Sequence Native CD Human dip

Delta3-9

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    protein search, using sw model

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                                                                                                                                        The invention relates to an alpha2-antiplasmin cleaving enzyme comprising a protein having a molecular weight of 180 kD in a dimeric form as determined by SDS-PAGE, where each subunit of the dimeric form has a molecular weight of 97 kD as determined by SDS-PAGE, and where the enzyme cleaves precursor alpha2-antiplasmin at the Pro12-Asn13 bond. The enzyme inhibitors of the enzyme and methods for detecting such inhibitors are useful for treating conditions involving fibrin, e.g. inflammatory conditions such as all forms of arthritis, organ fibrosis, undesirable scarring, cancer or its metastases; or atherothrombotic disease such as acconnary artery thrombosis, stroke, pulmonary embolism, all other forms of arterial and venous thromboses. This peptide is an internal sequence of the alpha2-antiplasmin cleaving enzyme corresponding to amino acids
                                                                     ywe, useful for treating conditions conditions such all forms of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000GB-00024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
 (JACK/) JACKSON K W.
(CHRI/) CHRISTIANSEN V J.
                                                                                                     atherothrombotic disease.
                                                                                                                                                                                                                                                                                                                                 10; Conservative
                                                                                                                                                                                                                                                                                                                                                     1 YALWWSPNGK 10
                                                                                                                                                                                                                                                                                                                                                                         YALWWSPNGK 10
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                               Lee KN,
                                                  WPI; 2004-625848/60
                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cervical cancer
                                                                                                                                                                                                                                                                                          Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200157278-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAY-2000;
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27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-AUG-2001
                               PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAM17490;
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                                Mckee
                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 2
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                                                                                                                                                                              (SENP: see AAI10068-AAI20459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notcably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genome-derived single exon nucleic acid probes useful for analyzing
Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.
                                                                                                                                                                 probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; foetal liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                              present invention relates to human single exon nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide #4017 encoded by human foetal liver single exon probe.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 65; DB 4; Length 51; 100.0%; Pred. No. 0.0078; ive 0; Mismatches 0; Indels
                                                                                                     Claim 27; SEQ ID NO 22316; 487pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen W, Rank DR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB36511 standard; peptide; 51 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0234687P.
2000US-0236359P.
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2000US-00608408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 51 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200157277-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-FEB-2000;
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human
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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human genome derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                        Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma.
                                                                                                                    Human bone marrow expressed probe encoded protein SEQ ID NO: 29984.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia; coronary heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 4; SEQ ID NO 29984; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 65; DB 4; L. 100.0%; Pred. No. 0.0078; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene expression in human bone marrow.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human liver peptide, SEQ ID No 30005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG51357 standard; peptide; 51 AA.
               AAM69678 standard; protein; 51 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                 03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
                                                                                                                                                                                                                                                                                                                                                            04-FEB-2000; 2000US-0180312P.
26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-0060840B.
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hes 10; Conservative (
                                                                                                                                                                                                                                                                                                                            2001WO-US000668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-OCT-2000; 2000GB-00024263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-488900/53
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                                                                                                                                                                                                                                                    WO200157276-A2.
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                                                                                                                                                                                                                  Homo sapiens.
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                                                                                      06-NOV-2001
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                                                    AAM69678;
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 AAM69678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to single exon nucleic acid probes (SENP: see AA131315-AA157546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders
part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                     Peptide #4047 encoded by probe for measuring placental gene expression.
                                                                                                                            Gaps
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                                                                                      Query Match
Best Local Similarity 100.0%; Pred. No. 0.0078;
Matches 10; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 27; SEQ ID NO 30279; 654pp; English.
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                                                                                                                                                                                                                                                                                            AAM30010 standard; protein; 51 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-0033366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0180312P.
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Best Local Similarity
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                                                        Sequence 51 AA;
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Length 51; Indele

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The invention relates to a single exon nucleic acid probe (SENP) (1) for measuring human gene expression in a sample derived from human adult liver. Comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (1) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis. Chyperlipoproctineemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. AB647348-AB655930 represent human liver single exon encoded peptides of the invention. Note: The sequence cirromation for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                 Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 65; DB 4; Length 51;
Pred. No. 0.0078;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          Claim 27; SEQ ID NO 30005; 658pp; English
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                                                                                                          2000US-0207456P.
2000US-00608408.
2000US-00632366.
                                                                                                                                             03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
24-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
                                                     30-JAN-2001; 2001WO-US000664
                                                                                                                                                                                                                                                                            Hanzel DK,
                                                                                                                                                                                                                                                                                                                 WPI; 2001-488898/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 51 AA;
                                                                                                            26-MAY-2000;
                                                                                           04-FEB-2000;
                 09-AUG-2001
                                                                                                                                                                                                                                                                              Penn SG,
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Spatially-addressable set of single exon nucleic acid probes, used to measure gene expression in human lung samples.

Chen W, Rank DR,

Hanzel DK,

SG, Penn WPI; 2002-114183/15.

(MOLE-) MOLECULAR DYNAMICS INC

26-MAY-2000; 2000US-0207456P. 30-JUN-2000; 2000US-00608408. 03-AUG-2000; 2000US-00632366. 21-SEP-2000; 2000US-0234687P. 27-SEP-2000; 2000US-023599P. 04-OCT-2000; 2000GB-00024263.

30-JAN-2001; 2001WO-US000665

15-NOV-2001

2000US-0180312P

04-FEB-2000;

The invention relates to a spatially-addressable set of single exon

Claim 27; SEQ ID NO 28959; 634pp; English.

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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of from human lung comprising single exon nucleic acid probes having one of from human lung comprising single exon nucleic acid sequences mentioned in the specification, or their complements or the 1237 open reading frames derived from the 12614 and compressed in the human lung; measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung comprising the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridiation of detectably clabeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included comprising (a) in the above mentioned microarray; assigning exons in several comprising (a) dentifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in the above with the exons, where a common pattern of expression of the exons in the tissues and/or cell types using hybridisation to a single exon comprising one of 12011 sequences, mentioned in the specification, or encoded by the corpsession of the exons in the tissues and/or cell types using hybridisation to a single comprising one of 12011 sequences, mentioned in the specification, or encoded by the corpsession of extremely frames (ORP). The probes are used for gene expression classes (ILD), familial idiopathic pulmonary fibrosis, pulmonary incodes each or pulmonary encodes each or pulmonary encodes each exonic pulminary encodes each exoni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                present sequence is a peptide/protein encoded by a single exon probe of
the invention. Note: The sequence data for this patent did not form part
of the printed specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary histiocytosis, lymphanapioleiomyomicosis, pulmonary alveolar proceinosis, Karagener syndrome, fibrocyseic pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension and hyaline membrane disease. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 65; DB 5; Length 51; 100.0%; Pred. No. 0.0078; etve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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chronic Obstructive pulmonary disease; interstital lung disease;
familial idiopathic pulmonary fibrosis; neurofibromatosis;
tuberous sclerosis; gaucher's disease; Niemann-Pick disease;
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ABG39294 standard; peptide; 51 AA.

RESULT 7 ABG39294 (first entry)

19-AUG-2002

ABG39294;

nyaline membrane disease

WO200186003-A2 Homo sapiens

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10; Conservative

Matches

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The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide equences in the specification, or their complements or fragments, and equences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acids sequences concoling at least 8 amino acids of any of the 6888 amino acids dequences of concoling at least 8 amino acids of any of the 6888 amino acids mander high stringency conditions to a nucleic acid molecule expression (comprising a plurality of single exon nucleic acid probes for measuring human gene expression, a method of probe cited above, where each of the plurality of probes is separately can addressably stolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a method of measuring human gene expression, a vector comprising the single exon probe cited above, an ORF-encoded peptide comprising at least 8 contiguous amino acids of any of the above-mentioned amino acid acuted antibody that binds specifically to a peptide cited above, methods of selling and/or licensing single exon probes or microarrays to measure gene expression, an achod of providing human gene expression date by subscription, and a computer-readable corrage methods of selling data by subscription, and a computer-readable corrage methods including data by subscription, and a computer-readable corrage methods including data by subscription, and a computer of the probes may be used as tools for surveying the expression analysis. The probes may be used as tools for surveying the probes of expression analysis. The probes may be used as tools for surveying the subscription in the probes are used in identifying and characterising grantler genomic alterations in the probes are used in identifying and characterising grantler genomic alterations. In the probes of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for surveying tissues.
                                                                                                                                                                                           Human, gene expression, single exon probe, microarray, alternative splicing event, genomic alteration.
                                                                                                                                              Human genome derived single exon protein #1892.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 45; SEQ ID NO 29292; 80pp; English.
                  ABO55658 standard; protein; 57 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Penn SG, Rank DR, Hanzel DK;
                                                                                                                                                                                                                                                                                                                                                                                                                                 03-APR-2002; 2002US-00029386.
                                                                                                                                                                                                                                                                                                                                                                                        03-APR-2002; 2002US-00029386
                                                                                                       (first entry)
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(RANK/) RANK D R.
(HANZ/) HANZEL D K.
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                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                       29-JUL-2004
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                                                               ABO55658;
AB05565
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The submitted of the su
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in need a fibroblast activation protein (FAP) alpha dimer enzyme in an
amount effective to down-regulate an immune response.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immune inhibition; fibroblast activation protein alpha dimer;
                                                                                                                    Length 57;
                                                                                                                                                                            0; Indels
seqdata.uspto.gov/sequence.html?DocID=20030194704
                                                                                                                    100.0%; Score 65; DB 8; 100.0%; Pred. No. 0.0088;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jesson MI;
                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human soluble FAP alpha dimer SEQ ID NO:70.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    AEB94227 standard; protein; 723 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jones B, Miller GT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-OCT-2005 (first entry)
                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                         1 YALWWSPNGK 10
                                                                                                                                                                                                                                                                          11 YALWWSPNGK 20
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                                                                Sequence 57 AA;
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of A657D; and a composition comprising a FAP alpha dimer enzyme lacking amino acids 269-448 from mouse FAP.

The method further comprises administering to the subject a second agent. The second agent is an anti-inflammatory agent, immunosuppressant, or anti-mycobacterial agent. The FAP alpha dimer enzyme is antibacterial, antiviral, antifungal, anti-parallel type FAP alpha dimer enzyme. The FAP alpha dimer enzyme is a truncation mutant. The FAP alpha dimer enzyme is a heteroidimer of a FAP alpha momer and a pPPIV/CD26 monomer. The FAP alpha dimer or symme is a heteroidimer of a FAP alpha monomer and a pPPIV/CD26 monomer. The FAP alpha dimer or acid substitution is present in the beta-propeller domain, the caralytic substitution is present in the beta-propeller domain, the caralytic condition, abnormal immune response selected from inflammation.

Condition, abnormal immune response selected from inflammation, continued disease, sepsis, graft versus host disease, transplant rejection, toxic shock syndrome, The approximate in mune entry allergy, asthma, atherosclerosis, contenting and allergy, asthma, atherosclerosis, contenting the parallel allergy, asthma, atherosclerosis, contenting and allergy and psy inferring the contenting and allergy asthma, atherosclerosis, contents and allergy and psy inferring the contents and allergy. autoimmune disease is selected from c, autoimmune thyroiditis, systemic lupus erythematosus (SLE), uveitis, hemolytic anemias, rheumatic fever, Crohn's disease, Guillain-Barre's syndrome, psoriasis, Graves' disease, myasthenia gravis, glomerulonephritis, autoimmune hepatitis and multiple sclerosis. The subject does not have cancer or a predisposition to cancer. The present sequence represents the amino acid sequence of human soluble fibroblast activation protein (FAP) alpha dimer (corresponding to AEB94159 minus N-terminal amino acids 1-37). response is subsequent to an infection, such as an RSV infection. The 8X99999999999999999999999999

Sequence 723 AA;

Gaps ö 100.0%; Score 65; DB 9; Length 723; 100.0%; Pred. No. 0.12; 0; Indels Mismatches ö Local Similarity 100. ses 10; Conservative Query Match Matches

1 YALWWSPNGK 10 ò

173 YALWWSPNGK 182 g

AEB94218 standard; protein; 734 AA. AEB94218; RESULT 10 AEB94218

Human soluble (FAP) alpha dimer SEQ ID NO:61. (first entry) 06-OCT-2005

immune inhibition, fibroblast activation protein alpha dimer;

PAP alpha dimer; guillain barre syndrome; antiinflammatory; cns-gen.;

fimmune disorder; neurological disease; autoimmune disease;

immunosuppressive; graft versus host disease; transplant rejection;

endotoxic shock; osteoarthritis; antiarthritic; osteopathic;

musculoskeletal disease; allergy; antiarlergic; asthma; antiasthmatic;

inflammation; respiratory disease; altergy; antiarlergic; antiarteriosclerotic;

cardiovascular disease; metabolic disorder; hashimotos disease;

antithyroid; endocrine disease; inflammatory bowel disease;

antinflammatory; gastrointestinal-gen.; gastrointestinal disease;

rheumatord arthritis; antirheumatic; multiple solerosis; neuroprotective;

autoimmune hepatitis; antinflammatory; hepatorropic; systemic lupus erythematosus; dermatological; dermatological disease; uveitis; ophthalmological; autoimmune hemolytic anemia; antianemic; hematological disease; rheumatic fever; antipyretic; Crohns disease; psoriasis; antiportic; graves disease; antithyroid; respiratory syncytial virus infection; respiratory-gen.; virucide. 

Homo sapiens

WO2005071073-A1

04-AUG-2005

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comportaing a FAP alpha dimer enzyme in a pharmaceutically acceptable carrier, where the composition is sterile and lacks an adjuvant; a carrier, where the composition is sterile and lacks an adjuvant; a composition comprising a FAP alpha dimer enzyme in a pharmaceutically acceptable carrier, and a non-adjuvant second agent; a composition comprising a FAP alpha dimer enzyme acking an enino acids 269-448 and comprising amino acids 269-448 from mouse FAP. The method further comprising amino acids 269-448 from mouse FAP. The method further comprising amino acids 269-448 from mouse FAP. The second agent is an anti-inflammatory agent, immunosuppressant, or anti-infective agent such as antibacterial, antifungal, anti-carrier agent such as antibacterial, antiviral, antifungal, anti-carrier agent such as antibacterial antiviral, antifungal, anti-carrier and anti-carrier and anti-carrier and an anti-carrier and an anti-carrier and an antibacterial agent. The FAP alpha dimer enzyme is a heterodimer of a PAP alpha monomer and a DPPIV/CD26 monomer. The FAP alpha dimer enzyme is a heterodimer of a PAP alpha monomer and a DPPIV/CD26 monomer. The FAP alpha dimer enzyme is a heterodimer of a DPPIV/CD26 monomer. The FAP alpha dimer enzyme comprises an amino acid substitution relative to wild type FAP alpha dimer. The mediated comman, or an N-linked glycosylation site and alters disulfide bond containing the munne response is an especially an IL-I mediated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a method of down-regulating an immune response, which comprises administering to a subject a fibroblast activation protein (FAP) alpha dimer enzyme in an amount effective to down-regulate an immune response. Also included are the following: a composition
                                                                                                                                                                                                                                                                                                                                                                                                                                          Down-regulating an immune response comprises administering to a subject in need a fibroblast activation protein (FAP) alpha dimer enzyme in an amount effective to down-regulate an immune response.
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lupus erythematosus (SLE), uveitis, hemolytic anemias, rheumatic fever,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                       Jesson MI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 134; SEQ ID NO 61; 177pp; English.
                                                                                                                                                                                                                                                                       Miller GT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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10-JAN-2005; 2005WO-US000709
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                                                                                                                                                                                                                                                                       Jones B,
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             %XGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCX8XLLLLXXXXXL
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RESULT 11

AEB94161 standard; protein; 750 AA 06-OCT-2005 (first entry) AEB94161; **AEB94161** 

Human soluble fibroblast activation protein (FAP) alpha dimer.

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Mclean PA, Jones B, Miller GT,
                                                           10-JAN-2005; 2005WO-US000709.
                                                                           WPI; 2005-564220/57.
                                                                             N-PSDB; AEB94160
                                             Misc-difference
                                                   WO2005071073-A1
                                        Homo sapiens
                                                       04-AUG-2005.
                                    enzyme.
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The plane dimer; guillain bare sortwarms, antiinflammatory; or, amount disease; autoimmune disease; meurological disease; autoimmune disease; meurological disease; autoimmune disease; mentological disease; transplant rejection; mentoroxic shock; osteoarthritis; antiarthritis; osteopathic; musculoskeletal disease; allergy; antiallergic; asthma; antiasthmatic; melammation; respiratory disease; atheroscierosis; antiasthmatic; antihyroid; endocrine disease; atheroscierosis; antiasthmatic; antihyroid; endocrine disease; allefammatory bowel disease; antithyroid; endocrine disease; antithammatory bowel disease; antithrematic; antihicumancory arthritis; antiinflammatory; multiple sclerosis; neuroprotective; when the hepatitis; antiinflammatory; dermatological; dermatological disease; utoimmune hepatitis; antiinflammatory; dermatological; dermatological disease; when the matological disease; antianemic; multiple sclerosis; antianemic; meatological disease; rheumatic fever; antipyretic; Crohns disease; psoriasis; antianemic; meatological antipocial disease; antithyroid; espiratory syncytial virus infection; respiratory-gen; virucide; inhibition; fibroblast activation protein alpha dimer;

'note= "Encoded by taa" Location/Qualifiers

09-JAN-2004; 2004US-0535577P.

(POIN-) POINT THERAPEUTICS INC

Jesson MI;

Down-regulating an immune response comprises administering to a subject in need a fibroblast activation protein (FAP) alpha dimer enzyme in an amount effective to down-regulate an immune response.

Claim 73; SEQ ID NO 4; 177pp; English

The invention relates to a method of down-regulating an immune response, which comprises administering to a subject a fibroblast activation protein (FAP) alpha dimer enzyme in a maneunt effective to down-regulate an immune response. Also included are the following: a composition comprising a FAP alpha dimer enzyme in a pharmaceutically acceptable carrier, where the composition is sterile and lacks an adjuvant; a composition comprising a FAP alpha dimer enzyme in a pharmaceutically acceptable carrier, and a non-adjuvant second agent; a composition comprising a FAP alpha dimer enzyme comprising an amino acid substitution of A657D; and a composition comprising a FAP alpha dimer enzyme lacking amino acids 269-448 and comprising amino acids 269-448 from mouse FAP.

The second agent is an anti-inflammatory agent, immunosuppressant, or anti-infective agent such as antibacterial, antivital, antifungal, anti-infective agent such as antibacterial, antivital, antifungal, anti-infective agent such as antibacterial, antivital, antifungal, anticarsing comparistion and anter enzyme. The FAP alpha dimer enzyme is a truncation mutant. The FAP alpha dimer enzyme is a fusion or chimeric protein. The FAP alpha dimer enzyme is a fusion or chimeric protein. The FAP alpha dimer enzyme is a fusion or chimeric protein. The FAP alpha dimer enzyme is a heterodimer of a FAP alpha monomer and a DPPIV/CDS monomer. The FAP alpha dimer enzyme comprises an amino acid substitution is present in the beta-propaller domain, the catalytic domain, or an N-linked glycosylation site and alters disulfide bond condition, abnormal immune response selected from inflammation, autodimmune disease, sepsie, graft versus host disease, transplant rejection, toxic shock syndrome, allergy, asthma, atherosclerosis,

(LUDW-) LUDWIG INST CANCER RES

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osteoarthritis, and Guillain-Barre's syndrome. The abnormal immune response is subsequent to an infection, such as an RSV infection. The autoimmune disease is selected from c, autoimmune thyroiditis, systemic lupus erythematosus (SLE), uveitis, hemolytic anemias, rheumatic fever, crohn's disease, Guillain-Barre's syndrome, psoriasis, Graves' disease, myasthenia gravis, glomerulonephritis, autoimmune hepatitis and multiple colloris. The subject does not have cancer or a predisposition to cancer. The present sequence represents the amino acid sequence of human soluble fibroblast activation protein (FAP) alpha dimer. Note: SEQ ID No:3 AEB94160 only encodes amino acids 84 to 750 the present sequence.
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in specification"
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/label= fap-2
/note= "Putative functional element; not defined further
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in specification"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Fibroblast activation protein alpha"
                                                                                                                                                                                  100.0%; Score 65; DB 9; Length 750; 100.0%; Pred. No. 0.12; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fibroblast activation protein-alpha; FAP-alpha; human;
type II integral membrane proteins; epithelial cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                           Human fibroblast activation protein-alpha (FAP-alpha).
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/note≕ "Asn is N-glycosylated"
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/note= "Asn is N-glycosylated"
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                                                                                                                                                                                                                                                                                                                                           AAW31963 standard; protein; 759 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .759
/label= FAP-alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in specification"
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                                                                                                                                                                                 Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                        199 YALWWSPNGK 208
                                                                                                                                                                                                                                             1 YALWWSPNGK 10
                                                                                                                                                            Sequence 750 AA;
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This sequence represents a dimeric fibroblast activation protein alpha rhe Pap-alpha) which is capable of degrading extracellular matrix proteins. The Fap-alpha molecule exhibits structural features typical of type II integral membrane proteins, including a large COOH-terminal extracellular domain, a hydrophobic transmembrane segment and a short cytoplasmic tail. Most common types of epithelial cancers including breast, lung, skin, pancreas and colorectal carcinomas contain abundant FaP-alpha reactive stronal fibroblasts which accompany tumour blood vessels. The induction of FAP-alpha fibroblasts at times and sites of tissue remodelling during fetal development, tissue repair and carcinogenesis is consistent with its putative role in normal fibroblast physiology. FAP alpha inhibitors, particularly a collagen derivative or (S)-valy1-pyrrolidine-2(R)-boronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acid, may be used to treat various epithelial cancers, e.g. breast, lung, skin, pancreas or colon cancer. Note: This sequence differs from the amino acid sequence of FAP-alpha found in AAW31963 between residues 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lillie J, Gannavarapu M, Glatt K, Hoersh S, Kamatkar S;
Mertens M, Monahan JE, Mýer V, Wang Y, Xu Y, Zhao X, Meyers RE;
Bast RC, Hortobagyi GN, Pusztai L, Meric F, Sahin A, Mills GB;
                                                                                                                                                                                       Dimeric fibroblast activation protein alpha - capable of degrading extracellular matrix protein, useful to treat epithelial cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 65; DB 2; Length 760; 100.0%; Pred. No. 0.12; ative 0; Mismatches 0; Indels
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                                                                   old LJ;
(LUDW-) LUDWIG INST CANCER RES. (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
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                                                                                                                                                                                                                                                                Claim 2; Page 25-28; 40pp; English
                                                                   Rettig W,
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27-UN-2001; 2001US-0301572P.
18-UU-2001; 2001US-0306501P.
25-SEP-2001; 2001US-0306501P.
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14-MAY-2002; 2002US-0380391P.
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hes 10; Conservative
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                                                                   Park JE,
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                                                                                                                   1997-480164/44.
                                                                                                                                            N-PSDB; AAT90148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 760 AA;
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                                                                      Zimmerman R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents the dimeric fibroblast activation protein alpha (FAP-alpha). The FAP-alpha molecule is capable of degrading extracellular matrix proteins and exhibits extructural features typical of type II integral membrane proteins, including a large COM+terminal extracellular domain, a hydrophobic transmembrane segment and a short cytoplasmic tail. The putative extracellular domain is described as containing five contential N-glycosylation sites, eleven conserved cysteine residues and three segments corresponding to highly conserved cysteine residues and three segments corresponding to highly conserved catalytic domains characteristic of serine proteases. Most common types of epithelial cancers including breast, lung, skin, pancreas and colorectal carcinomas contain abundant FAP-alpha reactive stromal fibroblasts which accompany tumour blood vessels. The induction of FAP-alpha fibroblasts at times and sites of tissue remodelling during foetal development, tissue repair and carcinogenesis is consistent with its putative role in normal fibroblast physiology FAP alpha inhibitors, particularly a collagen derivative or (S) vally pyrrolidine-2(R) boronic acid, may be used to treat various cepthelial cancers, e.g. breast, lung, skin, pancreas or colon cancer. Note: This sequence differs from the amino acid sequence of FAP-alpha
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                                                                                                                                                                   Dimeric fibroblast activation protein alpha - capable of degrading extracellular matrix protein, useful to treat epithelial cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        625. .670
/note= "alternative sequence found in AAW31963"
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    .760
    /label= FAP-alpha
    /note= "Fibroblast activation protein alpha"

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100.0%; Pred. No. 0.12;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     found in AAW27438 between residues 625 to 670
                                             old LJ;
(BOEH ) BOEHRINGER INGELHEIM INT GMBH.
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                                             Rettig W,
                                                                                                                                                                                                                                            Example 5; Fig 1; 40pp; English.
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Best Local Similarity 100.
Matches 10; Conservative
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                                               Park JE,
                                                                                               WPI; 1997-480164/44.
                                                                                                                      N-PSDB; AAT89286
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                                               Zimmerman R,
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expression

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The present invention describes a method for assessing whether a patient is afflicted with breast cancer. The method comprises comparing the level of expression of a marker (gene/polypeptide see ACCS0076 to ACCS0334 and ABR47386 to ABR47632) in a patient sample and the normal level of expression of the marker in a control non-breast cancer sample, where a patient sample and the normal level of patient sample and the normal level of expression of the marker in the patient sample and the normal level is an indication that the patient is afflicted with breast cancer. The breast cancer associated sequences from the present invention have cytostatic activities and can be used in gene therapy. The method is useful for diagnosing and treating breast cancer. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention relates to a method of differentially modulating the growth or differentiation of blood endothelial cells (BEC) or lymphatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              growth; differentiation; blood endothelial cell; BEC; lymphatic endothelial cell; LEC; hereditary lymphoedema; VEGFR-1; lymphatic growth agent; VEGF-C; VEGF-D; antianglogenic; cytostatic; vasotratic; antiinflammatory; gene therapy; endothelial cell disorder; inflammatory disease; cancer metastasis; lymphatic system; human.
                                                       Breast cancer diagnosis or treatment by comparing the level of expriof a marker in a patient sample with that in the control non-breast cancer sample.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 65; DB 6; Length 760; 100.0%; Pred. No. 0.12; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human BEC/LEC-related protein sequence SeqID475.
                                                                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                              Claim 1; SEQ ID NO 136; 128pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADN95552 standard; protein; 760 AA.
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Best Local Similarity 100.
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                 2003-210381/20
                                  N-PSDB; ACC50144.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 760 AA;
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composition comprising an agent that differentially modulates blood or lymphatic endothelial cells. Treating hereditary lymphates blood or lymphatic endothelial cells. Treating hereditary lymphoedema comprises identifying a human subject with lymphoedema and with a mutation in at least one allele of a gene encoding a LEC protein, where the mutation correlates with lymphoedema in human subjects, and with the proviso that composition comprising a lymphatic growth agent selected from VEGF-C or VEGF-D polypeptides and polymuclecides. The invention may be useful for the development of compounds with an antianglogenic, cytostatic, the development of compounds with an antianglogenic, cytostatic, wasotropic or antiinflammatory activity or for gene therapy. The method is useful in modulating the growth or differentiation of blood endothelial cells or lymphatic endothelial cells, in treating hereditary predisposition to the disporder or in monitoring the efficacy or toxicity of a drug on endothelial cells. The agent is useful in manufacturing a medicament for the differential modulation of blood vessel endothelial cell or lymphatic growth agent may also be used in manufacturing a medicament for the treatment of hereditary lymphoedema resulting from a mutation. The cllor of other diseases involving the lymphatic vessels, such as LEC gene or of other diseases involving the lymphatic vessels, such as LEC gene or of other diseases and cancer metastesis via the lymphatic synemial production which is related to the method of the invention. Our expressed protein which is related to the method of the invention. Our was expressed protein which is related to the method of the invention of a human LEC/BEC differentially which appears in the present sequence is that of a human LEC/BEC differentially and a present appear in the present and the process on the method of the invention. This sequence does not appear in the specification but was obtained by the indexer using the source data given in table 14 of the specification. 

Sequence 760 AA;

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Gaps

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Gape .. 0 100.0%; Score 65; DB 7; Length 760; 100.0%; Pred. No. 0.12; ive 0; Mismatches 0; Indels Query Match
Query Match
Best Local Similarity 10v.v.
Conservative

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210 YALWWSPNGK 219 1 YALWWSPNGK 10 셤 ઠે

ADQ21351 standard; protein; 760 AA. ADQ21351; RESULT 16 

26-AUG-2004 (first entry)

Human soft tissue sarcoma-upregulated protein - SEQ ID 4171.

soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.

WO2004048938-A2.

Homo sapiens.

10-JUN-2004

26-NOV-2003; 2003WO-US038193.

26-NOV-2002; 2002US-0429739P

(PROT-) PROTEIN DESIGN LABS INC.

Ginsburg WM,

Aziz N,

Zlotnik A;

WPI; 2004-441208/41.

Barly detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue

Example 2; SEQ ID NO 4171; 210pp; English

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The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual data and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples and comparing the expression in the first soft tissue sample indicates the presence of soft tissue sarcome amples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated protein of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Cytochrome c family heme-binding site signature"
470. 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumor-associated antigenic target; TAT430; cancer; neoplasm; cytostatic; ovary tumor; uterus tumor.
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Inote= "Tyrosine kinase phosphorylation site"
                                                                                                                                                                                                                                    Score 65; DB 8; Length 760; Pred. No. 0.12;
                                                                                                                                                                                                                                                                 0; Indels
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'note= "N-myristoylation site"
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note= "N-myristoylation site"
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te= "N-glycosylation site"
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note= "N-glycosylation site"
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                                                                                                                                                                                                                                                                   Mismatches
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/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  label= Mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                    ADW14775 standard; protein; 760 AA.
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                                                                                                                                                                                                                                       100.0%;
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nes 10; Conserv
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The present sequence is that of novel tumor-associated antigenic target polypeptide TAT430. TAT polypeptides have been identified ADM44770. ADM14776 whose expression is upregulated in particular tumor tissues. Tissue expression profiling using GeneExpress indicated that TAT430 is upregulated in breast, pancreatic, colon, adrenal, bladder, kidney, lymphoid, ovarian, prosters and stomach tumor stroma as compared to the corresponding healthy tissues. Upregulation in ovarian tumor tissue was confirmed by quantitative analysis of TAT mRNA expression, and upregulation in breast, pancreatic, colon, adrenal and bladder tumors was confirmed by gene expression profiling in silico (GEPIS) analysis. The TAT polypeptide may comprise the full-length polypeptide, or may lack the associated signal peptide, or may lack the associated signal peptide, or may be any of these fused to a heterologous polypeptide such as an epitope tag, or the Por region of an immunoglobulin. Tat polypeptide so the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Tumor-associated Antigenic Target polypeptides useful for diagnosing, preventing or treating cell proliferative disorders such as cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        encoding nucleic acids, provide targets for the
                                                                                                             'note= "Prolyl endopeptidase family serine active site"
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                                                   'note= "Prolyl oligopeptidase family homology'
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                                                                                                                                                                           note= "Glycosaminoglycan attachment site"
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                                                                                                                                               'note= "N-myristoylation site"
                                                                   566. .571
/note= "N-myristoylation site"
                                                                                                                                                                                                             "N-myristoylation site"
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                      "N-myristoylation site"
                                                                                                                                                                                                                                     /note= "N-glycosylation site"
738. .743
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Wu TD, Zhang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the invention, and their encodindiagnosis and therapy of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ashkenazi A, Cairns B, Dowd
Polakis P, Smith V, Wolf B,
                                                                                                                                                                                                                                                                                                                                                                     02-JUL-2004; 2004WO-US021353
                                                                                                                                                                                                                                                                                                                                                                                                  02-JUL-2003; 2003US-0484959P
/note= "N
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nes 10; Conservative
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N-PSDB; ADW14768.
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        Modified-Bite
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AEB94159
ID AEB94
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Disclosure; SEQ ID NO 2; 177pp; English. Mclean PA, Jones B, Miller GT, (POIN-) POINT THERAPEUTICS INC. 10-JAN-2005; 2005WO-US000709. 09-JAN-2004; 2004US-0535577P. (first entry) WPI; 2005-564220/57. N-PSDB; AEB94158 WO2005071073-A1. Homo sapiens. 06-OCT-2005 04-AUG-2005 AEB94159; 

immune inhibition; fibroblast activation protein alpha dimer;

PAP alpha dimer; guillain barre syndrome; antiinflammatory; cns-gen.;

FAP alpha dimer; guillain barre syndrome; antiinflammatory; cns-gen.;

immune disorder; neurological disease; autoimmune disease;

immunosuppressive; graft versus host disease; transplant rejection;

endotoxic shock; osteoarthritis; antiarthriti; osteopathic;

musculoskeletal disease; allergy; antiallergic; asthma; antiathmatic;

musculoskeletal disease; allergy; antiallergic; asthma; antiatehmatic;

antithyroid; endocrine disease; inflammatory bowel disease;

antiinflammatory gastrointestinal-gen.; gastrointestinal disease;

antiinflammatory sastrointestinal-gen.; gastrointestinal disease;

whenmatoid arthritis; antiinflammatory; hepatotropic;

systemic lupus erythematosus; dermatological; dermatological disease;

wutoimmune hepatitis; antiinflammatory; hepatotropic;

systemic lupus erythematosus; dermatological; dermatological disease;

whentis, ophitalmological; autoimmune hemolytic anemia;

hematological disease; rheumatic fever; antipyretic; Crohns disease;

periasis; antipsoriatic; graves disease; antithyroid;

respiratory syncytial virus infection; respiratory-gen.; virucide; Human wild type fibroblast activation protein (FAP) alpha dimer.

Jesson MI;

Down-regulating an immune response comprises administering to a subject in need a fibroblast activation protein (FAP) alpha dimer enzyme in an amount effective to down-regulate an immune response.

The invention relates to a method of down-regulating an immune response, which comprises administering to a subject a fibroblast activation protein in a place and activation and protein in a manount effective to down-regulate an immune response. Also included are the following: a composition comprising a FAP alpha dimer enzyme in a pharmaceutically acceptable comprising a FAP alpha dimer enzyme in a pharmaceutically acceptable carrier, and a non-adjuvant second agent; a composition comprising a FAP alpha dimer enzyme in a pharmaceutically acceptable carrier, and a non-adjuvant second agent; a composition comprising a FAP alpha dimer enzyme ladder absorbed as the most and a composition comprision a FAP alpha dimer enzyme as adjuvant; a manno acide 269-448 and comprises administering to the subject a second agent. The method further comprises administering to the subject as second agent. The faP alpha dimer enzyme is a truncation canti-infective agent such as antibacterial, antiviral, antifungal, anti-infective agent such as antibacterial, and a pharamator or an arti-mycobacterial agent. The FAP alpha dimer enzyme is a truncation and paper alpha dimer enzyme is a truncation and paper appla dimer enzyme is a ferencial agent. The FAP alpha dimer enzyme is a substitution relative to wild type FAP alpha dimer. The amuno acid substitution relative to wild type FAP alpha dimer. The amuno acid substitution, and noting all and an especially an il-infective formation. The immune response is an especially an inflammation, condition, abnormal immune response selected from inflammation,

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FAP alpha dimer; guillain barre syndrome; antiinflammatory; cns-gen.;

fimmune disorder; neurological disease; autoimmune disease;

immunosuppressive; praft versus host disease; transplant rejection;

endotoxic shock; osteoarthritis; antiarthritic; osteopathic;

endotoxic shock; osteoarthritis; antiarthritic; osteopathic;

inflammation; respiratory disease; antiarthritic; asthma; antiarteriosclerotic;

cardiovascular disease; metabolic disorder; hashimotos disease;

antithyroid; endocrine disease; inflammatory bowel disease;

antilnflammatory gastrointestinal-gen.; gastrointestinal disease;

rheumatord arthritis; antirheumatic; multiple sclerosis; neuroprotective;

antinflammatori antinflammatory; hepstotropic;

antinflammatori antinflammatory; hepstotropic;
autoimmune disease, sepsis, graft versus host disease, transplant rejection, toxic shock syndrome, allergy, asthma, atherosclerosis, osteoarthritis, and Guillain-Barre's syndrome. The abnormal immune response is subsequent to an infection, such as an RSV infection. The autoimmune disease is selected from c. autoimmune thyroiditis, systemic lupus exthematosus (SLE), uveitis, hemolytic anemias, rheumatic fever, Crohn's disease, Guillain-Barre's syndrome, psoriasis, Graves' disease, Crohn's disease, autoimmune hepatitis and multiple sclerosis. The subject does not have cancer or a predisposition to cancer. The present sequence represents the amino acid sequence of human wild type fibroblast activation protein (FAP) alpha dimer.
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in need a fibroblast activation protein (FAP) alpha dimer enzyme in an
amount effective to down-regulate an immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          systemic lupus erythematosus; dermatological; dermatological disease; uveitis; ophthalmological; autoimmune hemolytic anemia; antianemic; hematological disease; rheumatic fever; antipyretic; Crohns disease; psoriasis; antipsoriatic; graves disease; antithyroid;
                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         respiratory syncytial virus infection; respiratory-gen.; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse wild type fibroblast activation protein (FAP) alpha dimer.
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                                                                                                                                                                                                                                                                                                                               100.0%; Score 65; DB 9; Length 760; 100.0%; Pred. No. 0.12;
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                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POIN-) POINT THERAPEUTICS INC.
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Best Local Similarity 100...
Local 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2005-564220/57.
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                                                                                                                                                                                                                                                                                           Sequence 760 AA;
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The invention relates to a method of down-regulating an immune response, which comprises administering to a subject a fibroblast activation of protein (FAP) alpha dimer enzyme in an amount effective to down-regulate an immune response. Also included are the following: a composition comprising a FAP alpha dimer enzyme in a pharmaceutically acceptable carrier, where the composition is sterile and lacks an adjuvant; a composition comprising a FAP alpha dimer enzyme in a pharmaceutically acceptable carrier, and a non-adjuvant second agent; a composition comprising a FAP alpha dimer enzyme is a composition of A657D; and a composition comprising an unino acide 269-448 and comprising an inno acide 269-448 and comprising and no cide 269-448 from mouse FAP.

CC fromethod further comprises administering to the subject a second agent.

CC anti-infective agent is an anti-inflammatory agent, immunosuppressant, or anti-infective agent such as antibacterial, antiviral, antifungal, or anti-infective argume. The FAP alpha dimer enzyme is a truncation mutant. The FAP alpha dimer enzyme is a truncation causation or anni-infection or paragine or alpha dimer enzyme is a far an anti-infection, and an anti-infection and engaged and an especially an IL-I mediated condition, abnormal immune response is an especially an IL-I mediated condition, abnormal immune response is elected from inflammation, crant condition, abnormal immune response is an especially an IL-I mediated condition, abnormal immune response is an especially an IL-I mediated condition, abnormal immune response is subdiscer in the beta-propaler disease, transplant crejotion, costeoarthritis, and cuillain-Barre's syndrome. The abnormal immune disease, as an RSV streetion. The archimume disease, as all an anti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lupus erythematogus (SLB), uveitis, hemolytic anemias, rheumatic fever, crohn's disease, Guillain-Barre's syndrome, psoriasis, Graves' disease, myasthenia gravis, glomerulonephritis, autoimmune hepatitis and multiple sclerosis. The subject does not have cancer or a predisposition to cancer. The present sequence represents the amino acid sequence of mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  autoimmune disease is selected from c, autoimmune thyroiditis, systemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes; inflammation; autoimmune disorder; allergy; blood disorder; acquired immunodeficiency syndrome; AIDS; obesity; asthma; immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 60; DB 9; Length 761;
Pred. No. 0.74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer. The present sequence represents the amino acid secwild type fibroblast activation protein (FAP) alpha dimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polypeptide homologous to a human NOVX domain SeqID 863.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
 Disclosure; SEQ ID NO 6; 177pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alzheimer's disease; infection; str
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADI17327 standard; protein; 504 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      210 YALWWSPDGK 219
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 761 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unidentified.
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This invention relates to a novel nucleic acids, and encoded polypeptides thereof, which have properties related to the stimulation of biochemical
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Rastelli L, Miller CE;
Wolenc AR, Pena CEA;
1, Rieger DK, Burgess CE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New NOVX polypeptides and nucleic acids, useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis, or diabetes, and in chromosome mapping, tissue typing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zerhusen BD, Patturajan M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anderson DW, R. Y, Colman SD, JP, Lepley DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 863; 1498pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Li L. Gangolli EA, Padigaru M, And
Gerlach VL, Taupier RJ; Gusev VY,
Furtak K, Grosse WM, Alsobrook JP,
001US-0279884P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-706998/76.
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or physiological responses in a cell, tissue, organ or organism.

Specifically, it refers to the use of biologically active fragments for diagnostic assays and furthernore in the treatment of diverse pathological conditions. The present invention describes novel human and murine NOVX proteins, as well as methods to modulate their expression using antisense oligos, ribozymes and peptide nucleic acids.

The NOVX polypeptides, polymucleotides and antibodies are useful in treating or preventing NOVX-associated disorders, e.g. cardiomyopathy, creating or preventing diseases such as inflammation, autoimmune treating or preventing diseases such as inflammation, autoimmune disorders, allergies, blood disorders, acquired immunodeficiency syndrome treating or preventing diseases such as inflammation, autoimmune comparative, allergies, blood disorders, acquired immunodeficiency syndrome disorders, allergies, blood disorders, acquired immunodeficiency syndrome comparative, allergies, infections, stroke, muscular dystrophy and epilepsy. Accordingly, these molecules have many activities including cyclostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic, antisathmatic, nephrotropic, antiarteriosclerotic, anorectic, antisathmatic, nephrotropic, antibacterial, virucide, antiparasitic, crelaxant and anticonvulsant. In addition, they are useful in screening assays to identify small molecules that modulate or inhibit, for example, cused as in chromosome mapping, tissue typing, preventive medicine and pharmacogenesis, wound healing and anglogenesis. The nucleic acids are also used as in chromosome mapping, tissue typing, preventive medicine and pharmacogenesis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84.6%; Score 55; DB 5; Length 504;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cookson WOCM, Moffat MF, Allen M, Lench N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 2.9;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABP55609 standard; protein; 48 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human DPP4 amino acid sequence #3
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2001GB-00024575.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 504 AA;
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12-OCT-2001;
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The present invention describes a new isolated nucleic acid sequence (1) comprising a DPP10 mRNA sequence. DPP10 is a dipeptidyl peptidase (also known as prolyloligopeptidase). (1) has antinifammatory, antiasthmatic, antiasthmatic, antiasthmatic, antiathmatic and antirheumatic activities, and can be used in vaccines and gene therapy. A composition comprising (1) can be used for the manufacture of a medicament for regulating DPP10 expression or for preventing or treating inflammatory disease e.g., inflammatory bowel disease, asthma, atopy, rheumatoid arthritis or psoriasis. (1) can also be used in an assay for detecting or measuring DPP10 in a sample. A host cell comprising (1) can be used for producing recombinant DPP10 gene products, or in drug screening systems to identify agents for disgnosis or treatment of individuals having or susceptible to inflammatory disease. Human DPP10 is located on chromosome 2; more specifically chromosome 2414. Ag084254 to AB084612 and ABPS5559 to ABPS5629 represent chromosome and in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polypeptide fragments of CD26 - are capable of disrupting binding of CD45 and CD26 and thus interfering with T-cell activation.
for preventing or treating inflammatory disease e.g., inflammatory bowel
disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence of a CD26 fragment lacking a portion of the carboxy terminal
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                                                                                                                                                                                                                                                                                                                                                                                                                                           81.5%; Score 53; DB 6; Length 48; 100.0%; Pred. No. 0.56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR40916 standard; protein; 593 AA.
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                                                                   Disclosure, Fig 17; 321pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALWWSPNG 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 48 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAR-2003
05-FEB-1994
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Matches
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Pred. No.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               deficiencies. The peptides can be employed to increase immune function which has been impaired by use of immunosupressive drugs, such as certain chemotherapeutic drugs. (Updated on 25-MAR-2003 to correct PN field.)
the deletion of the segment of CD26 from AA 594 to the carboxy terminus of the wild-type protein. This deletion mutant, shown in AAR40916, lacks the putative catalytic site of CD26 and has a new carboxy terminus given in AAR40917. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polypeptide fragments and analogues of CD26 and encoding nucleic acid useful for stimulating immune response, e.g. for treatment of AIDS to counteract immunosuppressive drug, and as vaccine adjuvant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; T cell activation antigen; CD26; analogues; deletion; soluble; signal peptidase; immune-stimulating; response-stimulating; AIDS; immunosuppression; AIDS-related complex.
                                                                                                                                                       Gaps
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                                                                                                                   81.5%; Score 53; DB 2; Length 593; 100.0%; Pred. No. 7.1;
                                                                                                                                                     0; Indels
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                                                                                                                                100.0%; Pred ... o; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                             (revised)
(first entry)
                                                                                                                                                        Conservative
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                                                                                                                                                                                                                213 ALWWSPNG 220
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                                                                                                                                 Best Local Similarity
Matches 8, Conserv
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                                                                                    Sequence 593
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09-DEC-1994
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81.5%; Score 53; DB 2; Length 593,

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The specification describes a CD26 composition which, in conjunction with chemotherapeutic or radiotherapeutic agents, is used for the treatment and prevention of cancers. Expression of CD26 enhances the sensitivity of the cancer cell to the chemotherapeutic or radiotherapeutic agent. CD26 is a dipeptidyl peptidase IV (DPPIV). The chemotherapeutic agent is a useful for inhibitor. The CD26 composition of the invention is useful for inhibiting the growth of a cell, inducing cell cycle arrest in a cell, killing a cancer cell, potentiating the effect of a chemotherapeutic agent and/or a radiotherapeutic agent on a tumour cell, inducing or enhancing apoptosis of a cancer cell, treating cancer, or inducing tumour regression or tumour necrosis. The CD26 composition is further useful for increasing topolsomerase II expression in a cell, for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Use of a CD26 composition, and a chemotherapeutic and/or a radiotherapeutic agent for e.g. inhibiting the cell growth, inducing cell cycle arrest, killing a cancer cell, treating cancer, or inducing tumor regression or tumor necrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activating an antigen-presenting call, or for potentiating immune responses of an animal. The present sequence represents a CD26 protein, and is encoded by vectors which are used to produce compositions of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                    Gарв
                                                                                                                                                                                                                                                                                                  CD26; chemotherapeutic; radiotherapeutic; cancer; cell growth; dipeptidyl peptidase IV; DPPIV; topoisomerase II inhibitor; cell cycle arrest; tumour; tumour necrosis; immune response; human.
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                    Indels
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100.0%; Pred. No. 8.3;
:ive 0; Mismatches (
                                                                                                                                                                                                                                                                     of a human CD26 protein
                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 23; Page 170-171; 182pp; English.
                                                                                                                                                                       ADO71642 standard; protein; 688 AA.
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100.0%; Pro-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-MAY-2003; 2003WO-US015499.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-MAY-2002; 2002US-0381606P.
                                                                                                                                                                                                                                     26-AUG-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TEXA ) UNIV TEXAS SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      213 ALWWSPNG 220
                                                                                  213 ALWWSPNG 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Morimoto C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-420511/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 ALWWSPNG 9
                                                     6
                                                                                                                                                                                                                                                                     Amino acid sequence
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                      2 ALWWSPNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; ADO71641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 688 AA;
                                                                                                                                                                                                                                                                                                                                                                                                     WO2004045497-A2
                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                        03-JUN-2004.
                                                                                                                                                                                                    AD071642;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                       RESULT 24
ADO71642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New crystal of an extracellular domain of mammalian dipeptidyl-peptidase IV (DPP-IV) useful for identifying or designing inhibitors of DPP-IV
                                                                                                                                                                                                                                                                                          dipoptidyl-peptidase IV extracellular domain;
DPP-IV extracallular domain; three-dimensional structure; antidiabetic;
anorectic; cytostatic; type I diabetes; type II diabetes; IGT; obesity;
cancer; human; DPP-IV; enzyme; protein co-ordinate data; EC 3.4.14.5.
                                                                                                                                                                                                                                                               crystal; mammalian dipeptidyl-peptidase IV extracellular domain;
                                                                                                                                                                                                                  Human DPP-IV extracellular domain protein SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 31; SEQ ID NO 2; 215pp; English
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                                                                          ADO40240 standard; protein; 736 AA.
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                                                                                                                                                                        (first entry)
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N-PSDB; ADO40239.
                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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                                                                                                                                                                      12-AUG-2004
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                                                                                                                         ADO40240;
                                                 ADO40240
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The sequences given in AAR54612-14 represents analogues of the human T cell activation antigen CD26 which have internal deletions. The analogues pref. lack residues 3-9 or 24-34. These analogues are soluble under physiological conditions and lack enough amino acid residues to render them susceptible to cleavage by signal peptidase. The peptide fragments and analogues are useful as immune or response- stimulating therapeutics, eg. they may be used for treatment of disease conditions characterised by immunosuppression, eg. AIDS or AIDS-related complex, other virally or environmentally induced conditions, and certain congenital immune deficiencies. The peptides can be employed to increase immune function which has been impaired by use of immunosupressive drugs, such as certain chemotherapeutic drugs. (Updated on 25-MAR-2003 to correct PN field.)
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with an allosteric binding site of DPP-IV. The compound is an inhibitor of DPP-IV activity. (I) is useful for the identification and/or design of inhibitors of DPP-IV activity. (II) is useful as a therapeutic active substance, in particular for the treatment of diabetes type I, diabetes type II, iGT, obesity and cancer. (II) is useful for the manufacture of medicament for the treatment of above mentioned disease. The present sequence represents the extracellular domain of human DPP-IV, which is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, T cell activation antigen, CD26; analogues, deletion, soluble, signal peptidase, immune-stimulating, response-stimulating, AIDS; immunosuppression, AIDS-related complex.
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                                                                                                                                                                                                                                                                                                                                                                                         81.5%; Score 53; DB 8; Length 736;
100.0%; Pred. No. 8.9;
ive 0; Mismatches 0; Indels

    23. .24
    note= "Position of delta24-34 deletion"

                                                                                                                                                                                                                                                                used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR54613 standard; protein; 739 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93WO-US007923.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100..
Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 ALWWSPNG 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 ALWWSPNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Delta24-34 CD26.
                                                                                                                                                                                                                                                                                                                                          Sequence 736 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9409132-A1.
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AAR40909 Btandard; protein; 766 AA.
206 ALWWSPNG 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Region
                                                                                   RESULT 28
AAR40909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequences given in AARS4612-14 represents analogues of the human T cell activation antigen CD26 which have internal deletions. The analogues pref. lack residues 3-9 or 24-34. These analogues are soluble under physiological conditions and lack enough amino acid residues to render them susceptible to cleavage by signal peptidase. The peptide fragments and analogues are useful as immune or response- stimulating therapeutics, eg. they may be used for treatment of disease conditions characterised by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunosuppression, eg. AIDS or AIDS-related complex, other virally or environmentally-induced conditions, and certain congenital immune environmentally-induced conditions, and certain congenital immune which has been impaired by use of immunosupressive drugs, such as certain chemotherapeutic drugs. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polypeptide fragments and analogues of CD26 and encoding nucleic acid useful for stimulating immune response, e.g. for treatment of AIDS to counteract immunosuppressive drug, and as vaccine adjuvant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; T cell activation antigen; CD26; analogues; deletion; soluble; signal peptidase; immune-stimulating; response-stimulating; AIDS; immunosuppression; AIDS-related complex.
                                                                                                                Gaps
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                                                            Score 53; DB 2; Length 739;
Pred. No. 8.9;
                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2. .3
/note= "Position of delta3-9 deletion"
                                                                                      100.0%; Pred. No. 8.9
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tanaka T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Page 49-52; 85pp; English
                                                                                                                                                                                                                                                                                                                                            AAR54612 standard; protein; 759 AA
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                                                              81.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (revised)
                                                                                                                                                                                                              202 ALWWSPNG 209
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                                                                                                                                                               2 ALWWSPNG 9
                                                            Query Match
Best Local Similarity
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               Sequence 739 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Delta3-9 CD26
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09-DEC-1994
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                                                                                                                                                                                                                                                                                                                                                                                              AAR54612;
                                                                                                                                                                                                                                                                                          RESULT 27
AAR54612
                                                                                                                   Matches
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peptide fragments of CD26 - are capable of disrupting binding of CD45 CD26 and thus interfering with T-cell activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= C-terminal region of extracellular domain
/note= "1 N-linked glycosylation site & 1 catalytic site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    reactivity with the Mab Tal. C26 cDNA library was constructed from human PhA-activated Teals using the CDNA library was constructed from human the predicted CD26 polypeptide has the characteristics of a signal sequence of the type II membrane protein, which is reinforced by the observation that potential N-glycosylation sites are located in the carboxy side of the hydrophobic core. Therefore the N-terminal 6 AAs are predicted to be cytoplasmic, the next 22 AAs are predicted to transverse the cytoplasmic, the next 22 AAs are predicted to transverse the cytoplasmic membrane, and the 738 C-terminal AAs constitute the constitute the
                                                                                                                                                                                                                                                                                                                                                                                                                                    29. .323
/label= N-terminal glycosylated region of extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                predicted extracellular domain. (Updated on 25-MAR-2003 to correct PN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of extracellular domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= active site of serine protease/esterase /note= "fits the consensus sequence GXSXG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                           Human T cell activation antigen; monoclonal antibody Tal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "1 N-linked glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note= "8 sites for N-linked glycans"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 324. .551
/label= Cysteine rich region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure, Page 39-43; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (DAND ) DANA FARBER CANCER INST INC.
                                                                                                    Sequence encoded by human CD26 cDNA.
                                                                                                                                                                                                                                                                                                                                                                     . .28
|Tabel= hydrophobic
                                                                                                                                                                                                                                                                                                                    cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92US-00832211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92WO-US002892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Morimoto C, Schlossman SF,
                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  domain
(revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1993-272827/34.
N-PSDB; AAQ46089.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                             Ното варіепв.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-FEB-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polypeptide
25-MAR-2003
05-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Active-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Gaps

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Indels

DB 2; 9.1;

Query Match
81.5%; Score 53; DB
Best Local Similarity 100.0%; Pred. No. 9.1
Matches 8; Conservative 0; Mismatches

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AAR5461

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Treating a patient for mucosal inflammation associated with rhinitis, sinusitis or both, by intranasally administering a peptidase that cleaves at Xaa-Pro sequences, to the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thus invention relates to the treating of a patient for mucosal inflammation associated with rhinitis or sinualtis, comprising intransally administering a peptidase. The peptidase is considered antiasthmatic, antiallergic and antiinflammatory in its action. The peptidase cleaves at Xaa-Pro sequences and is useful for treating a patient for mucosal inflammation associated with rhinitis or sinusitis, which is the result of allergies or asthma. This sequence represents human dipeptidyl peptidase IV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Prostate cancer; prostate tumour tissue; human; mammal; cytostatic.
                                                                                                  Human, dipeptidyl peptidase IV; antiasthmatic; antiallergic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 5;
9.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81.5%; Score 53; DB 100.0%; Pred. No. 9.2 iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prostate cancer-associated protein #111.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Col 9-14; 13pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG61910 standard; protein; 766 AA.
                                                                                                                                                                                                                                                                                                                                                                                        Monod M;
                                                                     Human dipeptidyl peptidase IV.
                                                                                                                                                                                                                                                                            28-FEB-2001; 2001US-00794236.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-OCT-2001; 2001WO-US032045
                                                                                                                                                                                                                                                                                                                28-FEB-2001; 2001US-00794236
                                19-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry
                                                                                                                                                                                                                                                                                                                                                                                        Grouzmann E, Lacroix J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            213 ALWWSPNG 220
                                                                                                                                                                                                                                                                                                                                                   CORP BV
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Best Local Similarity
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                                                                                                                           antiinflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 766 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40200230268-A2
                                                                                                                                                                                                    US6337069-B1.
                                                                                                                                                                                                                                                                                                                                                     (BMRA-) BMRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-AUG-2002
                                                                                                                                                                  Ношо варіепв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-APR-2002
                                                                                                                                                                                                                                         08-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia.
ABB08991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABG61910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            요
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents the human T cell activation antigen CD26. The invention is concerned with polypeptide fragments and analogues of CD26 which have internal deletions (see also AAR54612-14). The analogues preflack residues 3-9 or 24-34. These analogues are soluble under physiological conditions and lack enough amino acid residues to render them susceptible to cleavage by signal peptidase. The peptide fragments and analogues are useful a immune or response- stimulating therapeutics, eg. they may be used for treatment of disease conditions characterised by immunosuppression, eg. AIDS or AIDS-related complex, other virally or environmentally-induced conditions, and certain congenital immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          deficiencies. The peptides can be employed to increase immune function which has been impaired by use of immunosupressive drugs, such as certain chemotherapeutic drugs. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polypeptide fragments and analogues of CD26 and encoding nucleic acid useful for stimulating immune response, e.g. for treatment of AIDS to counteract immunosuppressive drug, and as vaccine adjuvant.
                                                                                                                                                                                                                                                                                                               Human; T cell activation antigen; CD26; analogues; deletion; soluble; signal peptidase; immune-stimulating; response-stimulating; AIDS; immunosuppression; AIDS-related complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 46-49; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tanaka T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (DAND ) DANA FARBER CANCER INST INC.
                                                                                                                                                  AAR54611 standard; protein; 766 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92US-00934162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93WO-US007923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schlossman S,
                                                                                                                                                                                                                            (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALWWSPNG 220
                                                       213 ALWWSPNG 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 ALWWSPNG 9
                     2 ALWWSPNG 9
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 766 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9409132-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-AUG-1992;
                                                                                                                                                                                                                                                                                                                                                                                                sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Morimoto C,
                                                                                                                                                                                                                          25-MAR-2003
09-DEC-1994
                                                                                                                                                                                                                                                                                  Native CD26.
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Homo

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Gape

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13-OCT-2000; 2000US-00687576 08-DEC-2000; 2000US-00733288

ABB08991 standard; protein; 766 AA.

RESULT 30 ABB08991 ID ABB08 XX

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Length 766; 0; Indels 11-APR-2001; 2001WO-US040483 18-APR-2000; 2000US-0197508P (MILL-) MILLENNIUM PHARM INC

Williamson M;

Meyers RA,

WPI; 2002-034353/04.

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The present invention relates to methods of detecting a prostate cancerassociated transcript in a cell from a patient. The method comprises contearing a blological sample from the patient with prostate cancerassociated polynuclectides (designated PC genes) that selectively hybridise to a sequence that is at least 80% identical to them. The prostate cancerassociated polynuclectide sequences are differentially propersed in prostate tumour tissue or in prostate cancer and are derived from the tissues of various organisms such as humans or other mammals (e.g. mice, sheep and dogs). The methods of the invention are useful for diagnosing and treating prostate cancer in mammals. The prostate cancerase associated genes are useful for diagnosing or treating prostate cancer in associated genes are useful for diagnosing or treating prostate cancer.

The nucleic acid sequences are particularly useful in gene therapy, as a vaccine or in antisense applications.

ABG61800-ABG61944 represent prostate cancer-associated proteins
                                                                                                                                                                                                                                                                                                                                       Detecting a prostate cancer-associated transcript in a cell in a patient, useful for diagnosing prostate cancer (PC) or screening modulators of PC, by determining if prostate cancer-associated genes are expressed in a
                                                                                                                                                                                                                                     Hevezi P;
                                                                                                                                                                                                                                       Afar D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 27; Page 393; 436pp; English
                                                                                                                                                                                                                                     Gish KC, Mack DH, Wilson KE,
                 24-JAN-2001; 2001US-0263957P.

16-MAR-2001; 2001US-0276791P.

16-MAR-2001; 2001US-0276888P.

06-APR-2001; 2001US-0286214P.

30-APR-2001; 2001US-00847046.

04-MAY-2001; 2001US-0288589P.
                                                                                                                                                                                             (EOSB-) EOS BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                               2002-471335/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 766 AA;
                                                                                                                                                                                                                                                                                                 N-PSDB; ABK92227
                                                                                                                                                                                                                                                                                                                                                                                                               prostate tissue.
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This invention islance countries antiatehritic, neuroprotective, antithyroid, dermatological, antiatehritic, antiasthmatic, antiasthmatic, antiphyroid, dermatological, antiphyroid, antiasthmatic, antiasthmatic, antianthroid, cophthalmological, antiphyroid, antiandian, antianthroid, cardiant, antianthrosolerotic, anorectic and metabolic in its action. Uses include antiatherosolerotic, anorectic and metabolic in its action. Uses include therapy, expression or activity of 21953 protein modulator, it is gene therapy, expression or activity of 21953 protein modulator, it is preventing, treating or detecting a cellular proliferative or differentiative disorder. The 21953 molecules can act as novel diagnostic targets and therapeutic agents for controlling disorders associated with the cell differentiation and proliferation such as cancer, immune function, reproductive, neurological and cardiovascular function. The 21953 molecules are thus useful for treating and preventing cellular proliferative and differentiative disorders, haematopoietic neoplastic disorders, arthritis, multiple selezosis, asthma, grave's disease, mellitus, arthritis, multiple selezosis, asthma, grave's disease,

mellitus, arthritis, multiple sclerosis, asthma, Grave's disease, neuronal disorders, demyelinating diseases, vascular disorders and metabolism or pain disorders. This sequence represents the amino acid sequence of human dipeptidyl peptidase IV

Sequence 766 AA;

This invention relates to an isolated 21953 human prolyl oligopeptidase.

Disclosure; Fig 3; 121pp; English

New polypeptides 21953, member of human prolyl oligopeptidase family, useful as diagnostic targets and therapeutic agents for controlling cancer, lymphoma and leukemia.

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Human, angiodemic condition, angiotensin converting enzyme, ACE,
vasopeptidase inhibitor, dipeptidyl peptidase IV, aminopeptidase P;
DPP IV, aminopeptidase P; APP, hypertension, diabetes; cardiac disease;
     81.5%; Score 53; DB 5; Length 766; 100.0%; Pred. No. 9.2; 1.ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                      Human dipeptidyl peptidase IV (DPP IV).
                                                                                                                                                                                                                 AAO15555 standard; protein; 766 AA.
                                                                                                                                                                                                                                                                                     24-OCT-2002 (first entry)
Ouery Match
Best Local Similarity luv.
Restractive 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              renal disease; enzyme
                                                                                                                          213 ALWWSPNG 220
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                                                                                        2 ALWWSPNG
                                                                                                                                                                                                                                                    AA015555;
                                                                                                                                                                                RESULT 33
                                                                                                                                                                                                  AA015555
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                                                                                                                                                                                                                                                                                                                                                        21953 prolyl oligopeptidase; antibody; proline; endopeptidase; cancer; cardiovascular disease; autoimmune disease; atopic allergy; neuronal disorder; vaccular disorder; prostate disorder; cytostatic; antidathetic; antiathritic; antiathmatic; antinfiammatory; diabetes mellitus; arthritis; multiple sclerosis; asthma; grave's disease; neuronal disorder; demyelinating disease; dipeptidase.
                                                       Gaps
                    81.5%; Score 53; DB 5; Length 766;
                                                       0; Indels
                                                                                                                                                                                                                                                                                                                       Human dipeptidyl peptidase IV amino acid sequence.
                                      9.2;
                                      100.0%; Pred. No. 9.2 ive 0; Mismatches
                                                                                                                                                                                                                    AAG78417 standard; protein; 766 AA
                                                                                                                                                                                                                                                                                          (first entry)
                                                          8; Conservative
                                                                                                                              213 ALWWSPNG 220
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2 ALWWSPNG 9

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Matches

12-APR-2002

THE SECTION OF THE SE

AAG78417;

RESULT 32 AAG78417 31-OCT-2001; 2001WO-US045643

WO200259343-A2 Homo sapiens

01-AUG-2002.

WO200179473-A2 Homo sapiens,

25-OCT-2001

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Gaps

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                                                                                                                                                                                                                                                                  The invention comprises a method of identifying a subject that is susceptible to developing angiodemic conditions during a course of treatment. The method of the invention involves administering an angiotensin converting enzyme (ACE) inhibitor or a vasopetidase inhibitor and determining dipeptidial peptidase IV (DPP IV) enzyme activity or aminopeptidase P (APP) enzyme activity. The method of the invention is useful for identifying/diagnosing susceptibility to developing angiodemic conditions during a course of treatment involving the administration of an ACE inhibitor or a vasopeptidase inhibitor. The method is particularly useful during the treatment of a subject that is in med of or taking an ACE inhibitor and/or a vasopeptidase inhibitor, which are commonly used in the treatment of hypertension, diabetes, cardiac disease and renal diseases. The present amino acid sequence corresponds the human dipeptidyl peptidase IV (DPP IV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                         enzyme
                                                                                                                                                     Diagnosing susceptibility to developing an angiotensin converting enzyme
(ACE) inhibitor- or a vasopeptidase inhibitor-associated angioedema, by
measuring levels of dipeptidyl peptidase IV or aminopeptidase P enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DPP10; dipeptidyl peptidase; prolyloligopeptidase; enzyme; asthma; antiinflammatory; antiasthmatic; antipsoriatic; antiatthitic; antirheumatic; vaccine; gene therapy; inflammatory disease; inflammatory bowel disease; atopy; rheumatoid arthritis; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81.5%; Score 53; DB 5; Length 766; 100.0%; Pred. No. 9.2; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                           Disclosure; Page 62-64; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABP55629 standard; protein; 766 AA
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24-APR-2001; 2001GB-00010046.
12-OCT-2001; 2001GB-00024575.
12-OCT-2001; 2001GB-00024594.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-APR-2002; 2002WO-GB001887
31-OCT-2000; 2000US-0244524P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human dpp4 protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100 nes 8; Conservative
                                   (UYVA-) UNIV VANDERBILT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          213 ALWWSPNG 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 ALWWSPNG 9
                                                                                                       WPI; 2002-627422/67
                                                                                                                         N-PSDB; AAL44351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 766 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          сһготовоте 2q14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200286113-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-0CT-2002
                                                                                                                                                                                                           activities.
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                                                                     Brown NJ;
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The present invention describes a new isolated nucleic acid sequence (I) comprising a DPP10 mRNA sequence. DPP10 is a dipeptidyl peptidase (also known as prolylolidyopeptidase). (I) has antiinflammacory, antiaethmatic, antiaethmatic, antiaethmatic, antiaethmatic, antiaethmatic, antiaethmatic, antiaethmatic, antipeoriatic, and artirheumatic activities, and can be used in vaccines and gene therapy. A composition comprising (I) can be used in vaccines and gene therapy. A composition comprising (I) can be used disease, asthma, atopy, rheumatory disease e.g., inflammatory cor for preventing or treating inflammatory disease e.g., inflammatory cor for pused in an assay for detecting or measuring DPP10 expression cor products, or in drug screening systems to identify agents for diagnosis or treatment of individuals having or susceptible to inflammatory disease. Human DPP10 is located on chromosome 2, more specifically chromosome 2414. ABQ84254 to ABQ84612 and ABP55569 to ABP55629 represent correction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tissue-specific endothelial membrane protein; antibacterial; virucide; fungicide; antiparasitic; anticonvulsant; neuroleptic; cytostatic; antiparkinsonian; nootropic; neuroprotective; antiathmatic; infection; antidiabetic; hypotensive; nephrotropic; antiarthritic; antinflammatory; gene therapy; epilepsy; schizophrenia; cancer; Parkinson's disease; Alzheimer's disease; asthma; diabetes; hypertension; arthritis; polycystic kidney disease; tissue-specific luminally expressed protein;
                                                                         New nucleic acid sequence comprising DPP10 mRNA, useful for the manufacture of a medicament for regulating DPP10 protein expression or for preventing or treating inflammatory disease e.g., inflammatory bowel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human liver dipeptidyl peptidase IV (DPP4) protein SEQ ID NO:7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81.5%; Score 53; DB 6; Length 766; 100.0%; Pred. No. 9.2; ive 0; Mismatches 0; Indels
Lench N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TARG-) TARGET PROTEIN TECHNOLOGIES INC.
Cookson WOCM, Moffat MF, Allen M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABP56700 standard; protein; 766 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inflammatory bowel disease; enzyme
                                                                                                                                                                             Example 2; Fig 23; 321pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-JUN-2001; 2001US-0297021P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JUN-2002; 2002WO-US018185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-MAR-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.،
نامر 8، Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Roben PW, Stevens AC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             213 ALWWSPNG 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-167367/16
                                      WPI; 2003-093132/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 ALWWSPNG 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 766 AA;
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                                                                                                                                          disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 35
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The present invention describes a method (M1) for delivering an therapeutic agent to a specific tissue, comprising administering an encount of a therapeutic complex comprising a ligand which binds to a mount of a therapeutic complex comprising a ligand which binds to a c tissue-specific luminally expressed protein, a therapeutic group, and a complex membrane proteins from the present invention can have antibacterial, or virucide, fungicide, antiparasitic, anticonvulsant, neuroleptic, cycostatic, antiparkinsonian, noctropic, neuroprotective, antisathmatic, antidiabetic, hypotensive, nephrotropic, antiarthritic and antidiamatory activities, and can be used in gene therapy. (M1) is cuseful in targeting pharmaceuticals or other therapeutics to specific tissues using tissue-specific endothelial membrane proteins. A therapeutic complex may be used to treatment would be efficacious, such at in cases of infections (e.g. bacterial, viral, fungal and parasitic), chicases, asthma, diabetes hypertension, polycystic kidney disease, arthritis, and inflammatory bowel disease. The present sequence
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                       Delivering a therapeutic agent (e.g. immunosuppressant) to a specific tissue, comprises administering an amount of a therapeutic complex comprising a therapeutic group, a ligand that binds to a tissue-specific protein, and a linker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein tyrosinė kinase pathway; protein tyrosine kinase; cyto
gene therapy; drug sensitivity; genetic profile; cancer; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            predictor set; protein tyrosine kinase activity modulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81.5%; Score 53; DB 6; Length 766;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human src biomarker polypeptide SEQ ID NO:234.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Pred. No. 9.2; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lee FY, Shaw P;
                                                                                                                       Example 2; Page 106-107; 123pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADD14045 standard; protein; 766 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-JAN-2002; 2002US-0350061P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            213 ALWWSPNG 220
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-636735/60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 ALWWSPNG 9
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N-PSDB; ABZ22557.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 766 AA;
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The present invention describes a predictor set comprising a plurality of polymucleotides or polypeptides whose expression pattern is predictive of the response of cells to treatment with a compound that modulates protein tyrosine kinase activity or members of the protein tyrosine kinase activity of cells, comprising obtaining a sample of cells, pathway. Also described: (1) predicting whether a compound is capable of modulating the activity of cells, comprising obtaining a sample of cells, cerelating the expression of the markers to the compound's ability to modulate the activity of the cells; (2) a plurality of markers, and correlating the expression of the markers to the compound's ability to modulate the activity of the cells; (2) a plurality of cell lines for correlate with compound sensitivity or resistance of cells associated with a disease state, and (3) identifying polymucleotides and colypeptides that predict compounds, analysing the expression pattern of a microarray of polymucleotides tate, comprising subjecting the plurality of cell lines to one or more compounds, analysing the expression pattern of a microarray of polymucleotides or polypeptides that predict the sensitivity or censistance of cells associated with a disease state by using the expression pattern of the microarray. The polymucleotides and polypeptides are useful in predicting the activity of compounds that interact with protein tyrosine kinase pathways. These may be used in determining drug cancer) based on patient response at a molecular level. The present concern based on patient response at a molecular level. The present concerns and in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
that interact with protein tyrosine kinases and/or protein
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100.0%; Pred. No. 9.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                         Claim 10; SEQ ID NO 234; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human dipeptidyl peptidase IV (DPPIV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADD27855 standard; protein; 766 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81.5.,
100.0%; Pr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2001; 2001US-00794236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          is-JAN-2004 (first entry)
                       tyrosine kinase pathways.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               213 ALWWSPNG 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 766 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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22-MAY-2003
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                                                                                                                                                                                                                                                                                                                                             Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 39
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                                                                                                            method comprises intranasally administering to the patient a peptidase that cleaves at Xaa-Pro sequences or an agent that inhibits the binding of substance P (SP) to the neurokinin 1 (NK1) receptor. The peptidase is an exopeptidase, preferably selected from human dipeptidyl peptidase is peptidase 9, or human attractin. The method is useful for treating a patient for mucosal inflammation associated with rhintis and/or pinusitis which are the result of allergies or asthma. The invention provides an effective treatment of the inflammation associated with both rhintis and sinusitis. The present sequence represents human DPPIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                  Treatment of patient for mucosal inflammation associated with rhinitis and/or sinusitis involves intranasally administering peptidase that cleaves at Xaa-Pro sequences or agent inhibiting binding of Sp to
                                                                                                                                                                                                                                                                             Gaps
                                                                                             The present invention relates to a method of treating a patient for mucosal inflammation associated with rhinitis and/or sinusitis. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; pain; neuronal tissue; gene therapy;
spinal segmental nerve injury; chronic constriction injury; CCI;
spared nerve injury; SNI; Chung.
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                                                                                                                                                                                                                                                        81.5%; Score 53; DB 7; Length 766; 100.0%; Pred. No. 9.2;
                                                                                                                                                                                                                                                                              0; Indels
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                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human Protein AAA52308, SEQ ID NO 12620.
                                                                         Disclosure; SEQ ID NO 1; 14pp; English
                                                                                                                                                                                                                                                                                                                                                                             ADD46934 standard; protein; 766 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page; 1017pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-033347P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GEHO ) GEN HOSPITAL CORP. (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                              8; Conservative
                                                      neurokinin 1 receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                     (revised)
                                                                                                                                                                                                                                                                                                                        213 ALWWSPNG 220
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GENBANK; AAA52308.
WPI; 2003-811386/76.
                                                                                                                                                                                                                                                                                                    2 ALWWSPNG 9
                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                     Sequence 766 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2003016475-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Unidentified
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29-JAN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                  ADD46934;
                                                                                                                                                                                                                                                           Query Match
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the invention interiors a compression of the nucleic acid sequence. Also claimed are a vector comprising the nucleic acid sequence. Also comprising the nucleic acid sequence. Also comprising the nucleic acid sequence. Also comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that increases or decreases the expression of the polynucleotide sequence that increases or decreases the expression of a first animal of subjected to pain, a method for identifying an agent compound that regulates the activity of one or more of the expression an animal subjected to pain, a method for identifying a compound which regulates the activity of one or more of the compound that regulates the activity of one or more of the polypeptides or method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more of polypeptides or their antibodies. The polynucleotide or the compound that to reading the activity is useful for preparing a medicament for treating can animal segmental nerve injury (SNI) in an animal (e.g. gene therapy). The sequence presented is a human procein (described in Table 3 therapy). The sequence data for this parent did not form part of the printed or specification) which is differentially expressed during pain.

Note: The sequence data for this parent did not form part of the printed specification) which is differentially expressed during pain.
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The invention discloses a composition comprising two or more isolated rat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-NOV-2001; 2001US-0332464P.
29-NOV-2001; 2001US-0335394P.
03-DEC-2001; 2001US-035594P.
14-DEC-2001; 2001US-0340376P.
08-JAN-2002; 2002US-0347311P.
10-JAN-2002; 2002US-0347349P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-JUN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100.
nes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              213 ALWWSPNG 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           σ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 766 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2003042661-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-NOV-2001;
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2002US-0347211P. 2002US-0347349P. 2002US-0355250P.

2001US-0340376P

2002US-0356714P. 2002US-0359077P. 2002US-0368809P.

2002US-0372246P

2002US-0370110P

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13-NOV-2002; 2002WO-US036810
                        WO2003042661-A2.
Homo sapiens.
                                                                                                                                                                                    -JAN-2002;
-FEB-2002;
                                                                                                                                                                       08-JAN-2002;
                                                                                                                                                                                                                                                    04-APR-2002;
                                                  22-MAY-2003
                                                                                                                                                                                                                                       29-MAR-2002
                                                                                                                                                                                                                                                                  -APR-2002
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ADJ83981
ID ADJ83
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                                                                                                                                                                                                                                                                                                                                          The invention relates to nucleic acids and proteins (ADN38683-ADN40064)

whose expression is upregulated or downregulated in specific cancers or
cher diseases such as angiogenic or fibrotic disorders, and to methods
of determining the presence or absence of a pathological cell in a
c patient by detecting a nucleic acid at least 80% identical to those of
the invention or by detecting a polypeptide of the invention. The
conclination also relates to expression vectors and host cells comprising a
c nucleic acid of the invention; antibodies which specifically bind a
c polypeptide of the invention; use of such antibodies for drug targeting;
conclination of screening for modulators of activity or expression of the
polypeptides and nucleic acids. The nucleic acids, polypeptides,
c antibodies and methods are useful for diagnosing, prognosing and treating
cancer and other conditions such as psoriasis, ischaemia, heart disease,
atherosaclerosis, infilammatory diseases, autonimune diseases, retinal
c neovascularistation syndromes, scarring and uterine fibroids. They may
also be useful in wound healing and in contraception. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                              Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis; inflammatory disease; autoimmune disease; retinal neovascularistation syndrome; scarring; uterine fibroid; detection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; vulnerary; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:A204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                     Hevezi PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; differential expression; cancer; angiogenic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81.5%; Score 53; DB 7; Length 766; 100.0%; Pred. No. 9.2; ive 0; Mismatches 0; Indels
                                                                                                                                                                                    Gish KC, Glynne R, He Wilson KE, Zlotník A;
                                                                                                                                                                                                                                                                                                                      Claim 12; SEQ ID NO 590; 1385pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADN39604 standard; protein; 766 AA.
                                                                                                                                                                                                 Murray R, Watson SR,
                                                                                                                                                                                     Ginsburg WM,
                                                                                                                                                            (EOSB-) EOS BIOTECHNOLOGY INC.
                                       2002US-0368809P.
                                                                              05-JUN-2002; 2002US-0386614P.
                                                                                            16-JUL-2002; 2002US-0396839P.
                                                                                                       2002US-0397775P.
2002US-0397845P.
             2002US-0356714P
                          2002US-0359077P
                                                    2002US-0370110P
                                                                  2002US-0372246P
                                                                                                                                 09-SEP-2002; 2002US-0409450P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 81.5
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            213 ALWWSPNG 220
                                                                                                                                                                                                                          WPI; 2003-468649/44.
N-PSDB; ADN39271.
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                                                                                                                                                                                     Azız N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 766 AA;
                                                    04-APR-2002;
12-APR-2002;
                                                                                                                                                                                     Afar D, 1
Mack DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADN39604;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 40
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The invention relates to nucleic acids and proteins (ADN38683-ADN40064)

whose expression is upregulated or downregulated in specific cancers or
other diseases such as angiogenic or fibrotic disorders, and to methods
of determining the presence or absence of a pathological cell in a
patient by detecting a nucleic acid at least 80% identical to those of
the invention or by detecting a polypeptide of the invention. The
invention also relates to expression vectors and host cells comprising
nucleic acid of the invention; use of such antibodies for drug targeting;
polypeptide of the invention; use of such antibodies for drug targeting;
onlypeptides and nucleic acids. The nucleic acids, polypeptides,
antibodies and methods are useful for diagnosing, prognosing and treating
antibodies and methods are useful for diagnosing, isonosing and treating
antibodies and methods are useful for diagnosing, isonosing and treating
antibodies accountions such as posiasis, ischaemia, heart disease,
atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
antibodies and methods are useful for diagnosing, isonosing and part disease,
anterosclerosis, inflammatory diseases, autoimmune diseases, retinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           also be useful in wound healing and in contraception. The present sequence represents a polypeptide of the invention.
                                                                                                                                                                                                                      Glynne R, Hevezi PA;
E, Zlotnik A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81.5%; Score 53; DB 7; Length 766;
100.0%; Pred. No. 9.2;
ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                          Gish KC, Gl
Wilson KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 12; SEQ ID NO A204; 1385pp; English.
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                                                                                                                                                                                                                              Ginsburg WM,
R, Watson SR,
                                                                                                                                                     (EOSB-) EOS BIOTECHNOLOGY INC
                                    2002US-0397845P
2002US-039777SP
                                                                            09-SEP-2002; 2002US-0409450P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                                                                                                                                              Aziz N, Gir
Murray R,
                                                                                                                                                                                                                                                                                                                                                WPI; 2003-468649/44.
N-PSDB; ADN39603.
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                                                                                                                                                                                                                              Afar D, 1
Mack DH,
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bronchial asthma; chronic obstructive pulmonary disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel crystal of a dipeptidyl peptidase IV (DPPIV) which is sufficient to ensure a resolution capable of analysing its three-dimensional structure up to the side chain level by X-ray crystallographic structural unalysis. The crystal of the invention demonstrates immunomodulatory, antidiabetic, antinflammatory, antidiabetic, antinflammatory, antidiabetic, antinflammatory, structural cordinates and may be useful for providing a three-dimensional structural coordinate as the information for designing, identifying, structural coordinate as the information for designing, identifying, the effector may be useful as a modulatory agent of immune response and as a therapeutic or prophylactic agent for diabetes, inflammation, multiple sclerosis, grave's disease, chronic rheumatoid arthritis, AIDS or cancer. The current sequence is that of the human full-length colon dipeptidyl peptidase IV (DPPIV) protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dimensional structure, useful for designing, identifying, evaluating or searching an effector of the dipeptidyl peptidase IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New crystal of dipeptidyl peptidase IV capable of analyzing its three-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                               crystal; proteni co-ordinate data; dipeptidyl peptidase IV; DPPIV; immunomodulatory; antidiabetic; antinflammatory; neuroprotective; antithyroid; antithermatic; anti-HIV; cytostatic; immune response; diabetes; inflammation; multiple sclerosis; Grave's disease; chronic rheumatoid arthritis; AIDS; cancer; human;
                                                                                     Human full-length colon dipeptidyl peptidase IV (DPPIV) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Sugiyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; SEQ ID NO 2; 332pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Shima H,
                                                                                                                                                                                                                                                                                                                                          28-JUL-2003; 2003WO-JP009523
                                                                                                                                                                                                                                                                                                                                                                           29-JUL-2002; 2002US-0398761P
                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                          (TANA ) TANABE SEIYAKU CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Hiramatsu H, Kyono K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     213 ALWWSPNG 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-156830/15.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ADJ83980.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 766 AA;
                                                                                                                                                                                                                                                                         WO2004011640-A1
                                                                                                                                                                                                           colon; enzyme
                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-MAY-2004
                                                    36-MAY-2004
                                                                                                                                                                                                                                                                                                          05-FEB-2004.
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                    ADJ83981;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADJ75313
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Marker gene related amino acid sequence SEQ ID NO:565.

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The present invention describes a method of testing for bronchial asthma or chronic obstructive pulmonary disease. The method comprises or chronic obstructive pulmonary disease. The method comprises or chronic obstructive pulmonary disease. The marker gene in a biological sample from a subject, comparing the expression level determined with the expression level of the marker gene in a biological sample from a healthy campact, and judging whether the subject has bronchial asthma or chronic obstructive pulmonary disease. The marker gene comprises: (a) a group of genes (S1) whose expression levels increase when respiratory epithelial colls are calls are stimulated with interleukin-13; or (b) a group of genes (S2) whose expression levels decrease when respiratory epithelial cells are stimulated with interleukin-13; or (b) a group of genes (S2) whose expression levels decrease when respiratory epithelial cells are stimulated with interleukin-13; or (b) a group of genes (S2) whose expression levels action of obstructive pulmonary disease; (c) a kit for screening for a chronic obstructive pulmonary disease; (d) an inducer that induces bronchial asthma or chronic obstructive pulmonary disease; (d) an inducer that induces bronchial asthma or chronic obstructive pulmonary disease; (e) a marker gene or an antisense mucleic acid corresponding to a portion of the marker gene, a riboxyme, a polymucleotide that suppresses the expression of the gene through an RNAi effect or an antibody recognising to a protein encoded by a marker gene; and (7) a DNA chip for testing for bronchial asthma or a chronic obstructive pulmonary disease, on which a group contial antibod is an ensemble of the gene through an RNAi effect or an antibody and antiasthmatic activities, and can be used in gene therapy. The method can be used in gene therapy. The method can be used in gene therapy and particity and antiasthmatic activities, and can be used in gene therapy. The respection of the gene through and the particity and antiasthmatic activities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Resting for bronchial asthma or chronic obstructive pulmonary disease by
epithelial cell; interleukin-13; respiratory; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aring the expression level of a marker gene in a biological sample a subject with the expression level of the gene in a sample from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bronchial asthma or chronic obstructive pulmonary disease. The present sequence is used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nagai H,
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100.0%; Pred. No. 9.2;
:ive 0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 11; SEQ ID NO 565; 241pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kubo H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADO19398 standard; protein; 766 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                      06-AUG-2002; 2002JP-00229312.
20-MAR-2003; 2003JP-00077212.
                                                                                                                                                                                                                                                                                                                                               04-AUG-2003; 2003EP-00254857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENO-) GENOX RES INC
                                              gene therapy; marker.
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Best Local Similarity
Local 8; Conserve
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                                                                                                                                                                                               EP1394274-A2
                                                                                                                         Homo sapiens
       respiratory
                                                                                                                                                                                                                                                                         03-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ohtani N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             comparing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           213
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ID ADO1
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ADO19398;

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Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for treating an immune related disorder such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
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                                                                              autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis; diabetes mellitus; renal disease; demyelinating disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to human PRO polypeptides and the polynucleotides encoding them. The polypeptides and polynucleotides are useful for treating and diagnosing immune related disorders in mammals. The immune related disorders include systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, systemic arthritis, solutions, and arthritis, autoimmune haemolytic and arthritis, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            central or peripheral nervous system, demyelinating polyneuropathy, Guillain-Barre syndrome and chronic inflammatory demyelinating polyneuropathy. This sequence represents a human PRO polypeptide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schoenfeld J, Williams PM;
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                  related disorder; systemic lupus erythematosus;
                                  juvenile chronic arthritis;
                                       rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis
systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;
                                                                                                                        central nervous system; peripheral nervous system; demyelinating polyneuropathy; Guillain-Barre syndrome; chronic inflammatory demyelinating polyneuropathy.
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Pred. No. 9.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADO19806 standard; protein; 766 AA.
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Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  spondyloarthropathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dennis K,
Wu TD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 766 AA;
                                                                                                                                                                                                                                                                 WO2004043361-A2
                                                                                                                                                                                                                         Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for treating an immune related disorder such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
                                                                                                                                                    rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis; systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis; autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to human PRO polypeptides and the polynucleotides encoding them. The polypeptides and polynucleotides are useful for treating and diagnosing immune related disorders in mammals. The immune related disorders include systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, systemic arthritis, systemic haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central or peripheral nervous system, demyelinating diseases of the Guillain-Barre syndrome and chronic inflammatory demyelinating polyneuropathy, polyneuropathy. This sequence represents a human PRO polypeptide of the
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                                                                                                                               Human; PRO; immune related disorder; systemic lupus erythematosus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schoenfeld J, Williams PM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-NOV-2003; 2003WO-US035268
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                                         (first entry) .
                                                                                     Human PRO polypeptide #164
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Wu TD;
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Best Local Similarity
Matches 8; Conserv
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Human PRO polypeptide #165.

ADO19400;

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8; Length 766; 0; Indels

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N-PSDB; ADO71611, ADO71613
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nes 8; Conservative
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                                                                                                               Morimoto C;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to human PRO polypeptides and the polynucleotides encoding them. The polypeptides and polynucleotides are useful for treating and diagnosing immune related disorders in mammals. The immune related disorders include systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, systemic arthritis, syndrome, vasculitis, sarcoidosis, autoimmune haemolykic ansemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central or peripheral nervous system, demyelinating diseases of the Guillain-Barre syndrome and chronic inflammatory demyelinating polyneuropathy, polyneuropathy. This sequence represents a human PRO polypeptide of the
                                                                                                                                                                                                                                                                                                                                                                                PRO69614, PRO71106, or PRO86388 useful for
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               central nervous system; peripheral nervous system; demyelinating polyneuropathy; Guillain-Barre syndrome; chronic inflammatory demyelinating polyneuropathy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 7; SEQ ID NO 730; 1731pp; English.
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   diabetes mellitus; renal disease;
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Best Local Similarity
Matches 8; Conserv
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                                                                                     Homo sapiens,
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The specification describes a CD26 composition which, in conjunction with chemotherapeutic or radiotherapeutic agents, is used for the treatment and prevention of cancers. Expression of CD26 enhances the sensitivity of the cancer cell to the chemotherapeutic or radiotherapeutic agent. CD26 is a dipeptidyl peptidase IV (DPPIV). The chemotherapeutic agent is a copoisomerase II inhibitor. The CD26 composition of the invention is useful for inhibiting the growth of a cell, inducing cell cycle arrest in a cell, killing a cancer cell, potentiating the effect of a cell, chemotherapeutic agent and/or a radiotherapeutic agent on a tumour cell, inducing or enhancing apoptosis of a cancer cell, treating cancer, or inducing tumour regression or tumour necrosis. The CD26 composition is curther useful for increasing topoisomerase II expression in a cell, for activating an antigen-presenting cell, or for potentiating immune responses of an antigen-presenting cell, or for potentiating immune responses of an antimal. The present sequence represents a CD26 protein, and is encoded by vectors which are used to produce compositions of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of a CD26 composition, and a chemotherapeutic and/or a radiotherapeutic agent for e.g. inhibiting the cell growth, inducing cell cycle arrest, killing a cancer cell, treating cancer, or inducing tumor regression or tumor necrosis.
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100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 23; Page 151-153; 182pp; English.
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15-MAY-2003; 2003WO-US015499.
                                                                                            17-MAY-2002; 2002US-0381606P.
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modulator.
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                                                                                                                                                                                                                                                                   The specification describes a CD26 composition which, in conjunction with chemotherapeutic or radiotherapeutic agents, is used for the treatment that prevention of cancers. Expression of CD26 enhances the sensitivity of the cancer cell to the chemotherapeutic or radiotherapeutic agent. CD26 is a dipeptidyl peptidase IV (DPPIV). The chemotherapeutic agent is a useful for inhibiting the GD26 composition of the invention is a cell, killing a cancer cell, potentiating the effect of a chemotherapeutic agent and/or a radiotherapeutic agent on a tumour cell, inducing or enhancing apoptosis of a cancer cell, treating cancer, or inducing or enhancing apoptosis of a cancer cell, treating cancer, or inducing tumour regression or tumour necrosis. The CD26 composition is further useful for increasing topologemerase II expression in a cell, for
                                                                                                          Use of a CD26 composition, and a chemotherapeutic and/or a radiotherapeutic agent for e.g. inhibiting the cell growth, inducing cell cycle arrest, killing a cancer cell, treating cancer, or inducing tumor regression or tumor necrosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    activating an antigen-presenting cell, or for potentiating immune responses of an animal. The present sequence represents a CD26 protein, and is encoded by vectors which are used to produce compositions of the
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100.0%; Pred. No. 9.2
:ive 0; Mismatches
                                                                                                                                                                                                                                Claim 23; Page 175-176; 182pp; English.
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  Dang NH, Morimoto C;
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                                                 2004-420511/39.
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                                                                      N-PSDB; AD071643
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Matches
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The invention relates to a method of identifying a mammal that will respond therapeutically to a method of treating cancer by administering an epidermal growth factor receptor (EGFR) modulator by comparing the cancer by comparing the level of a biomarker in a mammal before and after exposure to an EGFR modulator. The method comprises: (a) measuring, in the mammal, the level of at least one biomarker identified in the specification; (b) exposing the mammal to the EGFR modulator; and (c) measuring in the mammal the level of the biomarker, where a difference in the level in step (c) therapeutically to the method of treating cancer. The method and compared to step (a) indicates that the mammal will respond therapeutically to a method of treating cancer. The method and therapeutically to a method of treating cancer by administering an epidermal growth factor receptor (EGFR) modulator. This sequence corresponds to one of the biomarkers whose levels of expression is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumour-associated antigenic target (TAT) polypeptide PRO80881, SEQ:895
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 766;
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100.0%; Pred. No. 9.2;
ive 0; Mismatches
Disclosure; SEQ ID NO 137; 520pp; English.
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Best Local Similarity 100..
... 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 766 AA;
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The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide perves as least 80% identical to the TAT nucleic acids and polypeptide polypeptides; expression vectors and host cells comprising a TAT nucleic acid; an antibody specific for a TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptide; fusion proteins comprising a TAT polypeptide; and methods and compositions for the treatment or atibodies, antagonists, binding molecules and compositions are useful for diagnosin or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, cervical cancer, liver cancer, bacterial cancer, cervical cancer, cancers of the central cancer, melanoma and leukaemia. TAT nucleic acids may further be used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence represents a TAT polypeptide.
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Sequence 766 AA;

Gaps ö 81.5%; Score 53; DB 8; Length 766; 100.0%; Pred. No. 9.2; ive 0; Mismatches 0; Indels Query Match Best Local Similarity 100. Matches 8; Conservative 2 ALWWSPNG 9 δ

213 ALWWSPNG 220 g

Human PRO protein sequence SEQ ID NO:434. ADP54458 standard; protein; 766 AA. 18-NOV-2004 (first entry) ADP54458; RESULT 50 ADP54458 

immune response stimulation; antiallergic; antianemic; antiarthritic; antiasthmatic; antidiabetic; antinflammatory; antipsoriatic; antihritic; antirhrematic; antidiabetic; antinflammatory; antipsoriatic; harithyroid; CNS; dermatological; gastrointestinal; haemostatic; hepatotropic; immunostimulant; immunosuppressive; muscular; nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic; human; PRO; immune related disease; inflammatory immune response; virucide, gene therapy

Ното варіелв.

WO2004039956-A2.

13-MAY-2004.

28-OCT-2003; 2003WO-US034381

29-OCT-2002; 2002US-0422472P.

(GETH ) GENENTECH INC

Gurney AL, Schoenfeld J, Williams PM; Aggarwal S, Clark H, Wood WI, Wu TD; Wood WI,

WPI; 2004-376182/35. N-PSDB; ADP54457. New PRO polynucleotides and polypeptides, useful in useful in diagnosing and treating an immune related disease, e.g. systemic lupus erythematosus, rheumatoid arthritis, diabetes mellitus or asthma and in stimulating an immune response.

Hermann K, Kinnemann H; Rosenthal A, Pilarsky C;

T, Heiden E,

ich D, Bruemmendorf T Roepcke S, Staub E,

Mennerich D,

Li X,

WPI; 2004-786403/78. N-PSDB; ADU06201.

(HINZ/) HINZMANN B. (HERM/) HERMANN K. (CAST/) HEIDEN CASTANOS-VELEZ B.

09-APR-2003; 2003DE-01016701. 09-APR-2003; 2003DE-01016701.

DE10316701-A1.

04-NOV-2004.

c described; (1) a vector comprising (1); (2) a host cell comprising the vector of (1); (3) a process for producing a PRO polypeptides; (4) an isolated PRO polypeptide; (5) a chimeric molecule comprising the isolated PRO polypeptide; (5) a chimeric molecule comprising the polypeptide of (4) fused to a heterologous amino acid sequence; (6) an antibody which specifically binds to a polypeptide of (4); (7) a chimeric molecule of (4); (7) a chimeric molecule of (4); (7) a netbody which specifically binds to a polypeptide of (4); (7) a netbod of matter comprising a container, a label on the container and a composition of comprising a container, a label on the container and a composition of matter of (7); (9) a method of treating an immune related disease in a companing an immune related disease or an inflammatory immune response to a mammal; (10) a method of disease or an inflammatory immune response or an inflammatory immune response. The present sequence represents a human or stimulating an immune response. The present sequence represents a human or stimulating an immune response. The present represents and method or resp ö Gaps The present invention describes an isolated PRO nucleic acid (I). ; 0 DB 8; Length 766; 9.2; Novel bronchial cancer-associated human protein SegID914. Indels cancer; cytostatic; tumour-associated protein; tection; metastasis; tumour; human. ö 81.5%; Score 53; DB 100.0%; Pred. No. 9.2 cive 0; Mismatches Claim 1; SEQ ID NO 434; 3009pp; English ADU06688 standard; protein; 766 AA. Conservative 213 ALWWSPNG 220 σ Local Similarity 2 ALWWSPNG cancer detection; Sequence 766 AA; Homo sapiens. 27-JAN-2005 bronchial ADU06688; Query Match Best Loc Matches RESULT 51  $\overset{\circ}{\mathbf{A}}\overset{\bullet}{\mathbf{A}}\overset{\circ}$ à

Summer H; 12-MAY-2004; 2004WO-EP005071. 21-MAY-2003; 2003EP-00011481. (FARB ) BAYER HEALTHCARE AG. (first entry) Query Match Best Local Similarity 100.. L.a 8; Conservative Golz S, Brueggemeier U, 213 ALWWSPNG 220 WPI; 2004-834301/82. N-PSDB; ADV25524. 2 ALWWSPNG 9 Sequence 766 AA; WO2004104216-A2. Homo sapiens 24-FEB-2005 02-DEC-2004 ADV25525; RESULT 52 ADV25525 g ð

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bronchial cancer comprising 489 defined sequences given in the bronchial cancer comprising 489 defined sequences given in the bronchial cancer comprising 489 defined sequences given in the compounds with a cytostatic activity through the inhibition of expression or activity of tumour-associated proteins. The novel DNA sequences and cor activity of tumour-associated by them are used for detecting bronchial cancer or determining the risk of developing it and to screen for specific binding partners of the DNA or protein sequences, where the binding partners are potentially useful as agents for treating or diagnosing bronchial cancer. The DNA or protein sequences can also be used for prognosis, detection of metastases and for secondary treatment of tumours that have been stabilised or are no longer detectable). Detecting abnormal expression of the DNA sequences provides early diagnosis of bronchial cancers. The present sequence is that of a protein encoded by a novel bronchial cancer-associated human gene sequence of the
New nucleic acid, and derived proteins, useful for diagnosis of bronchial cancer and in screening for therapeutic and diagnostic agents.
                                                                                                                                                                                                Claim 2; SEQ ID NO 914; 1381pp; German.
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ö Gaps ö 81.5%; Score 53; DB 8; Length 766; 0; Indels Pred. No. 9.2; 100.0%; Pred. ...

ADV25525 standard; protein; 766 AA Human dipeptidyl-peptidase IV.

respiratory disease; gastrointestinal disease; liver disease; metabolic disorder; Cardiovascular-Gen.; Endocrine-Gen.; Antiinflammatory; Gastrointestinal-Gen.; Gynecological; Hepatotropic; Neuroprotective; Cytostatic; Antiparkinsonian; Nootropic; Cardiant; Antiarrhythmic; Antiatresriosclerotic; Antianemic; Antidabetic; Dermatological; Immunosuppressive; Muscular-Gen.; Antirheumatic; Antiarthritic; Antipsoriatic; Antinfertility; Gene Therapy. dermatological disease; cancer; neoplasm; hematological disease; Dipeptidyl-peptidase IV; DPP4; cardiovascular disease;

Antiinflammatory, Immune disorder, Dermatological, Immunosuppressive,

Antirheumatic; Antlarthritic; Osteopathic; Hemostatic; Antlanemic; Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic; Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic;

Antiallergic; ds; gene; diagnosis

Use of dipeptidylpeptidase IV (DPP4) polypeptides or polynucleotides for screening therapeutic agents or for diagnosing or treating diseases

New nucleic acid encoding PRO polypeptide, useful for diagnosing and treating an immune related disorder, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.

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Wood WI,

Ouyang W, Williams MP,

Clark H,

Abbas A,

(GETH ) GENENTECH INC.

WPI; 2005-182330/19.

11-AUG-2004; 2004WO-US026249 11;AUG-2003; 2003US-0493546P

WO2005016962-A2 Homo sapiens.

24-FEB-2005.

The present sequence is the protein sequence of human dipeptidylpeptidse IV (DPP4). The invention relates to novel disease associations of DPP4 polypeptides and polymucleotides and to novel methods of screening for therapeutic agents for the treatment of cardiovascular disorders, cancer, hematological disorders and metabolic diseases. Pharmaceutical compositions are provided for treatment of these diseases and disorders and comprise a DPP4 polypeptide, an DPP4 polymucleotide, or regulators of DPP4 or modulators of DPP4 molecule, an antibody or a riboxyme. The invention also provides methods of disagnosing diseases and disorders associated with DPP4 by amount of a DPP4 polymucleotide in a sample amount of a DPP4 polymucleotide in a sample amount in a sample from a healthy and/or diseased mammal. The diseases and disorders include Parkinson's disease, and disorders include Parkinson's disease, and disorders include Parkinson's disease, and an antibody or a riboxyme of disease, and disorders include Parkinson's disease, and disorders include Parkinson's disease, and disorders include Parkinson's disease, and an antibody or a riboxyme or a parkinson's disease, and disorders include Parkinson's disease, and disorders include Parkinson's disease, and disorders and disease. ö myocardial infarction, arrhythmias, atherosclerosis, anemia, eosinophilic disorders, leukemia, panoreatitis, Crohn's disease, inflammatory bowel disease, diabetes, Cushing's syndrome, systemic lupus erythematosus, myaerhenia gravis, rheumatoid arthritis, psoriasis, scleroderma, or e.g. cardiovascular, metabolic, inflammatory, or Gaps ö Length .766; 0; Indels Score 53; DB 8; Pred. No. 9.2; 81.5%; Scor. 100.0%; Pred. No. Disclosure; SEQ ID NO 2; 128pp; English. ADY15161 standard; protein; 766 PRO polypeptide SEQ ID NO 967. (first entry) Conservative neurological disorders. associated with DPP4, 213 ALWWSPNG 220 σ Local Similarity 2 ALWWSPNG Sequence 766 AA; 05-MAY-2005 infertility ADY15161; Query Match Matches RESULT 53 ADY15161 ð

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(first entry)

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diabetes, antidiabetic, endocrine disease; gastrointestinal disease; metabolic disorder; dipeptidyl peptidase IV; CD26; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Diagnosing pre-diabetes, diabetes or susceptibility to diabetes, by obtaining biological sample, and detecting or measuring level of polypeptide marker comprising polypeptide e.g. vascular endothelial growth factor B, apolipoprotein D.
                                                                                                                                               Human dipeptidyl peptidase IV protein.
                                                                 ADZ14038 standard; protein; 766
                                                                                                                                                                                                                                                                                                                                                    (HOFF ) HOFFMANN LA ROCHE INC
                                                                                                                                                                                                                                                                                               28-SEP-2004; 2004US-00952459.
                                                                                                                                                                                                                                                                                                                           03-OCT-2003; 2003US-0508699P
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213 ALWWSPNG 220
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N-PSDB; ADZ14037.
REFSEQ; NP_001926.
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                                                                                                                                                                                                                   Homo sapiens.
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                                        polypeptide. The polypeptide, agonist or an antagonist, antibody, composition, and method are useful for diagnosing and treating an immune related disorder, e.g. systemic lupus erythematosus, rheumatoid arthritis. The present sequence represents a DNA encoding a PRO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         treating an immune related digorder, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus
                                                                                                                                                                                                                                                                                                                                                                                                       Antinflammatory, Immune disorder, Dermatological, Immunosuppressive, Antirheumatic, Antiarthritic, Osteopathic, Hemostatic, Antianemic, Antithyroid, Antiabbtic, Nephrotrropic, CNS-Gen., Hepatotropic, Virucide, Gastrointestinal-Gen., Antipsoriatic, Antiasthmatic, Antiallergic, ds, gene, diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid encoding PRO polypeptide, useful for diagnosing and
                                                                                                                                                                              Gaps
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                             The invention relates to an isolated nucleic acid encoding a PRO
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9.2;
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                                                                                                                                                  Score 53;
Pred. No.
    Claim 8; SEQ ID NO 967; 158pp; English
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100.0%; Pre
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                 polypeptide.
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Rosinski JA;

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                               The present invention relates to a method for diagnosing of pre-diabetes, diabetes or susceptibility to diabetes. The method involves obtaining a biological sample and detecting or measuring the level of a polypeptide marker, such as vascular endothelial growth factor B or apolipoprotein of the invention is useful for treating diabetes and pre-diabetes. The present sequence is the human diapetidyl apptidates IV (DPDIV, DPP4) protein. Diapetidyl peptidates IV is also known as CD26, ADCP2, TP103, ADABP: adenosine deaminase complexing protein 2 and Tcell activation
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100.0%; Pred. No....
0; Mismatches
Claim 1; SEQ ID NO 18; 66pp; English.
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0; Indels

81.5%; Score 53; DB 9; Length 766; 100.0%; Pred. No. 9.2;

100.0%; Pred. ...

8; Conservative

Best Local Similarity Matches 8; Conserv

Query Match

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immunosuppressive; graft versus host disease; transplant rejection; endotoxic shock; osteoarthritis; antiarthritic; osteopathic; musculookeletal disease; allergy; antiarthritic; osteopathic; musculookeletal disease; allergy; antialthritic; osteopathic; antialthritic; osteopathic; antialthritic; antiarteriosclerosis; antiarteriosclerosis; antiarteriosclerosis; antithyroid; endocrine disease; inflammatory bowel disease; antithyroid; endocrine disease; inflammatory bowel disease; antithyroid; antihestinal-gen.; gastrointestinal disease; antithematory; hepatotropic; autoprotective; systemic lupus erythematocous; dermatological, dermatological disease; uveitis; ophthalmological; autoimmune hemolytic anemia; antianemic; hematological disease; rheumatic fever; antipyretic; Crohns disease; psoriasis; antipsoriatic; graves disease; antithyroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention comprises a method of determining etiology of an autistic spectrum disorder in a patient. The method involves determining the level of an infectious agent, toxic chemical, or dietary protein derived antigen, or their antibodies in samples of patient, and comparing antigens/antibodies levels with normal levels of antigens/antibodies from control subjects. The method of the invention is useful for determining the etiology of an autistic spectrum disorder, such as autism, pervasive development disorder and Asperger's syndrome. The present amino acid sequence represents a human dispetidyl peptidase IV enzyme that was used
                                                                                                                                                                                                                                                                                                                                                       Determining etiology of autistic spectrum disorder in patient, by determining level of infectious agent/toxic chemical/dietary protein derived antigen in samples of patient, comparing it with normal level of antigens of control subjects.
autism; nootropic; asperger syndrome; enzyme; dipeptidyl peptidase IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immune inhibition; fibroblast activation protein alpha dimer; FAP alpha dimer; guillain barre syndrome; antiinflammatory; cns-gen.; immune disorder; neurological disease; autoimmune disease;
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Pred. No.
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Local Similarity 100.0%; Pries 8; Conservative 0;
                                                                                                                                                                03-FEB-2004; 2004US-00770712
                                                                                                                                                                                                     03-FEB-2004; 2004US-00770712.
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                                                                                 US2005170333-A1.
                                             Homo sapiens.
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The invention relates to a method of down-regulating an immune response, which comprises administering to a subject a fibroblast activation protein (FAP) alpha dimer enzyme in an amount effective to down-regulate protein (FAP) alpha dimer enzyme in an amount effective to down-regulate carrier, where the composition is sterile and lacks an adjuvant; a composition comprising a FAP alpha dimer enzyme in a pharmaceutically acceptable carrier, where the composition is sterile and lacks an adjuvant; a composition comprising a FAP alpha dimer enzyme in a pharmaceutically acceptable carrier, and a non-adjuvant second agent; a composition comprising a RAP alpha dimer enzyme lacking amino acids 269-448 and comprising a RAP alpha dimer enzyme lacking amino acids 269-448 and comprising a mino acids 269-448 from mouse FAP.

The second agent is an anti-inflammatory agent, immunosuppressant, or anti-infective agent such as antibacterial, antiviral, antifungal, anti-infective agent such as antibacterial agent. The FAP alpha dimer enzyme is a fusion or chimeric protein. The FAP alpha dimer enzyme is a heterodimer of a FAP alpha monomer and a ppriv, CD26 monomer. The FAP alpha dimer enzyme is a fusion or chimeric protein. The FAP alpha dimer enzyme is a heterodimer of a FAP alpha monomer and a ppriv, CD26 monomer. The FAP alpha dimer enzyme is a heterodimer of a FAP alpha dimer enzyme is comprised an amino acid substitution is present in the beta-propeller (formit on an N-linked glycosylation site and alters disulfide bond formation, abnormal immune response selected from inflammation, controlled acceptable, graft versus host disease, transplant response is subsequent to an infection, such amenatic fever; catchimume disease, sepsie, graft versus host disease, rheumatic graves, disease, continumne disease is selected from c, autoimmune disease is selected from c, autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Crohn's disease, Guillain-Barrer's syndrome, psoriasis, Graves' disease, myasthenia gravis, glomerulonephritis, autoimmune hepatitis and multiple sclerosis. The subject does not have cancer or a predisposition to cancer. The present sequence represents the amino acid sequence of human CD26/dipeptidyl peptidase IV (DPPIV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Down-regulating an immune response comprises administering to a subject in need a fibroblast activation protein (FAP) alpha dimer enzyme in an amount effective to down-regulate an immune response.
respiratory syncytial virus infection; respiratory-gen.; virucide; CD26 dipeptidyl peptidase IV; DPPIV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 66; 177pp; English.
                                                                                                                                                                                                                                                                                                                                                                          Miller GT,
                                                                                                                                                                                                                                                                                                                           (POIN-) POINT THERAPEUTICS INC
                                                                                                                                                                                                                                  10-JAN-2005; 2005WO-US000709.
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                                                                                         Homo sapiens.
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Length 766; 0; Indels

81.5%; Score 53; DB 9; 100.0%; Pred. No. 9.2; iive 0; Mismatches (

Local Similarity 100. nes 8; Conservative

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                                                                                                       F-16 monoclonal antibody, complement mediated cytotoxicity, cell damage, myocardial infarction, reperfusion injury, multiple sclerosis, nephritis, neuropathy, arthritis, cardiant, neuroprotective, vasotropic,
                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents rat dipeptidyl peptidase IV (DPPIV). The invention relates to the murine monoclonal antibody F-16 (FERMP-17016), which suppresses complement-mediated cell damage by specifically binding too DPPIV, thereby inhibiting complement activation. The invention also relates to the F-16 hybridoma which secrets the monoclonal antibody and and DPPIV. The F-16 hybridoma was produced by fusion of a mouse myeloma cell and a splenocyte obtained from a mouse incculated with rat glomerulus protein extract. The F-16 antibody was subsequently found to bind to DPPIV. The F-16 antibody is useful for treating diseases caused by complement—ediated cytocoxicity, such as myocardial infarction,
                                                                                                                                                                                                                                                                                                                                                        Monoclonal antibody specific for dipeptidyl peptidase, useful for prevention and treatment of nephritis, arthritis, neuropathy and myocardial infarction resulting from complement-dependent cell damage.
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                                                                                                                                                                                                      "This region is specifically claimed"
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100.0%; Pred. No. 9.2;
ive 0; Mismatches 0; Indels
                                                                                                Dipeptidyl peptidase IV; DPPIV; rat; glomerulus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  potential complement suppression activity
                                                                         Rat dipeptidyl peptidase IV (DPPIV).
                                                                                                                                                                                   Location/Qualifiers
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           AAB11748 standard; protein; 767 AA
                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Page 7-9; 11pp; Japanese
                                                                                                                                                                                                                                                                                           98JP-00321079.
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                                                     (first entry)
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Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                                                          antiarthritic
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                                                                 Tissue-specific endothelial membrane protein; antibacterial; virucide; fungicide; antiparasitic; anticonvulsant; neuroleptic; cytostatic; antiparkinsonian; nootropic; neuroprotective; antiatehmatic; infection; antidiabetic; hypotensive; nephrotropic; antiatrhritic; antinflammatory; gene therapy; epilepsy; schizophrenia; cancer; Parkinson's disease; Alzheimer's disease; ashma; diabetes; hypertension; arthritis; polycystic kidney disease; tissue-specific luminally expressed protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Delivering a therapeutic agent (e.g. immunosuppressant) to a specific tissue, comprises administering an amount of a therapeutic complex comprising a therapeutic group, a ligand that binds to a tissue-specific protein, and a linker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a method (M1) for delivering a therapeutic agent to a specific tissue, comprising administering an amount of a therapeutic complex comprising a ligand which binds to a tissue-specific luminally expressed protein, a therapeutic group, and a linker which links the group to the ligand. Tissue-specific endothelial membrane proteins from the present invention can have antibacterial, virucide, fungicide, antiparsitic, anticonvulsant, neuroleptic, cytostatic, antiparkinsonian, nootropic, neuroprotective, antiasthmatic, antidiabetic, hypotenaive, nephrotropic, antiarthritic and antiinflammatory activities, and can be used in gene therapeutice to specific tissues using tissue-specific endothelial membrane proteins.
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Rat liver dipeptidyl peptidase IV (DPP4) protein SEQ ID NO:4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                 inflammatory bowel disease; enzyme.
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Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                               Rat Protein AAA41096, SEQ ID NO 12618.
             ADD46932 standard; protein; 767 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page; 1017pp; English
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                                                                                                                                                                                                                                                                                                                                     01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                                                                                        14-AUG-2001; 2001US-0312147P.
                                                                                                                                                                                                                                                                                         14-AUG-2002; 2002WO-US025765
                                                                     (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention discloses
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GENBANK; AAA41096.
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                                                                                                                                                                                       Rattus norvegicus.
Unidentified.
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                                                                     02-DEC-2004
29-JAN-2004
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                                          ADD46932;
ADD46932
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Costigan M;

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or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polypeptides or their antibodies. The polynoclectide or the compound that modulates its activity is useful for preparing a medicament for treating ann (e.g. spinal segmental nerve injury (Chung), chronic construction injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene therapy). The sequence presented is a rat protein (described in Table 3
a composition comprising two or more isolated rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   therapy). The sequence presented is a rat protein (described in Table 3 of the specification) which is differentially expressed during pain. Mote: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the expression of a polymuleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polymuleotides, a method for producing a pharmaceutical composition, is method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating
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Sequence 767 AA;

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probable secreted protein C17H12.1 [ 4-alpha-glucanotra	structural protein	structural protein	structural protein	probable s/n-oxide	biotin sulfoxide r	probable (imported	for related protei	Valy1-tkNA Byntnas R giihtilia VfhO n	mannan endo-1.4-be	sericin1B - silkwo	chitinase (EC 3.2.	hypothetical prote	hypothetical prote	hypothetical prote	probable ammonium	H+-transporting tw h:mothotical prote	hypothetical prote	hypothetical prote	hypothetical 12.4K	hypothetical prote	lg gamma-za chain hymothetical prote	hypothetical prote	potassium channel	hypothetical prote	conserved hypothet	hypothetical prote	transcription init	hypothetical prote	hypothetical prote	hypothetical prote	transcription init	potassium channel	type II Site-Speci hymothetical prote	ketopantoate reduc	deoxyhypusine synt	tolb protein [impo	probable outer mem	probable transcrip	transcription init	AppA [imported] -	hypothetical prote	ferrochelatase nom	RNA polymerase sig	conserved hypothet	probable aldo-keto	probable transcrip transcription init	gene WNT3 protein	hypothetical prote	serine/threonine p	wingless homolog X	Wnt-3A protein - m	hypothetical prote wnt-1 protein - mo	iron utilization p	nucleotide-binding	heterogeneous ribo
2 T35234 2 H88712 2 AC0016	н-		н.	٦ ٢	~	7	~	N (	4 0	۱ ۸	1 (1	~	N	7	01 0	7	4 (	7	7	0	7 0	N (1	0	~	N (	1 (1)	~	7 0	7 0	1 (1	0	00	N C	1 (1	7	<b>(4</b> )	1.0	0	<b>7</b> 0	10	0	0 0	N 64	7	~	7 (7	4 0	7	0	4 (	7	2 12	N 6	10	~ .
631 643 698	708	708	708	796	196	806	849	988	1001	1217	1635	1638	142	293	512	20.0	100	104	107	108	112	157	160	160	182	192	193	197	220	231	246	256	263	281	292	293	293	295	2 6 6	303	305	300	310	318	329	332	3 6	338	350	352	352	353	350	356	365
53.8 53.8 8.8.8	<u>-</u> : -	: _:	_: .	: :	: _:	-:	ᆣ.	ᆣ.	: .	: _	: _:	_	_:	<u>.</u> :	<u>.</u> .	∹.	: ~	~	ď.	؞.	~i ~		:	٠i.	.i ^		~i.	~i ~			~:	~ .	vi c	i	Ni.	~. ⋅	i	oi o	v	i	oi.	oi o	i	N	oi (	o o	N C	N	o o	NO	N	00	4 0	N	2
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A;Molecule type: protein
A;Residues: 281-302 <IWA>
A;Cross-references: UNIPARC:UP10000172A3A
            81.5%; Sc.
100.0%; Pre
                                                                                                                         8; Conservative
                                                                                                                                                                                                                                                                                213 ALWWSPNG 220
                                                                                                                                                                                                     2 ALWWSPNG 9
                                         Query Match
Best Local Similarity
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A; Residues: 1-792 <HON>
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Timmunol. 149, 481-486, 1992.
Title: Cloning and functional expression of the T cell activation antigen CD26.
Reference number: 156154; MUID:92325476; PMID:1352530
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A; Introns: 2/3: 32/1; 65/1; 95/3; 122/3; 140/2; 164/3; 205/1; 258/3; 296/2; 341/3; 356/3

A; Introns: 2/3: 32/1; 65/1; 95/3; 122/3; 140/2; 164/3; 205/1; 258/3; 296/2; 341/3; 356/3

C; Superfamily: dipeptidy1-peptidse IV

C; Superfamily: dipeptidy1-peptidse IV

C; Superfamily: dipeptidy1-peptidse IV

F; 1-6/Domain: intracellular #status predicted <IVIX>

F; 1-6/Domain: intracellular #status predicted <IVIX>

F; 29-76/Domain: extracellular #status predicted <IVIX>

F; 85, 92, 150, 219, 229, 281, 321, 520, 685/Binding site: carbohydrate (Asn) (covalent) #status

F; 630, 708, 740/Active site: Ser, Asp, His #status predicted
                                     C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence revision 23-Aug-1996 #text change 09-Jul-2004
C;Date: 31-Dec-1993 #sequence revision 23-Aug-1996 #text change 09-Jul-2004
C;Accession: S24313; B42408; B61136; S59510; I56154; S59857; S15520
R;Misumi, Y.; Hayashi, Y.; Arakawa, F.; Ikehara, Y.
Biochim. Biophys. Acta 1131, 333-336, 1992
A;Title: Molecular cloning and sequence analysis of human dipeptidyl peptidase IV, a ser
A;Accession: S24313
A;MUD:92329551; PMID:1352704
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-6,'I', 8-766 <MIS>
A;Residues: 1-6,'I', 8-766 <MIS>
A;Residues: 1-6,'I', 8-764 + 4833, 1992
A;Cross-references: UNIPROT:P27487; UNIPARC:UPI000016AE80; EMBL:X60708; NID:g35335; PIDN
R;Darmoul, D; Lacasa, M; Baricault, L; Marguet, D; Sapin, C; Trotot, P; Barbat, A.
A;Title: Dipeptidyl peptidase IV (CD 26) gene expression in enterocyte-like colon cancer
IV mRNA levels during cell differentiation.
A;Reference number: A42408; MUID:92165847; PMID:1347043
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;Molecule type: mRNA
;Residues: 1-436,'S',198-766 <TAN>
;Cross-references: UN193R-766 <TAN>
;Abbott, C.A.; Baker, E.; Sutherland, G.R.; McCaughan, G.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: B42408
A;Molecule type: mRNA
A;Residues: 1-5, 'R', 7-436,'S',438-556,'I',558-662,'E',664-766 <DABI>
A;Cross-references: UNIPARC:UPI0000052ACB; GB:M80536; NID:g181569; PIDN:AAA52308.1; PID:
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N;Alternate names: cell surface glycoprotein CD26; thymocyte-activating molecule (THAM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochem. J. 311, 835-843, 1995
A;Title: Human dipeptidyl peptidase IV gene promoter: tissue-specific regulation from
A;Reference number: S59510; MUID:96067599; PMID:7487939
A;Accession: S59510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source: intestine
A; Note: this sequence corresponds with the author's translation
A; Note: this sequence corresponds with the author's translation
A; Accession: A4108
A; Accession: A4208
A; Molecule type: mRNA
A; Residues: 1-5, R', 7-436, 'S', 438-556, 'I', 558-662, 'E', 664-711, 'G', 713-766 < DAR2>
A; Cross-references: UNIPARC: UPI0000172AB; GB: M80536; NID: G191569
A; Note: sequence extracted from NCBI backbone (NCBIN: 83986, NCBIE: 83988); this set R; Gorvel, J. P.; Ferrero, A.; Chambraud, L.; Rigal, A.; Bonicel, J.; Maroux, S. Gastroenterology 101, 618-625, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Molecule type: protein
Residues: 1-15, X,17-22 <GOR>
Cross-references: UNIPARC:UPI0000172A2C
Hoehm, S.K.; Gum Jr., J.R.; Erickson, R.H.; Hicks, J.W.; Kim, Y.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cross-references: UNIPARC:UPI000004F7BF; EMBL:U13734
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Residues: 1-31 <BOE>
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A;Cross-references: UNIPROT:P14740; UNIPARC:UP1000017098A; GB:J02997; NID:g204463; PIDN R;Ogata, S.; Misumi, Y.; Ikehara, Y. J. Biol. Chem. 264, 3596-3601, 1989
J. Biol. Chem. 264, 3596-3601, 1989
A;Title: Primary structure of rat liver dipeptidyl peptidase IV deduced from its cDNA as A;Reference number: A33315; MUID:89123496; PMID:2563382
A;Accession: A33315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: mRNA
A;Residues: 1-37,'A', 39-182,'I',184-331,'T',333-351,'C',353-393,'V',395-561,'L',563-623,
A;Cress-references: UNIPARC:UP10000129841; GB:004591; NID:9203973; PIDN:AAA41096.1; PID
A;Note: the authors translated the codon GCG for residue 38 as Arg, ACC for residue 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A36; UNIPARC:UP10000172A37
K;McCaughan, G.W.; Wickenson, J.B.; Creswick, P.F.; Gorrell, M.D.
Hepatology 11, 534-544, 1990
A;Title: Identification of the bile canalicular cell surface molecule GP110 as the ector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    residues in dipeptidyl peptidase IV by affin
PMID:1347701
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;Residues: 1-20;35-54;427-443;505-509;511-520;530-538;593-600;602-608;618-627 <HO2>
;Cross-references: UNIPARC:UP10000172A2E; UNIPARC:UP10000172A30; UNIPARC:UP10000172A31
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A;Residues: 'R',625-630,'X',632-648 <OG2>
A;Cross-references: UNIPARC:UPI0000172A39
R;InwakL-Egawa, S.; Watanabe, Y.; Fujinuoto, Y.
Biol. Chem. Hoppe-Seyler 374, 973-975, 1993
A;Title: N-terminal amino acid sequence of the 60-kDa protein of rat kidney dipeptidyl
A;Reference number: S38949; MUID:94128239; PMID:7905271
                                                                                                                                                                                                                                                                                                                                                                                    NyAlternate names: GP110; membrane glycoprotein 110K; OX-61
N;Contains: dipeptidyl-peptidase IV, soluble form
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Accession: A39914; A33315; E33315; A60730; A42203; S38949; A31781
R;HONG, W.; Doyle, D.
R;HONG, W.; Doyle, D.
R;HONG, W.; Acad. Sci. U.S.A. 84, 7962-7966, 1987
A;Title: CDNA cloning for a bile canaliculus domain-specific membrane glycoprotein of A;Reference number: A39914; MUID:88068516; PMID:3479775
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PMID:3182821
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   DB 1;
                                                                    Mismatches
   Score 53;
Pred. No.
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J. Biol. Ghem. 263, 16892-16898, 1988
A;Title: Membrane orientation of rat gpl10
A;Reference number: A31781; MUID:89034185;
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A;Map position: X
A;Introns: 4/3; 51/1; 123/3; 166/3; 188/2; 279/2; 392/3; 501/3; 553/1; 583/1; 606/2; 647
C;Superfamily: dipeptidyl-peptidase IV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F2214.11 protein - Arabidopsis thaliana (Governorm)

C;Species: Arabidopsis thaliana (Mouse-ear cress)

C;Species: Arabidopsis thaliana (Mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C;Accession: D86146

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Mature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, X.; Liu, Z.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Titles: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A66141; MUID:21016719; PMID:11130712
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A;Cross-references: UNIPROT:Q9LMM4; UNIPARC:UPI00000A1319; GB:AE005172; NID:g8920593; PI
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C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:Q18253; UNIPARC:UPI000007DC53; EMBL:Z69883; PIDN:CAA93743.1; A;Experimental source: clone C27C12
                                                                                                                                                                hypothetical protein C27C12.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T19514
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Pred. No. 9.1;
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C;Superfamily: Arabidopsis hypothetical protein Fl3M22.23
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-829 <WIL>
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7
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Pred. No. 10;
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, March 1996
A;Reference number: Z19134
A;Accession: T19514
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ilarity 75.0%;
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Matches 6; Conservative
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   207 ALWWSPN 213
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nes 6; Conserv
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A; Molecule type: DNA
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NiAlternate names: CD26 alpha subunit; THAM alpha subunit
C;Species Nus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S23752; A46665; A56030
C;Accession: S23752; A46665; A56030
J; Biol. Chem. 267, 2200-2208, 1992
A;Title: cDNA cloning for mouse thymocyre-activating molecule. A multifunctional ecto-di
A;Accession: S23752; MUID:92129288; PMID:1370813
A;Accession: S23752
A;Cross-references: UNIPARC:UPI0000172A3B
C;Comment: This protein is localized to the bile canaliculus, which is the apical domain C;Comment: This protein is localized to the bile canaliculus, which is the apical domain C;Comment: This protein is localized to the bile canaliculus, which is the apical domain: c;Superfamily: dipeptidyl-peptidase, membrane-bound form #status experimental <MATM>F;1-792/Product: dipeptidyl-peptidase, membrane-bound form #status experimental <MATM>F;1-28/Domain: signal sequence #link MATS #status experimental <SIG>F;1-6/Domain: intracellular #status predicted <IMN>F;2-8/Domain: extracellular #status predicted <IMN>F;2-9/Domain: extracellular #status predicted <IMN>F;2-9/Domain: extracellular #status predicted <IMN>F;2-9/Domain: dipeptidyl-peptidase, soluble form #status experimental <MATS>F;3-9/14/Active site: Ser #status experimental
F;30-747/Active site: Ser #status predicted
F;709,741/Active site: Asp, His #status predicted
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A; Residues: 1-76 cNARA
A; Residues: 1-76 cNARA
A; A; Cross-references: UNIPARC:UP10000172A2D; EMBL:X58384
B; Vivier, I.; Marguet, D.; Naquet, P.; Bonicel, J.; Black, D.; Li, C.X.; Bernard, A.M.;
R; Vivier, I.; Marguet, D.; Naquet, P.; Bonicel, J.; Black, D.; Li, C.X.; Bernard, A.M.;
A; Immunol. 147, 447-454, 1991
A; Title: Evidence that thymocyte-activating molecule is mouse CD26 (dipeptidyl peptidase A; Reference number: A46465; MUID:91302787; PMID:1712807
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C;Keywords: dipeptidylpeptide hydrolase; glycoprotein; transmembrane protein
F213, 223, 315, 514, 679/Binding tie: carbohydrate (Aan) (covalent) #status predicted
F;624,702,734/Active site: Ser, Asp, His #status predicted
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Reference number: A56010; MUID:95092780; PMID:7999781
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A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-20 «VIV»
A; Molecule type: protein
A; Residues: 1-20 «VIV»
A; Cross-references: UNIPARC: UPI0000172A2E
A; Cross-references: UNIPARC: UPI0000172A2E
A; Experimental source: M14.T thymoma cells, Swiss nu/nu
A; Note: sequence extracted from NCB1 backbone (NCBIP:42236)
R; Bernard, A.M.; Mattei, M.G.; Pierres, M.; Marguet, D.
Biochemistry 33, 15204-15214, 1994
A; Reference number: A56030; MUID:95092780; PMID:7999781
A; Accession: A56030
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 746-760 «BER»
A; Cross-references: UNIPARC: UPI0000172A2F; GB:U12620
C; Genetics:
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Best Local Similarity 100.
Matches 8; Conservative
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A; Experimental source: clone W07A8
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A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
Modecule type: DNA
A;Readues: 1-250 «KUR»
A;Cross-references: UNIPROT:Q8UA66; UNIPARC:UP1000013799C; GB:AE007870; PIDN:AAK89887.1;
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A;Experimental source: strain C58 (Dupont)
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C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
   C,Accession: AC2988
R,Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
                                                                                                ; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                         ster, E.W.
AyItle: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AC2988
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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A;Map positIon: linear chromosome
C;Superfamily: 3-demethylubiquinone-9 3-0-methyltransferase; bioC homology
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C;Superfamily: 3-demethylubiquinone-9 3-0-methyltransferase; bioC homology
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Best Local Similarity 77.8%; Pred. No. 6.7;
Matches 7; Conservative 0; Mismatches
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A;Accession: T26259
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R, Goodner, B.: Hink
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probable dipeptidyl aminopeptidase - fission yeast (Schizosaccharomyces pombe) (fragmen
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A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000; MUID:95350630; PMID:7542800
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A;Residues: 1-699 <TIGR>
A;Cross-references: UNIPROT:P45176; UNIPARC:UPI000012EB5B; GB:U32815; GB:L42023; NID:91
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Species: Schizosaccharomyces pombe
Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 15-Sep-2000
Accession: T37700
                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Devlin, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, submitted to the EMBL Data Library, August 1997
A;Reference number: Z21737
A;Accession: T37700
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A;Map position: 5
A;Introns: 83/1; 141/3; 256/3
C;Superfamily: Caenorhabditis elegans hypothetical protein W07A8.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 45; DB 2; Length 743;
Pred. No. 19;
2; Mismatches 0; Indels
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A;Molecule type: DNA
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                                                                                                             69.2%; Score 45; DB 2;
illarity 100.0%; Pred. No. 8.4;
Conservative 0; Mismatches
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Pred. No. 25;
1; Mismatches
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C;Superfamily: 4-alpha-glucanotransferase
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75.0%;
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Local Similarity 60.0%;
es 6; Conservative
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178 AVWWSPDG 185
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Best Local Similarity
Matches 6; Conserv
                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                   74 WWSPNG 79
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C;Accession: 138028; G02274; I38046; S78011; S45341; S71384

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R;Will, H.; Hinzmann, B.
Bur. J. Blochem. 231, 605-608, 1995
A;Title: CDNA sequence and mRNA tissue distribution of a novel human matrix metalloprote
A;Reference number: 138028; MUID:95377289; PMID:7649159
                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-582 <WILL>
A;Cross_references: UNIPROT:P50281; UNIPARC:UPI000048136; EMBL:Z48481; NID:g963053; PID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-582 actio>
A;Cross-references: UNIPARC: UPI0000048136; EMBL: U41078; NID: 91127836; PIDN: AAA83770.1; P
R;Okada, A.; Bellocq, J.P.; Rouyer, N.; Chenard, M.P.; Rio, M.C.; Chambon, P.; Basset, P
Proc. Natl. Acad. Sci. U.S.A. 92, 2730-2734, 1995
A;Title: Membrane-type matrix metalloproteinase (Mr-MMP) gene is expressed in stromal ce
A;Reference number: I38046; MUID: 95224014; PMID: 7708715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: translated from GB/EMBL/DDBJ
A;Molecule translated mRNA
A;Residues: 1-7,'S',9-582 <OKA>
A;Cross-references: UNIPARC:UPI000003096F; EMBL:X83535; NID:g804993; PIDN:CAA58519.1; PI
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C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproted;
C;Superfamily: interstitial collagenase; metalloproteinase; zinc; zymogen
C;Keywords: glycoprotein; hydrolase; metalloproteinase; zinc; zymogen
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-97/Domain: activation peptide #status predicted <PRO>
F;61-284/Domain: matrix metalloproteinase homology <MMP>
F;88-582/Product: matrix metalloproteinase la membrane type #status predicted <MAT>
F;285-313/Domain: hinge #status predicted <HNG>.
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F;339-562/Domain: transmembrane #status predicted <TMM>
F;539-562/Domain: transmembrane #status predicted <TMM>
F;93,243,249/Binding site: zinc, catalytic (Cys, His, His, His, His) (inhibited) #status F;33,243/Binding site: zinc, catalytic (His) (active) #status predicted
F;240/Active site: Ju #status predicted
F;319-508/Disulfide bonds: #status predicted
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A; Residues: 1-7 'S', 9-188, 'R', 190, 'A', 192-267, 'K', 269-272, 'HY', 275,'P', 277-285, 'KQ', 288, A; Residues: 1-7 'S', 9-188, 'R', 190000157586; EMBL: D26512
R; Cross-references: UNIPARC: UPI0000157586; EMBL: D26512
R; Sato, H.; Kinoshita, T.; Takino, T.; Nakayama, K.; Seiki, M.
FEBS Lett. 393, 101-104, 1996
A; Title: Activation of a recombinant membrane type 1-matrix metalloproteinase (MTI-MMP)
A; Reference number: S71384; MUID: 96397540; PMID: 8804434
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A/Residues: 1-7, 'S', 9-337, 'K', 339-582 <SEI>
A/Crossidues: 1-7, 'S', 9-337, 'K', 339-582 <SEI>
A/Crossidues: 1-7, 'S', 9-337, 'K', 339-582 <SEI>
A/Crossidues: 1-7, 'S', 9-337, 'K', 339-582 <SEI
A/Crossidues: 1-7, 'S', 9-337, 'K', 339-582 <SEI
Nature 370, 61-65, 1994
A/TILLE: A matrix metalloproteinase expressed on the surface of invasive tumour cells.
A/Reference number: 845341, MUID:94286011, PMID:8015608
A/Status: nucleic acid sequence not shown
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A,Molecule type: mRNA
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73
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Pred. No.
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A;Residues: 112-116 <SAW>
A;Cross-references: UNIPARC:UP10000175D8E
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77.8%;
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Best Local Similarity 77.8
Matches 7; Conservative
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C;Species: Mus musculus (house mouse)
C;Species: O2-Jul-1996 #text_change 22-Jun-1999
C;Accession: 148673
R;Okada, A.; Bellocq, J.P.; Rouyer, N.; Chenard, M.P.; Rio, M.C.; Chambon, P.; Basset, F. Proc. Natl. Acad. Sci. U.S.A. 92, 273-2734, 1995
A;Title: Membrane-type matrix metalloproteinase (MT-MMP) gene is expressed in stromal ce A;Reference number: 138046; MUID:95224014; PMID:7708715
A;Accession: 148673
A;Reterence number: 138046; MUID:95224014; PMID:7708715
A;Reterence number: 138046; MUID:95224014; PMID:7708715
A;Reterence number: 148673
A;Reterence number: 148674
A;Reterence
                                                                                                                                                                                                                                                                                                       CyAccession: G7536

R/White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
AyTitle: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: G75316
A;Accession: G75
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                                                                                                                                                      probable lipase - Deinococcus radiodurans (strain R1)
C,Species: Deinococcus radiodurans
C,Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
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Pred. No. 13;
0; Mismatches 1; Indels
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Pred. No. 31;
1; Mismatches 1; Indels
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85.7%;
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Best Local Similarity 77.8%;
Matches 7; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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Gene: DR2078
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A72050
GlpT/PgpT/UhpT family protein CP0082 [imported] - Chlamydophila pneumoniae (strains CWLC
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A;Molecule type: DNA
A;Molecule type: DNA
A;Rosidues: 1-455 <ARN>
A;Cross-references: UNIPROT:Q927N9; UNIPARC:UPI0000137B1F; GB:AE001649; GB:AE001363; NI:
A;Experimental source: strain CWL029
A;Experimental source: strain CWL029
A;Experimental source: strain CWL029
A;Experimental source: strain (WL029
A;Experimental sour
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A,Residues: 1-455 <REA>
A,Cross-references: UNIPARC:UPI0000137B1F; GB:AE002171; GB:AE002161; NID:G7189009; PIDN
A,Experimental source: strain AR39, HL cells
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RjShirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; I
RiShirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; I
Nucleic Acids Ree. 28, 2311-2314, 2000
A;Title: Comparison of Whole genome sequences of chlamydia pneumoniae J138.
A;Title: Comparison of Whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349; PMID:10871362
A;Accession: F86573
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A)Cross-references: UNIPROT:0927N9; UNIPARC:UPI0000137B1F; GB:BA000008; NID:98979037; P
A)Experimental source: strain J138
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A;Reference number: A81500; MUID:20150255; PMID:10684935
A;Accession: F81616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, Nature Genet. 21, 385-389, 1999
A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
A;Reference number: A72000; MUID:99206606; PMID:10192388
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C,Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C,Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                            N'Alternate names: hexosphosphate transport protein
C'Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C'Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C'Accession: A72050; P81616
   Gaps
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Pred. No. 35;
1; Mismatches 2; Indels
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Pred. No. 35;
1; Mismatches 2; Indels
   3; Indels
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Best Local Similarity 66.7
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       Conservative
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                                                                                   2 ALWWSPNGK 10
                                                                                                                                                              22 AQWWDPQGK 30
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A,Gene: uhpC
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A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hexaprenyldihydroxybenzoate methyltransferase (EC 2.1.1.114) [imported] - Brucella meliq
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Experimental source: strain 16M
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A;Residues: 1-582 «RES»
A;Cross-references: UNIPROT:Q10739; UNIPARC:UPI0000030970; EMBL:X83537; NID:g805012; PIL
A;Accession: 161946
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;Guperfamily; interstitial collagenase; hemopexin repeat homology; matrix metalloprotei;
;Reywords: hydrolase; metalloproteinase; zinc; zymogen
;1-23/Domain: signal sequence #status predicted <SIG>
;24-97/Domain: activation peptide #status predicted <PRO>
;61-284/Domain: matrix metalloproteinase homology <MMP>
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                                                                                                                                                                                                                                                                                                        matrix metalloproteinase (EC 3.4.24.-) membrane type precursor - rat
NyAlternate names: membrane-type metalloproteinase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: 184471; 161946
R;Okada, A.; Bellocq, J.P.; Rouyer, N.; Chenard, M.P.; Rio, M.C.; Chambon, P.; Basset, Proc. Natl. Acad. Sci. U.S.A. 92, 2370-2734, 1995
A;Title: Membrane-type matrix metalloproteinase (MT-MMP) gene is expressed in stromal characteric number: 138046; MUID:95224014; PMID:7708715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;MOJecule type: mRNA
A;Residues: 1-67, M', 69-254, A', 256-582 <RE2>
A;Cross-references: UNIPARC:UP100001679D1; EMBL:X91785; NID:g1001926; PIDN:CAA62897.1;
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C.Species: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
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S.Superfamily: 3-demethylubiquinone-9 3-O-methyltransferase; bioC homology
C;Koywords: methyltransferase
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Pred. No. 31;
1; Mismatches 1; Indels
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Pred. No.
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66.7%;
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ilarity 77.8%;
Conservative 1
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ALFWMPNGK 426
                                                                                              418 ALFWMPNGK 426
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Best Local Similarity
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Best Local Similarity
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 09-Jul-2004
C;Accession: 138029; G00041
R;Will, H.; Hinzmann, B.
R;Will, H.; Hinzmann, B.
A;Title: CDNA sequence and mRNA tissue distribution of a novel human matrix metalloprote A;Reference number: 138028; WUID:95377289; PMID:7649159
A;Accession: 138029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cross-references: UNIPROT:P51511; UNIPARC:UPI000003DC75; EMBL:Z48482; NID:g963055; PID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 106-608,'R',610-669 <SEI>
A;Cross-references: UNIPARC:UP100000705A7; GB:D86331; NID:91418214; PIDN:BAA13071.1; PID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Genes GDB:MMP15; MT2-MMP
A;Gross-references: GDB:44246
A;Cross-references: GDB:44246
C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotei
C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotei
C;Keywords: glycoprotein; hydrolase; metalloproteinase homology canc; zymogen
P;141/Domain: activation peptide #status predicted <AT>
P;142-125/Domain: activation peptide #status predicted <AT>
P;133-669/Domain: matrix metalloproteinase homology cand.
P;133-669/Domain: hemopexin repeat homology cand.
P;134-559/Domain: hemopexin repeat homology cand.
P;140-059/Domain: transmembrane #status predicted <TRM>
P;259,263,269/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
P;150/Binding site: azinc, catalytic (His) (active) #status predicted
P;259,263,269/Binding site: zinc, catalytic (His) (active) #status predicted
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NyAlternate names: membrane-type matrix metalloproteinase 2 (MT2MMP); MMP15
C;Species: Homo sapiens (man)
C;Date: 17-May-1996 #semience revision 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: CC0840
C;Superfamily: 3-demethylubiquinone-9 3-O-methyltransferase; bioC homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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A;Molecule type: mRNA
A;Residues: 1-669 <WIL>
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Pred. No. 28;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 63.1
Best Local Similarity 66.7
Matches 6; Conservative
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A, Accession: G00041
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                             FAIWWALNG 30
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N.Alternate names: protein YHRO286

C, Species: Saccharomyces cerevisiae

C, Species: Saccharomyces cerevisiae

C, Species: O7-Jun-1999 #sequence_revision 30-May-1997 #text_change 09-Jul-2004

C, Accession: S46780, A30107

R, Du.

A, Accession: S46780

A, Accession: S46773

A, Accession: S46780

A, Roberta to the EMBL Data Library, June 1994

A, Roberta to The sequence of S. cerevisiae cosmid 8082.

A, Roberta to The sequence of S. cerevisiae cosmid 8082.

A, Roberta type: DNA

A, Roberta C. J.; Pohlig, G.; Rothman, J.H.; Stevens, T.H.

J. Cell Biol. 108, 1363-1373, 1989

A; Title: Structure, Diosynthesis, and localization of dipeptidyl aminopeptidase B, an in A; Reference number: A30107; MUID:89174971; PMID:2647766

A, Accession: A30107

A, Roberta type: DNA

A, Reference: UNIPARC:UPI0000172A3C; EMBL:X15484

A, Cross-references: UNIPARC:UPI0000172A3C; EMBL:X15484

A, Cross-references: UNIPARC:UPI0000172A3C; EMBL:X15484

A, Gene: SGD:DAP2; STE13; MIPS:YHRO28C

A, Map position: 8R

C, Superfeanily: dispeptidyl publicate IV
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Caccession: 701868
R;Latraile, P.; Elliott, G.; Le, T.
Submitted to the EMBL Data Library, August 1998
A;Description: The sequence of A. thaliana T24M8.
A;Reference number: 214449
A;Accession: 701868
A;Accession: 701868
A;Accession: 701868
A;Accession: T01868
A;Residues: 1-246 <LAT>
A;Molecule type: DNA
A;Residues: 1-246 <LAT>
A;Residue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 64.6%; Score 42; DB 1; Length 818; Best Local Similarity 75.0%; Pred. No. 60; Matches 6; Conservative 0; Mismatches 2; Indels
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124 FALWWGLNG 132
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1 YALWWSPNG 9

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C;Accession: I54331
R;Yokotani, N.; Doi, K.; Wenthold, R.J.; Wada, K.
Hum. Mol. Genet. 2, 1037-1039, 1993
A;Title: Non-conservation of a catalytic residue in a dipeptidyl aminopeptidase IV-rela:
A;Reference number: I54331; MUID:93372805; PMID:8103397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Accession: 154331
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Molecule type: mRNA
A,Residues: 1-865 < RES>
A,Cross-references: UNIPROT:P42658; UNIPARC:UPI0000047378; GB:M96859; NID:g306705; PIDN
C,Superfamily: dipeptidyl-peptidase IV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Cross-references: UNIPROT:Q05894; UNIPARC:UP10000135E3A; GB:L08077; NID:G329565; PIDN
                                                                                                                                                                                                                                  GB:M76429; NID:9408719; PIDN
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J. Gen. Virol. 74, 1811-1818, 1993
J. Gen. Virol. 74, 1811-1818, 1993
J. Gen. Virol. 74, 1811-1818, 1993
A;Titles A gene encoding a highly expressed spindle body protein of Heliothis armigera A;Reference number: JQ2166; MUID:93389435; PMID:8376960
A;Accession: JQ2166
Proc. Natl. Acad. Sci. U.S.A. 89, 197-201, 1992
A,Title: Differential expression of two distinct forms of mRNA encoding members of A,Reference number: A41793; MUID:92108018; PMID:1729689
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C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
C;Accession: JQ2166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C,Species: Homo sapiens (man)
C,Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
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                                                                                                                                          A;Status: preliminary; not compared with conceptual translation
A;Status: preliminary; not compared with conceptual translation
A;Residues: 1-803 <WAD>
A;Residues: 1-803 <WAD>
A;Cross-references: UNIPROT:P42659; UNIPARC:UPI00002A83C; GB:M76429; NI
A;Note: sequence extracted from NCBI backbone (NCBIP:75138)
C;Superfamily: dipeptidy1-peptidase IV
C;Reywords: dipeptidy1-peptide hydrolase; glycoprotein
F;257,342/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Pred. No. 85;
1; Mismatches 1; Indels
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F;21-351/Product: spindle body protein #status predicted <MAT>
F;195/Binding site: carbohydrate (Asn) (covalent) #status pred
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Pred. No. 91;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dipeptidyl aminopeptidase like protein - human
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83.3%;
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Best Local Similarity 75.0%;
Matches 6; Conservative
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Best Local Similarity 75.0%;
Matches 6; Conservative
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Best Local Similarity 83.33,
Best Local Similarity 63.33,
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C, Keywords: glycoprotein
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A; Residues: 1-351 < DAL>
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C;Species: Homo sapiens (man)
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 21-Jul-2000
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 21-Jul-2000
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 21-Jul-2000
R;Yokotani, N.; Doi, K.; Wenthold, R.J.; Wada, K.
Hum. Mol. Genet. 2, 1037-1039, 1993
A;Title: Non-conservation of a catalytic residue in a dipeptidyl aminopeptidase IV-relat A;Title: Non-conservation of a catalytic residue in a dipeptidyl aminopeptidase IV-relat A;Title: Non-conservation of a catalytic residue in a dipeptidyl-peptidase IV
A;Molecule munber: 154331; MUID:9372805; PMID:8103397
A;Residues: 1-803 -RES>
A;Residues: 1-803 -RES>
A;Residues: 1-803 -RES>
A;Cross-references: UNIPARC:UPIO00016A7F9; GB:M96860; NID:g306707; PIDN:AAA35761.1; PID:C;Superfamily: dipeptidyl-peptidase IV
                                                                                                                                                                                                                                                                                                                                                                                                                                   R; Andrews S. S. Submitted to the EMBL Data Library, July 1997
A; Description: The sequence of A. thaliana IG005110.
A; Reference number: 214347
A; Accession: T01541
A; Reterence number: 214347
A; Reterence number: 214347
A; Residues: 1701541
A; Residues: 1-785 < AND-A; Residues: 1-785 < AND-A; Residues: 1-785 < AND-A; Cosser-references: UNIPARC: UNIPARC: UPI00000A0893; EMBL: AF013293; NID: G2252823; A; Experimental source: cultivar Columbia
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C; Species: Bos primigenius taurus (cattle)
C; Sate: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004 C; Accession: A41793
R; Wada, K.; Yokotani, N.; Hunter, C.; Doi, K.; Wenthold, R.J.; Shimasaki, S.
                                                                                                                                                                                                                                                                                                                                                                                /pothetical protein A_IG005110.16 - Arabidopsis thaliana
/species: Arabidopsis thaliana (mouse-ear cress)
/bate: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 09-Jul-2004
/Accession: T01541
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                                                                                  Length 669
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                                                                                                                                     Indels
                                                                            Query Match 63.1%; Score 41; DB 2; Best Local Similarity 62.5%; Pred. No. 72; Matches 5; Conservative 1; Mismatches 2
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Pred. No. 85;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B3;
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Pred. No.
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75.0%;
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les 5, Conservative
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Best Local Similarity
Matches 6; Conserv
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A;Introns: 284/3; 467/3
A;Note: A_IG005110.16
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Best Local S
Matches 5
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Gaps

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phosphoenolpyruvate carboxykinase (ATP) (EC 4.1.1.49) - Salmonella enterica subsp. enter C; Species: Salmonella enterica subsp. enterica serovar Typhi A,Note: this species has also been called Salmonella typhi C; Spate: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Oct-2003 C; Accession: AF0998 R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, F; Parkhill, J.; Connerton, P.; Cronin, A.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P. Nature 413, 848-852, 2001 A; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Athichers: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Reference number: AB0502; MUID:21534947; PMID:11677608
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                                                                                                                                                                                                                                                                                                                A;Gross-references: UNIPROT:Q19614; UNIPARC:UP1000017B912; EMBL:U53150; PIDN:AAA96130.1; A;Experimental source: strain Bristol N2; clone F20A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: UNIPARC: UPI00005A7B8; GB: AL513382; PIDN: CAD08114.1; PID: 916505093;
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A;Introns: 45/3; 122/1; 271/3; 294/2; 315/3; 381/3; 423/2
                      C;Accession: T30040
R;Gattung, S.; Wu, X.
submitted to the EMBL Data Library, March 1996
A;Description: The sequence of C. elegans cosmid F20Al.
A;Reference number: Z20726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: STY4296
C;Superfamily: phosphoenolpyruvate carboxykinase [ATP]
C;Keywords: carbon-carbon lyase; carboxy-lyase
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A;Reference number: 219277
A;Accession: T20450
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-618 <****IL>>
                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-466 <GAT>
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83;
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0; Mismatches
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75.0%;
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Best Local Similarity 62.5%;
Matches 5; Conservative
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Best Local Similarity
Matches 6; Conserv
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A;Molecule type: DNA
A;Residues: 1-539 <PAR>
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                                                                                                                                                                                                    A; Accession: T30040
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A;Reference number: 219027
A;Accession: Ti8825
A;Cross-references: UNIPARC:UP10000082BD8; EMBL:Z81030; PIDN:CAB02716.1; GSPDB:GN00023; A;Experimental source: clone C01G10
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Pred. No. 56;
0; Mismatches 1; Indels
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66;
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A,Map position: 5
A;Introns: 13/2; 72/3; 122/2; 177/1; 272/3; 315/1; 353/2
C;Superfamily: O-staloglycoprotein endopeptidase
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Best Local Similarity 71.4%; Pred. No. 4
Matches 5; Conservative 1; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
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356 AIWWRPN 362
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Gaps

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A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-2329 <FAV>
A,Cross-references: UNIPROT:P34369; UNIPARC:UPI000013B834; EMBL:L14433; NID:g289649; PII
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R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.; submitted to the Protein Sequence Database, March 1999
A;Reference number: 215184
A;Accession: T06077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein F18B13.15 [imported] - Arabidopsis thaliana CSBC arabidopsis thaliana (mouse-ear cress) CSBC arabidopsis thaliana (mouse-ear cress) CSBC arabidopsis thaliana (mouse-ear cress) CSBC are 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004 CSBC are 186832 A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. Nasnen, N.F.; Hughes, B.; Hutzar, L. Nature 408 Nulce 1820, 2000 A.; A.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;MOlecule type: DNA
A;Reaidues: 1-2352 <BEV>
A;Cross-references: UNIPROT:Q9T016; UNIPARC:UP10000A4642; EMBL:AL035656; GSPDB:GN00062
A;Experimental source: cultivar Columbia; BAC clone T9A14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Map position: 4
A;Introns: 94/3; 132/3; 158/3; 289/1; 453/2; 717/1; 806/3; 911/3; 1013/2; 1165/1; 1207/-
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                                                                                                                                                                                                               C5003.6 protein - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
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Pred. No. 3.4e+02;
1; Mismatches 1; Indels
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Pred. No. 3.38+02;
1; Mismatches 1; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                splicing factor PRP8 homolog T9A14.60 - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                 C, Accession: S44625
R, Favello, A.D.
submitted to the EMBL Data Library, May 1993
A, Description: Sequence of the C. elegans cosmid C50C3.
A, Reference number: S44627
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Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 61.5%;
Best Local Similarity 71.4%;
Matches 5; Conservative
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1527 FTLWWSP 1533
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FTLWWSP 1357
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A,Gene: ATSP:T9A14.60
A,Map position: 4
1 YALWWSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Accession: S44625
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                                                           1351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Rei
Nature 410, 1091-1096, 2001
A;Title: The highly reduced genome of an enslaved algal nucleus.
A;Reference number: A99082; MUID:11323671; PMID:11323671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Sajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the blology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
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A,Molecule type: DNA
A,Residues: 1-2057 «DOU»
A,Cross-references: UNIPROT:Q9AW36; UNIPARC:UPI00000A2A43; GB:AJ010592; NID:G12580717;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable 4-ALPHA-GLUCANOTRANSFERASE - Mycobacterium tuberculosis (strain H37RV)
C,Species: Mycobacterium tuberculosis
C,Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
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Pred. No. 1.1e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                                     Query Match 61.5%; Score 40; DB 2; Length 618; Best Local Similarity 60.0%; Pred. No. 95; Matches 6; Conservative 2; Mismatches 2; Indels
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                                    C;Genetics:
A;Gene: CESP:E04D5.1
A;Map position: 2
A;Introns: 57/1; 81/2; 107/2; 151/3; 212/1; 305/3; 586/3
C;Superfamily: translation initiation factor eIF-2A
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      A; Experimental source: clone E04D5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match . 61.5%;
Best Local Similarity 55.6%;
Matches 5; Conservative ?
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A;Cross-references: UNIPARC:UP1000013213D; EMBL:U00027; NID:9551319; PID:9551320; MIPS:Y R;Hodges, P.E.; Jackson, S.P.; Brown, J.D.; Beggs, J.D.
A;Title: Extraordinary sequence conservation of the PRPB splicing factor.
A;Reference number: S55355, MUID:95304847; PMID:7785334
A;Accession: S55355, MUID:95304847; PMID:7785334
A;Accession: S55355, MUID:95304847; PMID:7785334
A;Accession: S55355
A;Texas: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-2413 <HOW>A;Residues: 1-2413 <HOWA;D:195-1956 <HOWA;D:195-1957 <HOWA;D:195-1956 <HOWA;D:195-1957 <HOWA;D:1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Description: pre-mRNA splicing C, Keywords: nucleus; pre-mRNA splicing
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Best Local Similarity 75.0
Matches 6; Conservative
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1606 FTLWWSP 1612
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Nyllearnate names: DBP3 protein; protein YHR165c
C; Species: Saccharomyces cerevisiae
C; Date: 31-Dec-1993 #equence revision 31-Dec-1993 #text_change 09-Jul-2004
C; Date: 31-Dec-1993 #equence revision 31-Dec-1993 #text_change 09-Jul-2004
C; Accession: S34670; S48905; $55355; S53613; S51873
R; Hodges, P.E.; Jackson, S.P.; Brown, J.D.; Beggs, J.D.
Submitted to the EMBL Data Library, July 1993
A; Description: Predicted protein sequence of the yeast splicing factor PRPB and of a Nem A; Reference number: S34670
A; Reference number: S34670
A; Accession: S34670
A; Accession: S34670
A; Residues: 1-2413 < HOD>
A; Residues: 1-2413 CHOD>
A; Residues: 1-2413 CHOD>
A; Residues: C.
Experimental Company of the company of
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C; Date: Schizosaccharomyces pombe
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C; Accession: T38841
R; Gentles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
R; Reference number: 221815
A; Accession: T38841
A; Accession: T38841
A; Residues: prellminary; translated from GB/EMBL/DDBJ
A; Residues: 1-2383 - GENA
A; Comperimental source: strain 972h; cosmid c4F8
C; Canetics:
C; Canetics: Comperimental source: strain 972h; cosmid c4F8
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                        Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Scaession: B96832
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-2359 <STO>
A;Residues: 1-2359 <STO>
A;Cross-references: UNIPROT:Q9SSD2; UNIPARC:UP1000009D7F0; GB:AE005173; NID:G5902365; PI
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Pred. No. 3.4e+02;
1; Mismatches 1; Indels
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Pred. No. 3.4e+02;
1; Mismatches 1; Indels
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A, Description: The sequence of S. cerevisiae cosmid 9986.
A, Reference number: $46673
A, Accession: $48905
A, Molecule type: DNA
A, Residues: 1-2413 < MAC>
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71.4%;
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Best Local Similarity 71.4
Matches 5; Conservative
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Best Local Similarity 71.4
Matches 5; Conservative
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1558 FTLWWSP 1564
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1558 FTLWWSP 1564
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Gene: SPDB:SPAC4F8.12c
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A;Map position: 1
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Gape

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Length 2413;

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Conserved hypothetical protein CC2496 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: G87558
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolo:
n, J; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-168 <BES>
A;Cross-references: UNIPROT:Q9XAE9; UNIPARC:UPI0000DB18F; EMBL:AL079356; PIDN:CAB45624.
A;Experimental source: strain A3(2)
C;Genetics:
hypothetical protein SC669.33 - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C;Accession: T35629
R;Seeger, K.J.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, June 1999
A;Reference number: Z21584
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Pred. No. 40;
0; Mismatches
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Gispecies: Helicobacter pylori
Cispecies: Helicobacter pylori
Cipate: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
CiAccession: F64610
Firomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A.Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A; Fitle: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A; Reference number: A64520; MUID:97394467; PMID:9252185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-305 <TOM>
A;Cross-references: UNIPROT:025426; UNIPARC:UPI0000C088D; GB:AE000585; GB:AE000511; NIE
C;Superfamily: Helicobacter hypothetical protein HP0726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: T08544
S.; Savan, M.; Grueneisen, A.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Ma; Subvin, M.; Zimmermann, W.; Grueneisen, A.; Way 1999
Submitted to the Protein Sequence Database, May 1999
A;Reference number: 216442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Accession: T08544
A,Molecule type: DNA
A,Residues: 1-321 <BEV>
A,Residues: 1-321 <BEV>
A,Cross-references: UNIPROT:098205; UNIPARC:UPI00000A3578; EMBL:AL050352; GSPDB:GN00062
A,Experimental source: cultivar Columbia; BAC clone F27B13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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phenylalanine-tRNA ligase (BC 6.1.1.20) alpha chain [validated] - Thermus aq
phenylalanine-tRNA ligase (BC 6.1.1.20) alpha chain
N.Alternate names: phenylalanyl-tRNA synthetase alpha chain
C.Species: Thermus aquaticus
C.Species: Thermus aquaticus
C.Species: 22-Nov-1993 #sequence revision 23-Feb-1996 #text_change 03-Jun-2002
C.Accession: S22366; S25717; $61093; T52502; S21468
R.Keller, B.; Kast, P.; Hennecke, H.
FEBS Lett. 301, 83-88, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 05-Oct-2004
                                                                                                                                                                                              hypothetical protein HP0726 - Helicobacter pylori (strain 26695)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 321;
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Pred. No. 73;
0; Mismatches
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Pred. No. 70;
1; Mismatches
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75.0%;
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Best Local Similarity 75...
6; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
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213 YAILWSPN 220
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LWWRPDG 34
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                LWWSPNG 9
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R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.
; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-1-223 <WIL>
A;Cross-references: UNIPROT:O45276; UNIPARC:UPI000008256C; EMBL:Z81044; PIDN:CAB02810.1;
A;Experimental source: clone C3046
                                                                                                   A,Molecule type: DNA
A,Residues: 1-185 <STO>
A,Cross-references: UNIPROT:Q9ASF4; UNIPARC:UPI00000C7750; GB:AE005673; NID:g13424051; F
C;Genetics:
A;Gene: CC2496
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C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb.2001 #sequence_revision 02-Feb-2001 #text_change 16-Aug-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'Species: Caenorhabditis elegans
'Species: Caenorhabditis elegans
'Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
'Macessimore, B.
'Mortimore, B.
ubmitted to the EMBL Data Library, October 1996
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                      Reference number: A87249; MUID:21173698; PMID:11259647

    Caenorhabditis elegans

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Pred. No. 69;
1; Mismatches
                                                                                                                                                                                                                                                           Score 39; DB 2;
Pred. No. 43;
0; Mismatches 2
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Status: preliminary; translated from GB/EMBL/DDBJ
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Pred. No. 52;
0; Mismatches
A; Title: Complete Genome Sequence of Caulobacter
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C;Superfamily: N-glycosylase/DNA lyase
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ilarity 71.4%;
Conservative
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83.3%;
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Best Local Similarity 75.0
Matches 6; Conservative
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A;Introns: 28/1; 153/1; 171/3
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Matches 5; Conserva
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Best Local Similarity
Matches 5; Conserv
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A, Molecule type: DNA
                                                    A;Accession: G87558
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 LWWSPN
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- Thermus aquaticus

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C;Accession: A27478
R;McClung, C.R.; Somerville, J.E.; Guerinot, M.L.; Chelm, B.K.
R;mclung, C.R.; Somerville, J.E.; Guerinot, M.L.; Chelm, B.K.
A; Miller, 133-139, 1987
A; Title: Structure of the Bradyrhizobium japonicum gene hemA encoding 5-aminolevulinic a A;Reference number: A27478; MUID:87277426; PMID:3609750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:P08262; UNIPARC:UPI000016E709; GB:M16751; NID:g152096; PIDN:
C;Comment: This pyridoxal phosphate enzyme catalyzes the formation of 5-aminolevulinic a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-465 < cbJO>
A; Residues: 1-465 < cbJO>
A; Residues: 1-465 < cbJO>
A; Cross-references: UNIPROT: P20053; UNIPARC: UPI00000530DA; GB: M26597; NID: g172282; PIDN: R; Banroques, J.; Abelson, J.N.
Mol. Cell. Biol. 9, 3710-3719, 1989
A; Title: PRP4: a protein of the yeast U4/U6 small nuclear ribonucleoprotein particle. A; Title: PRP4: a protein of the yeast U4/U6 small nuclear ribonucleoprotein particle. A; Areference number: A32570; MUID: 89384597; PMID: 2528687
A; Accession: A32570
A; Residues: 1-465 < cbAN>
A; Residues: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C.Superfamily: 5-aminolevulinate synthase; glycine C-acetyltransferase homology C;Superfamily: scyltransferase; coenzyme A; phosphoprotein; porphyrin biosynthesis; pyridox P;SO-388/Domain: glycine C-acetyltransferase homology <GCA>F;247/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04/06 snRNP 52K protein - yeast (Saccharomyces cerevisiae)
N/Alternate names: protein P9705.6; protein YPR178w; U4/06 small nuclear ribonucleoprote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Saccharomyces cerevisiae
C;Date: 07-Sep-1990 #sequence revision 07-Sep-1990 #text_change 31-Dec-2004
C;Date: 07-Sep-1990 #sequence revision 07-Sep-1990 #text_change 31-Dec-2004
C;Acession: A32569; A32570; S9835, S07613
R;Petersen-Bjorn, S.; Soltyk, A.; Beggs, J.D.; Friesen, J.D.
Mol. Cell. Biol. 9, 3698-3709, 1989
Mol. Cell. Biol. 9, 3698-3709, 1989
A;Title: PRP4 (RNA4) from Saccharomyces cerevisiae: its gene product is associated with A;Reference number: A93112; MUID:89384596; PMID:2528686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: UNIPARC: UPI00000530DA; EMBL: M28518; NID: 9172280; PIDN: AAA79011.1; P1
                                                                                                                                                                                                                                                                                                        N;Alternate names: delta-aminolevulinate synthase
C;Species: Bradyrhizobium japonicum
C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 39; DB 1;
Pred. No. 92;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-409 <MCC>
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A; Reference number: S22366; MUID:93083630; PMID:1451792
A; Accession: S22366
A; Molecule type: DNA
A; Residues: 1-350 «KEL-
A; Cross-references: UNIPARC:UP100001107A3; EMBL:Z12118; NID:948253; PIDN:CAA78104.1; PID
A; Note: the source is designated as Thermus thermophilus
R; Kreutzer, R.; Kruft, V.; Bobkova, E.V.; Lavrik, O.I.; Sprinzl, M.
Nucleic Acids Res. 20, 4173-4178, 1992
A; Title: Structure of the phenylalanyl-tRNA synthetase genes from Thermus thermophilus H
A; Recence number: S25717; MUID:92375722; PMID:1508711
A; Molecule type: DNA
A; Residues: 1-350 «KRS
A; Cross-references: UNIPARC:UP100001107A3; EMBL:X65609; NID:948250; PIDN:CAA46559.1; PID
A; Note: the source is designated as Thermus thermophilus
A; Accession: S61094
A; Recession: S61094
A; Recession: S61094
A; Recession: S61094
A; Recession: S61094
A; Redule type: protein
A; Recession: S61094
A; Redule type: protein
A; Redules: 1-29 «KMX»
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A;Cress-references: UNIPARC:UPI0000176201
B;Lechler, A.; Kreutzer, R.
J. Mol. Biol. 278, 897-901, 1998
A;Title: The phenylanyl-tRNA synthetase specifically binds DNA.
A;Reference number: 226096
A;Reference number: 226096
A;Residues: 175202
A;Residues: 175202
A;Residues: 17502
A;Residues: 17502
A;Residues: 17502
A;Residues: 17502
A;Residues: 17502
A;Residues: 17502
A;Generces: UNIPARC:UPI00001107A3; EMBL:Y15464; PIDN:CAA75644.1
A;Experimental source: strain HB8
C;Generics:
A;Gene: phes
C;Generics:
A;Gene: phes
C;Generics:
A;Gene: phes
C;Superfamily: phenylalanine-tRNA ligase alpha chain
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
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C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Dec-2004
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Dec-2004
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Dec-2004
C;Accession: Tajandream, M.A.; Barrell, B.G.; Wedler, H.; Kutzner, M.; Wambutt, R.
submitted to the EMBL Data Library, January 1999
A;Reference number: 221944
A;Reference number: 221944
A;Accession: T40673
A;Accession: T40673
A;Residues: DNA
A;Residues: 1-376 <LXN>
A;Residues: 1-376 <LXN>
A;Cross-references: UNIPROT:094671; UNIPARC:UPI0000129356; EMBL:AL035263; PIDN:CAA22876.
C;Genetics:
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C;Species: Schizosaccharomyces pombe
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Pred. No. 79;
2; Mismatches 3; Indels
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85;
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50.0%;
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Best Local Similarity 50.0
Matches 5; Conservative
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267 FAVWWPEGGK 276
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hypothetical protein F12P21.10 [imported] - Arabidopsis thaliana
C;Species Arabidopsis thaliana (mouse-ear cress)
C;Species Arabidopsis thaliana (mouse-ear cress)
C;Accession: C86427
C;Accession: C86427
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
A;Authors: Hunder, J.L.; Janklns, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.C.; Davis, R.W.
A;Authors: Salzberg, S.L.; Schwartz, J.C.; Davis, R.W.
A;Title: Sequence and analyals of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rischulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura submitted to the Protein Sequence Database, May 2000
A;Reference number: Z25022
A;Reference number: Z25022
A;Accession: T49796
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-879 <SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:Q9P549; UNIPARC:UP1000006C5C3; EMBL:AL356324; GSPDB:GN00116
A;Experimental source: BAC clone B9J10; strain OR74A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-802 <STO>
A;Gross-references: UNIPROT:Q9C751; UNIPARC:UPI00000AA76F; GB:AE005172; NID:g11120775;
C;Genetics:
C;Genetics:
A;Genes SGD:SFL1; MIDS:YOR140w
A;Genes SGD:SCD1;
A;Genes SGD:SFL1; MIPS:YOR140w; SGD:SO005666
A;Map position: 15R
C;Superfamily: flocculation suppression protein SFL1; HSF DNA-binding domain homology
C;Reywords: DNA binding; nucleus; transcription regulation
F;65-170/Domain: HSF DNA-binding domain homology <HSF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species; Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 05-Oct-2004
                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                              Length 766
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                                                                                                                                                                                                                                 Score 39; DB 1; I
Pred. No. 1.7e+02;
3; Mismatches 0;
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N,Alternate names: protein B9J10.330
                                                                                                                                                                                                                                    60.0%;
                                                                                                                                                                                                                                                                                                 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                              82 IWWTPSG 88
                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                        3 LWWSPNG 9
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Title: Domains of the SFL1 protein of yeasts are homologous to Myc oncoproteins or year Reference number: JQ0384; MUID:90185205; PMID:2697640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    flocculation suppression protein SFL1 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein 03339; protein YOR140w; protein YOR3339w
C;Species: Saccharomyces cerevisiae
C;Date: 09-Mar-1996 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
C;Accession: S61694; JQ0384; S67025
R;Benes, V.; Andrade, M.A.; Rechmann, S.; Teodoru, C.; Banrevi, A.; Sander, C.; Valencia bubmitted to the EMBL Data Library, December 1995
A;Description: Nucleotide sequence and analysis of a 130 kb fragment of yeast chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :Comment: This protein is involved in cell surface assembly and regulation of the gene
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A;Cross-references: UNIPROT:013670; UNIPARC:UPI000013920F; EMBL:AL031262; PIDN:CAA20319-A;Experimental source: strain 972h-; cosmid c30B4
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Reference number: S66965
                                                                                                                                                                                                                                                                                                                                                                                                                       ucose inhibited division protein a - fission yeast (Schizosaccharomyces pombe)
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C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T40172
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Hilbert, H.; Duesterhoeft, A.
Submitted to the EMBL Data Library, August 1998
A;Reference number: Z21909
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                                                                                           Length 465;
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Cross-references: UNIPARC:UPI000017459F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 39; DB 2; I
Pred. No. 1.5e+02;
                                                                                           Score 39; DB 2;
Pred. No. 1e+02;
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                                                                                                                                                     1; Mismatches
         F;389-424/Domain: WD repeat homology <WD4>F;433-465/Domain: WD repeat homology <WD5>
                                                                                           60.0%;
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83.3%;
                                                                                                                         Best Local Similarity 66.7
Matches 6; Conservative
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C, Superfamily: gidA protein
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353 YTVAWSPNG 361
                                                                                                                                                                                                           1 YALWWSPNG 9
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Gene: SPDB:SPBC30B4.06c
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Length 1072;

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A;Residues: 1-1072 <GLA>
A;Residues: 1-1072 <GLA>
A;Cross-references: UNIPROT:Q8Y6P0; UNIPARC:UPI000005500C; GB:NC_003210; PIDN:CAC99722.1
A;Genetics:
A;Genetics:
                                                                                                                                                                                                         Score 39; DB 2; I
Pred. No. 2.3e+02;
1; Mismatches 1;
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71.4%;
                                                                                                                                                                                                         60.0%;
71.4%;
                                                                                                                                                                                                         Query Match
Best Local Similarity 71.4
Matches 5; Conservative
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Best Local Similarity
Local 5; Conserve
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A;Molecule type: DNA
A;Residues: 1-1223 <STO>
                                                                                                                                                                                                                                                                                                                             1 YALWWSP 7
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A,Gene: lin1685
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NyAlternate names: carboxypeptidase Y

Cispecies: Schizosaccharomyces pombe

Cispecies: Schizosaccharomyces pombe

Cipacies: 11-3na-2000 #sequence_revision 11-Jan-2000 #text_change 05-Oct-2004

CiAccession: T43236; T37997

Ciaccession: T43236; T37997

Dispecies: 05-Oct-2000 #sequence_revision 11-Jan-2000 #text_change 05-Oct-2004

Circustion: T43236; T37997

Dispecies: 07-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 05-Oct-2004

Circustion: T43236; T37997

A;Reference number: Z22357; MUID:97352672; PMID:9209031

A;Reference number: Z22357; MUID:97352672; PMID:9209031

A;Reference number: Z22357; MUID:97352672; PMID:9209031

A;Residues: 1-1002 - TABA

A;Residues: 1-1002 - TABA

A;Residues: 1-1002 - TABA

A;Cross-references: UNIPRO:1013849; UNIPARC:UPI00001271DE; EMBL:D86560; NID:g3046860; PI

R;Oliver, K.; Harris, D.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AD1280
SNF2-type helicase homolog lmol644 [imported] - Listeria monocytogenes (strain EGD-e)
SNF2-type helicase homocytogenes
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AD1280
C;Accession: AD1280
C;Accession: AD1280
C;Accession: AD1280
C;Accession: AD1280
C;Accession: AD1280
D; Jones, L.M.; Karst, U.
D; Jones, L.M.; Karst, U.
D; Jones, L.M.; Karst, U.
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Msok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Experimental source: strain 972h(-); cosmid c19G12; Comment: The mature carboxypeptidase exists as a heterodimer held together by a disulf; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A Map position: I Serine carboxypeptidase (Superfamily: Serine carboxypeptidase (Superfamily: Serine carboxypeptidase (Superfamily: Serine carboxypeptidase (Superfamily: Serine carboxypeptidase (Steywords: disulfide bond: glycoprotein; heterodimer, hydrolase; serine carboxypeptidase (S.19-51/Domain: signal sequence #stetus predicted <8RD- Fig.519-521/Domain: propeptide #stetus predicted <8RD- Fig.510-51/Region: 13-residue repeats (H-H-[RK]-P-G-E-H-M-P-P-P-P-[MF]) Fig.44-425/Region: 13-residue repeats (E-H-H-[RKQ]-G-G-[KE]-[DB]-K) Fig.21-002/Product: carboxypeptidase (E-H-H-[RKQ]-G-G-[KE]-[DB]-K) Fig.7-800/Disulfide bonds: #status predicted Fig.7-800/Disulfide bonds: #status predicted Fig.7-921,978/Active site: Ser, Asp, His #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1002 <OLI>
A;Cross-references: UNIPARC:UPI00001271DE; EMBL:297209; PIDN:CAB10121.1; GSPDB:GN00066; A;Experimental source: strain 972h(-); cosmid c19G12
C;Comment: The mature carbournerist.
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                                    Gaps
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                                 Indels
      Pred. No. 1.9e+02;
0; Mismatches 1;
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87.5%;
                                    7; Conservative
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                                                                                                                                               239 ALSWSPNG 246
                                                                                        2 ALWWSPNG 9
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Best Local Similarity
Matches 6; Conserv
      Similarity
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      Best Local
Matches
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C;Species: Listeria innocus
C;Species: Listeria innocus
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AD1643
C;Accession: AD1643
C;Accession: AD1643
C;Accession: A.; Barcheser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker.
C;Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihl, H.
C; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihl, H.
Science 294, 449-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
A;Authors: Kreft, J.; Kuhn, M.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Reference number: AB1077; MUD::21537279; PMID::11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-1072 <GLA>
A;Cross-references: UNIPROT:Q92B65; UNIPARC:UPI0000CC622; GB:AL592022; PIDN:CAC96916.1;
A;Experimental source: strain Clip11262
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C,Accession: B88451
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog.
A;Reference number: A75000; WID:99069613; PMID:9851916
A;Roces see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele A;Note: published errata appeared in Science 283, 1999; Science 283, 2103, 1999; and A;Accession: E88451
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C;Genetics:
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C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
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Pred. No. 2.3e+02;
1; Mismatches 1;
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Gaps

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Length 3473; Indels

Score 39; DB 1; Pred. No. 7e+02; 2; Mismatches

60.0**%**; 62.5**%**;

5 WSPNGK 10

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A;Cross-references: UNIPROT:QB3034; UNIPARC:UP100000F231A; GB:S57835
C;Superfamily: rice tungro spherical virus genome polyprotein
C;Swyworfs: glycoprotein; polyprotein
F;106,367,903,1018,1274,1311,1385,1665,1755,2291,2779/Binding site: carbohydrate (Asn)
UNIPROT: 083034; UNIPARC: UPI00000F231A; GB: S57835
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A;Molecule type: DNA
A;Residues: 1-2403 <LUE>
A;Cross-references: UNIPROT:015881; UNIPARC:UPI000080703; EMBL:Y12638; NID:e1044898; PI
C;Genetics:
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A;Molecule type: DNA
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A;Residues: 1-2924 <BAR>
A;Cross-references: UNIPROT:Q25733; UNIPARC:UPIO000079077; EMBL:U27338; NID:g914918; PID
C;Genetics:
A;Gene: EMP1
A;Introns: 2476/3
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C;Accession: T18378
R;Baruch, D.I.; Pasloske, B.L.; Singh, H.B.; Bi, X.; Ma, X.C.; Feldman, M.; Taraschi, T.Cell 82, 77-87, 1995
A;Title: Cloning the P. falciparum gene encoding PfEMP1, a malarial variant antigen and A;Reference number: Z18925; MUID:95330812; PMID:7541722
                                                                                                                                                                                                                                                                                                                      EMBO J. 16, 4433-4440, 1997
A;Title: Trans mRNA splicing in trypanosomes: cloning and analysis of a PRP8-homologuos
A;Reference number: Z20915; MUID:97392473; PMID:9250687
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Virology 193, 621-630, 1993
A;Title: Nucleotide sequence and genomic organization of rice tungro spherical virus.
A;Reference number: A46112; MUID:93212494; PMID:8460478
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N,Alternate names: erythrocyte membrane binding protein 1 (BMP1)
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                                                                                                                                                                                                                                   Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
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C;Species: rice tungro spherical virus
                                                                                                                                                                                                                                                                                         Luecke, S.; Kloeckner, T.; Palfi, Z.; Boshart, M.; Bindereif, A.
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A, Molecule type: genomic RNA
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Mammalia, Butheria, Euarchontoglires; Primates; Catarrhini; Hominidae;
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Charge relay system (By similarity).
Charge relay system (By similarity).
N-linked (GlCNAC...) (Potential).
Missing (in isoform 2).
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InterPro; IPR001375; Peptidase_S9.
InterPro; IPR001375; Peptidase_S9B.
InterPro; IPR001379; Ser setrs.
Pfam; PF00930; DPPIV N; 1.
Pfam; PF00326; Peptidase_S9; 1.
PROSITE; PS00708; PRO EMBER S9; 1.
PROSITE; PS00708; PRO EMBER SBR; 1.
SD_structure; Alternative splicing; Direct protein sequencing; Glycoprotein; Hydrolase; Polymorphism; Protease; Serine protease;
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Signal-anchor for type II membrane
protein (Potential).
Extracellular (Potential).
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R -> T (in dbSNP:1126507)
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Ensembl; ENSG00000078098; Homo sapiens:
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EMBL; BC026250; AAH26250.1; -; mRNA.
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1D 05
1D 05
1D 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Atlauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A plopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hashe F.,
A papleton M., Soarse M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
Brownstein M.J., Usdin T.B., Toobhlyuki S., Carninci P., Prange C.,
A Brownstein M.J., Usdin T.B., Toobhlyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Hitlalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
A Halton E., Ketreman M., Madan A., Sodingues S., Sanchez A.,
A Hitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Hutterfield Y.S.N., Krzywinski M.I., Schalbka U., Smallus D.E.,
A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
A mouse onth services "...
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MEDLINE-94327249; PubMed=7519584;
Rettig W.J., Su S.L., Fortunato S.R., Scanlan M.J., Raj B.K.M.,
Rettig W.J., Su S.L., Portunato S.R., Scanlan M.J., Raj B.K.M.,
Fibroblast activation protein: purification, epitope mapping and
induction by growth factors.";
Int. J. Cancer 58:385-392(1994).
Int. J. Cancer 58:385-392(1994).
and wound healing, and may contribute to invasiveness in malignant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=2; Synonyms=S, Truncated; 18016-2; Squence-VSP_005367; 18016-612884-2; Sequence-VSP_005367; TISSUE SPECIFICITY: Fibroblasts at times and sites of tissue remodeling during development, tissue repair, and carcinogenesis. PTM: N-q1ycosylated. PTM: The N-terminus may be blocked. SIMILARITY: Belongs to the peptidase S9B family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Goldstein L.A., Chen W.T.; "Identification of an alternatively spliced seprase mRNA that encodes a novel intracellular isoform."; J. Biol. Chem. 275:2554-2559(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATALYTIC ACTIVITY: Degrades gelatin and heat-denatured type I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Type II membrane protein. Found in cell surface lamellipodia, invadopodia and on shed vesicles. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     type IV collagen, but not native type I or type IV collagen. not cleave laminin, fibronectin, fibrin or casein. SUBUNIT: Homodimer, or heterodimer with DPP4. The monomer is
                                                                                                                                                                                                                      "dentification of the 170-kDa melanoma membrane-bound gelatinase (seprase) as a serine integral membrane protease.";
                                                                                                     MEDLINE=97218181; PubMed=9065413; DOI=10.1074/jbc.272.12.7595; Pineiro-Sanchez M.L., Goldstein L.A., Dodt J., Howard L., Yeh Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1), AND VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20112818; PubMed=10644713; DOI=10.1074/jbc.275.4.2554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=1; Synonyms=L;
IsoId=Q12884-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                  (вергаве) ав а serine integral mem
J. Biol. Chem. 272:7595-7601(1997)
                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE (ISOFORM 2). TISSUE=Melanoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note=Major isoform;
                                461-472 AND 511-518
                                                                        TISSUE=Melanoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Placenta;
                                                                                                                                                                                         Chen W.-T.;
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11 XENLA
Q91651 XENLA PRELIMINARY;
Q91651;
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Best Local Similarity 90.0
Matches 9; Conservative
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                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
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(C. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murines; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A Wilson K.A. Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases. EMBL; AC007750; AAY24205.1; -; Genomic_DNA.

R GO; GO:0016020; C:membrane; IEA.

R GO; GO:0003824; F:catalytic activity; IEA.

GO; GO:0004274; F:dipeptidy1-peptidase IV activity; IEA.

GO; GO:0004277; F:proly1 oligopeptidase activity; IEA.

GO; GO:0004277; P:proly1 oligopeptidase activity; IEA.

R InterPro; IPR001375; Peptidase_S9.

R InterPro; IPR001375; Peptidase_S9.

R InterPro; IPR001375; Peptidase_S9.

R Pfam; PF00930; DPPIV N, I.

R Pfam; PF00930; Peptidase_S9: I.

R Pfam; PF00930; PRO_ENDOPEP SER; I.

R PROSITE; PS00708; PRO_ENDOPEP SER; I.

W Hydrolase; Hypothetical protein; Transmembrane.

SEQUENCE 760 AA; 87713 MW; 7FF817B5A4F75142 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 65; DB 2; Length 760; 100.0%; Pred. No. 0.081; ive 0; Mismatches 0; Indels
                                                                                 Cotton M., Maupin R., Hawkins M., Harkins R.; "The sequence of Homo sapiens BAC clone RPI1-576I16."; Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                    Waterston R.H.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                   Waterston R.; -
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
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Q6P7D6;
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                                                         NUCLEOTIDE SEQUENCE.
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NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fap protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=Fap
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Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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MEDLINE=96312514; PubMed=8700860; DOI=10.1073/pnas.93.5.1924;
Brown D.D., Wang Z., Furlow J.D., Kanamori A., Schwartzman R.A.,
Remo D.F., Pinder A.;
"The thyroid hormone-induced tail resorption program during Xenopus
laevis metamorphosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xenopus laevis (African clawed frog).
Subtayota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Amura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Xenopus.
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                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; BC061713; AAH61713.1; -; mRNA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0004274; F:dipeptidy1-peptidase IV activity; IEA.
GO; GO:0006508; P:proteclysis and peptidolysis; IEA.
InterPro; IPR02469; Peptidase_S9B.
Pfam; PF00930; DPPIV N; 1.
SEQUENCE 350 AA; 40869 MW; 49FF2846A9CF0F7F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. (U.S.A. 93:1924-1929(1996).

EMBL; U41856; AAC59872.1; -; mRNA.

HSSP; P27487; 1PPQ.

GO: 00004177; F:aminopeptidase activity; IEA.

GO: GO:0004274; F:dipeptidyl-peptidase IV activity; IEA.

GO: GO:0006287; F:pydrolyge activity; IEA.

GO: GO:0006487; F:pydrolyl oligopeptidase activity; IEA.

GO: GO:0006508; P:proteolygis and peptidolysis; IEA.
                                                                                                                                                                                                                                                                                                                                        TISSUE=Prostate;
NIH MGC Project;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                  and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92.3%; Score 60; DB 2;
90.0%; Pred. No. 0.51;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92.3%; Score 60; DB 2;
90.0%; Pred. No. 0.23;
iive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       755 AA.
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Pfam; PF00326; Peptidase S9; 1.
PROSITE; PS00708; PRO_ENDOPEP_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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Name=gene 13;
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InterPro; IPR001375; Peptidase S9.
InterPro; IPR002469; Peptidase S9B.
InterPro; IPR000379; Ser estrs.
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embryos from day 7-19 and in new-born mice (P1).
SIMILARITY: Belongs to the peptidase S9B family.
                                                                                                           removed.
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haiteh F.,

D. Bratchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glbbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mynting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

B Butterfield Y.S.N., Krzywinski M.I., Schalk U., Smallus D.E.,

B Cheretion and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: Degrades gelatin and heat-denatured type I and
                                                                                                                                                                                                                                                                                                                                                        STRAIN=BALB/c; TISSUE=Embryo;
MEDLINE=97284459; PubMed=9139873;
Niedermeyer J., Scanlan M.J., Garin-Chesa P., Daiber C., Fiebig H.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences."; Proc. 0.16903 (2002).

Proc. Natl. Acad. 561. U.5.A. 99:16899-16903 (2002).

-!- FUNCTION: May have a role in tissue remodeling during development and wound healing, and contribute to invasiveness in malignant
                                                                                                                                                                      28-FBB-2003 (Rel. 41, Last sequence update)
10-MAY-2005 (Rel. 4), Last annotation update)
Seprase (BC 3.4.21.-) (Fibroblast activation protein alpha) (Integral
membrane serine protease).
                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=P97321-3; Sequence=VSP_005369;
TISSUE SPECIFICITY: Detected in fibroblasts, in placenta, uterus,
                                                                                                                                                                                                                                                                                                                                                                                                  Old L.J., Rettig W.J., Schnapp A.; "Mouse fibroblast activation protein: molecular cloning, alternative splicing and expression in the reactive stroma of epithelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     type IV collagen, but not native type I or type IV collagen. Do not cleave laminin, fibronectin, fibrin or casein.
--- SUBUNIT: Homodimer, or heterodimer with DPP4. The monomer is inactive (By similarity).
--- SUBCELLULAR LOCATION: Type II membrane protein (By similarity).
--- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Event=Alternative splicing; Named isoforms=3;
                                                                                                                           761 AA
                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE (ISOFORMS 1; 2 AND 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=P97321-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               int. J. Cancer 71:383-389(1997).
                                                                                                                                                        28-FEB-2003 (Rel. 41, Created)
                                                                                                                           STANDARD;
                                          207 YATWWSPNGK 216
                     1 YALWWSPNGK 10
                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=1;
                                                                                                                           MOUSE
                                                                                                                                                                                                                                     Name=Fap;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancers
                                                                                                             MOUSE
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Charge relay system (By similarity).
Charge relay system (By similarity).
Charge relay system (By similarity).
N.linked (GlCNAc. ) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Signal anchor for type II membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 60; DB 1; Length 761;
                                                                                                                                                                                                                                                                                                                                                                                                        Zuckschwerdt K., Park J.E.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF493782; AAM11677.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Extracellular (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9174C3AEDA213B25 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Pibroblast activation protein alpha subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Missing (in isoform /FTId=VSP_005369.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-linked (GlcNAc.
N-linked (GlcNAc.
N-linked (GlcNAc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 0.51;
                                                                                                                                                                                                                                MINEMENT, MOST ENSWISSON MOSON 192; Mus musculus. MGI; MGI:109608; Fap. GO; GO:0016021; C:integral to membrane; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
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                                                                                                                                           EMBL, Y10007, CAA71116.1; -; mRNA.
EMBL; BC019190; AAH19190.1; -; mRNA.
HSSP; P27487; 1PFQ.
                                                                                                                                                                                                                                                                                                InterPro; IRR002471; Pept. S9_MS.
InterPro; IPR001375; Peptidase_S9.
InterPro; IPR002469; Peptidase_S9B.
InterPro; IPR00349; Ser estrs.
Pfam; PF00300; DPPVV_N; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87945 MW;
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01-JUN-2002 (TrEMBLrel. 21,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8R492 RAT
ID Q8R492 RAT PRELIMINARY;
AC Q8R492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   210 YALWWSPDGK 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    761 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10116;
                                                                                                                                                                                                               MEROPS; S09.007;
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CARBOHYD
CARBOHYD
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Name=DPP4a;
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                                                                                                                                                  075583
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name-DPP4b;
Agkistrodon halys brevicaudus (Korean slamosa snake) (Gloydius halys
brevicaudus).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
Viperidae, Crotalinae, Gloydius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                   REROPS, SOB. 007; -...
RENGORS, SOB. 007; -...
REGEMEN, ENSRNOG0000005679; Rattus norvegicus.
RGD; 621253; Fap.
GO; GO:0014077; F:aminopeptidase activity; IEA.
GO; GO:0004274; Fidpeptidyl-peptidase IV activity; IEA.
GO; GO:0004274; F:hydrolase activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
R GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
R InterPro; IPR002471; Pept S9 AS.
R InterPro; IPR002471; Peptidase_S9.
R InterPro; IPR002469; Peptidase_S9.
R InterPro; IPR00347; Peptidase_S9.
R Pfam; PF00303; DPPIV N; I.
R Pfam; PF00303; Peptidase_S9; R Pfam; PF00304; Peptidase_S9; R Pfam; PF00305; Pfam; Pfam; Pf00305; Pfam; Pfam; Pf00305; Pfam; Pf00305; Pfam; Pf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.6%; Score 55; DB 2; Length 751;
88.9%; Pred. No. 3.1;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92.3%; Score 60; DB 2; Length 761; 90.0%; Pred. No. 0.51; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolage; Transmembrāne.
SEQUENCE 761 AA; 87843 MW; EB214BBE4BB14F2C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86155 MW; DAF219B4FEE7629A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00326; Peptidase_S9; 1.
PROSTITE; PS00708; PRO_ENDOPEP_SER; 1.
Hydrolase; Transmembrane.
SEQUENCE 751 AA; 86155 WW; DAF2191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dipeptidy peptidase 4b (EC 3.4.14.5)
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Q75S82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               110 YALWWSPDGK 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 YALWWSPNGK 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
HSSP; P27487; 1PFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=259325;
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Plaviviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLECTIDE SEQUENCE.

NUCLECTIDE SEQUENCE.

A Richard M., Lamson D., Wroblewski D., Reilly A., Philpott S.,

A Kleiner M., Lamson D., Wroblewski D., Reilly A., Philpott S.,

A Kleiner D., Holman S., Augenbraun M., Taylor J.;

AT FOURTO Confected Subjects.;

BY HCV/HIV Coinfected Subjects.;

RL Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.

BR GNHS, ANGBS622, AAT94269.1; -; Genomic_RNA.

BR SMR, Q68K44: 1-552.

BR GO, GO:000524; F:AFT binding; IEA.

GO, GO:000524; F:AFT dependent helicase activity; IEA.

GO, GO:000676; F:AFT-dependent helicase activity; IEA.

GO; GO:000676; F:Ndrolase activity; IEA.
                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Gloydius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Venom gland;
A Ogawa Y., Yanoshita R., Murayama N., Higuchi S., Samejima Y.;
Lisbuaitred (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; ABI58224; BAD063212.1; -; mRNA.
EMBL; ABI58224; BAD06323.1; -; mRNA.
GO; GO:000477; F:aminopeptidase activity; IEA.
GO; GO:0004774; F:iminopeptidase activity; IEA.
GO; GO:0004774; F:iminopeptidase activity; IEA.
GO; GO:0004274; F:iprolyl oligopeptidase activity; IEA.
GO; GO:000508; P:proteolysis and peptidolysis; IEA.
R GO; GO:000508; P:proteolysis and peptidolysis; IEA.
R InterPro; IPR002471; Peptidase_S9.
R InterPro; IPR001375; Peptidase_S9.
R InterPro; IPR001375; Ser_estrs.
R Pfam; PF00930; DPPIV N; I.
R Pfam; PF00930; DPPIV N; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       751 AA; 86127 MW; 6EA3F2D829BE97D4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update).
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Polyprotein (Fragment).
                                                                05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84.6%; Score 55; DB 2;
88.9%; Pred. No. 3.1;
ive 1; Mismatches (
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                                                                                                                                                       Dipeptidylpeptidase 4a (EC 3.4.14.5)
Q75583 AGKHB PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q68K44_9HEPC PRELIMINARY;
Q68K44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hydrolase; Transmembrane
SEQUENCE 751 AA; 8612
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NCBI_TaxID=11103;
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212 ALWWSPNG 219
211 ALWWSPNG 218
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                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Kidney
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P27487;
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DPP4_HUMAN
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-CB; TISSUE-Bursa;
Caldwell R.B., Kierzek A.M., Arakawa H., Bezzubov Y., Zaim J.,
Fiedler P., Kutrer S., Blagodatski A., Kostovska D., Koter M.,
Plachy J., Carninci P., Hayashizaki Y., Buerstedde J.M.;
"Full-length cDNAs from chicken bursal lymphocytes to facilitate
genefunction analysis.";
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                                                                                                                                                                                                                                          SMART; SM00490; DEZDC; ].
SMART; SM00490; HELICC; 1.
ATP-binding; Capsid protein; Helicase; Hydrolase; Polyprotein;
Structural protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Score 54; DB 2; Length 659;
Pred. No. 4;
1; Mismatches 0; Indels
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0004177; F:aminopeptidase activity; IEA.
GO; GO:0004274; F:dipeptidyl-peptidase IV activity; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0004287; F:hydrolase activity; IEA.
GO; GO:0006287; F:prolyl oligopeptidase activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
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PR0SITE; PS00708; PR0 ENDOPEP: SER; 1.
Hydrolase; Hypothetical protein; Transmembrane.
SEQUENCE 759 AA; 86343 WW; B9A0C38CCB8644AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                     659
70398 MW; 2ACAEB1F20ADF453 CRC64;
      GO:0008236; F:serine-type peptidase activity; IEA. GO:0006508; P:proteolysis and peptidolysis; IEA. GO:0019087; P:viral transformation; IEA.
                           proteolysis and peptidolysis; IEA.
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Last annotation update)
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100.0%; Pred. No. 6.6;
iive 0; Mismatches (
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                                                                   InterPro: IPR001410; DEAD.
InterPro: IPR001416; DEAD/DEAH N.
InterPro: IPR001045; HCV NS4a.
InterPro: IPR001045; HCV NS4a.
InterPro: IPR004109; Peptidase_S29.
Ffan; PF001006; HCV NS3; 1.
Ffan; PF001006; HCV NS4; 1.
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Interpro; IPR001375; Peptidase S9.
Interpro; IPR001469; Peptidase S9.
Interpro; IPR000379; Ser estrs.
Pfam; PF00930; DPPIV N; I
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25-OCT-2004 (TrEMBLrel. 28, Le
25-OCT-2004 (TrEMBLrel. 28, Le
Hypothetical protein.
ORFNames=RCJMB04 29g21,
Gallus gallus (Chicken).
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88.9%;
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Best Local Similarity 88.55,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QSZIB1_CHICK PRELIMINARY;
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Best Local Similarity
Matches 8; Conserv
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NON TER
SEQUENCE
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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01-FBS-1996 (Rel. 33, Last sequence update)
13-SEB-2005 (Rel. 48, Last annotation update)
13-SEB-2005 (Rel. 48, Last annotation update)
13-SEP-2005 (Rel. 49, Last annotation update)
10-peptidase 4 (EC 3.4.14.5) (Dipeptidyl peptidase IV) (DPP
1V) (T-cell activation antigen CD26) (TP103) (Adenosine deaminase
complexing protein 2) (ADABP) (Contains Dipeptidyl peptidase 4
membrane form (Dipeptidyl peptidase IV membrane form); Dipeptidyl
peptidase 4 soluble form (Dipeptidyl peptidase IV soluble form)].
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Pred. No. 6.7;
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GO; GO:0004177; F:aminopeptidase activity; IEA.
GO; GO:0004274; F:dipeptidy1-peptidase IV activity; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0004287; F:proly1 oligopeptidase activity; IEA.
GO; GO:0006508; P:proteolygis and peptidolygis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002471; Pept 59_AS.
InterPro; IPR001375; Peptidase S9.
InterPro; IPR00379; Ser estrs
InterPro; IPR000379; Ser estrs
Pfam; PF00326; Peptidase S9; 1.
PROSITE; PS00708; PRO ENDOPEP SER; 1.
Hydrolase; Hypotherical protein; Transmembrane.
SEQUENCE 765 AA; 88038 MW; 6F81ECD98C3D2397 CRC64;
                                                                        Last sequence update)
Last annotation update)
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100.0%; Pred. No. c.
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                                                    Created)
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SMR; Q5R7G7; 38-765.
     PRT;
                                              01-FEB-2005 (TrEMBLrel. 29, Created 01-FEB-2005 (TrEMBLrel. 29, Last se 01-FEB-2005 (TrEMBLrel. 29, Last an Hypothetical protein DKFZp469P1419.
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                                                                                                                                                                                                                                                                                                                                                                            The German cDNA Consortium;
                                                                                                                                                                                 Pongo pygmaeus (Orangutan)
QSR7G7 PONPY PRELIMINARY;
QSR7G7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Conservative
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TISSUE=Liver;
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NUCLECTIDE SEQUENCE [LARGE SCALE MRNA].

NUCLECTIDE SEQUENCE [LARGE SCALE MRNA].

TISSUE-Prostate, and Uterus;

A Straubberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

A Straubberg R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Alschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Alschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopking R.F., Jordan H., Moore T., Max S.I., Wang J., Hoish F.,

Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Tochhyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Wakin P.M., Sodergren B.J., Lu X., Glibbs R.A.,

Brownstein M. Madan P.J., McKernan M., Madan A., Glibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Whiting M., Madan A., Young A., Schenko Y., Bouffard G.G.,

Rhakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rhakesley R.W., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

R. Generation and initial analysis of more than 15,000 full-length human
MEDLINE=92329551; PubMed=1352704; DOI=10.1016/0167-4781(92)90036-Y; Misumi Y., Hayashi Y., Arakawa F., Ikehara Y.; "Molecular clonfing and sequence analysis of human dipeptidyl peptidase IV, a serine proteinase on the cell surface."; Biochim. Biophys. Acta 1131:333-336(1992).
                                                                                                                                                                                                                                                                                                                                TISSUE-Peripheral blood, MEDINE-92325476; PubMed=1352530; Tanaka T., Camerini D., Seed B., Torimoto Y., Dang N.H., Kameoka J., Dahlberg H.N., Schlossman S.F., Morimoto C.; Cloning and functional expression of the T cell activation antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Dipoptidy's peptidase IV (CD 26) gene expression in enterocyte-like colon cancer cell lines HT-29 and Caco-2. Cloning of the complete human coding sequence and changes of dipoptidyl peptidase IV mRNA levels during cell differentiation."; ippoptidyl peptidase IV mRNA J. Biol. Chem. 267:4824-4833(1992).
                                                                                                                                                                            MEDLINE=95012454; PubMed=7927537;
Abbott C.A., Baker E., Sutherland G.R., McCaughan G.W.;
"Genomic organization, exact localization, and tissue expression of
the human CD26 (dipeptida) peptidase IV) gene.";
Immunogenetics 40:331-338(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Darmoul D., Lacasa M., Baricault L., Marguet D., Sapin C., Trotot
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92165847; PubMed=1347043;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=93171637; PubMed=8094732;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunol. 150:2090-2090(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Immunol. 149:481-486(1992).
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NUCLEOTIDE SEQUENCE OF 1-31.
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                                                                                                                                        NUCLEOTIDE SEQUENCE.
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                                                                                                                                                              TISSUE-Placenta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tanaka T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                               CD26.";
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Zaa-, from a polypeptide, preferentially when Yaa is Pro, provided Zaa is neither Pro nor hydroxyproline.
SUBUNIT: Homodimer or heterodimer with Seprase (FAP).
SUBCELLULAR LOCATION: Type II membrane protein. Also exists in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE SPECIFICITY: Expressed in the poorly differentiated crypt cells of the small intestine as well as in the mature villous cells. Expressed at very low levels in the colon.

FIM: The soluble form (SDPP) derives from the membrane form (MDPP) by proteolytic processing.

SIMILARITY: Belongs to the peptidase S9B family. DPPIV subfamily.
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PubMed=12906826; DOI=10.1016/S0969-2126 (03) 00160-6;
PubMed=12906826; DOI=10.1016/S0969-2126 (03) 00160-6;
PubMed=12906826; DOI=10.1016/S0969-2126 (03) 00160-6;
Structural basis of proline-specific exopeptidase activity as observed in human dipeptidy peptidase-IV.";
Structure 11:947-959(2003)
-!- FUNCTION: Removes N-terminal dipeptides sequentially from polypeptides having unsubstituted N-termini provided that the penultimate residue is proline. Plays a role in T cell activation.
-!- CATALYTIC ACTIVITY: Release of an N-terminal dipeptide, Xaa-Yaa-|-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 39-766, HOMODIMERIZATION, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 35-771, HOMODIMERIZATION, AND
                                                                                                                                                                                                                                          "Expression of sucrase-isomaltase and dipeptidylpeptidase IV in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "High-resolution structure of human apo dipeptidyl peptidase IV/CD26 and its complex with 1-[([2-[(5-iodopyridin-2-yl)amino]-ethyl]amino) acetyl]-2-cyano-(S)-pyrrolidine.";
Acta Crystallogr. D 59:1206-1212(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-GLYCOSYLATION SITES.
PubMed=12483204; DOI=10.1018/nsb882;
Rasmussen H.B., Branner S., Wiberg F.C., Wagtmann N.;
"Crystal structure of human dipeptidyl peptidase IV/CD26 in complex
                                                                                                                                                                                                                                                                                                                                                                                                                                         "A marker for neoplastic progression of human melanocytes is a cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 38-766 IN COMPLEX WITH
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                  Boehm S.K., Gum J.R. Jr., Erickson R.H., Hicks J.W., Kim Y.S.; "Human dipeptidyl peptidase IV gene promoter: tissue-specific regulation from a TATA-less GC-rich sequence characteristic of housekeeping gene promoter."
                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93210468; PubMed=8096237; DOI=10.1084/jem.177.4.1135; Morrison M.E., Vijayasaradhi S., Engelstein D., Albino A.P., Houghton A.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-GLYCOSYLATION SITES.
PubMed=12646248; DOI=10.1016/S0006-291X (03) 00258-4;
PubMed=12646248; DOI=10.1016/S0006-291X (03) 00258-4;
Hiramatsu H., Kyono K., Higashiyama C., Fukushima C., Shima H. Sugiyama S., Inaka K., Yamamoto A., Shimizu R.;
The structure and function of human dipeptidyl peptidase IV, possessing a unique eight-bladed beta-propeller fold.";
Biochem. Biophys. Res. Commun. 302:849-854(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oefner C., D'Arcy A., Mac Sweeney A., Pierau S., Gardiner R.,
                                                                                                                                                                                          Gorvel J.P., Ferrero A., Chambraud L., Rigal A., Bonicel J.,
                                                                                                                                                   PROTEIN SEQUENCE OF 1-22, AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INHIBITOR, AND HOMODIMERIZATION.
PubMed=12832764; DOI=10.1107/S0907444903010059;
                                                                                                                                                                                                                                                                                        Gastroenterology 101:618-625(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Struct. Biol. 10:19-25(2003).
MEDLINE=96067599; PubMed=7487939;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       surface ectopeptidase.";
J. Exp. Med. 177:1135-1143(1993)
                                                                                       housekeeping gene promoter.";
Biochem. J. 311:835-843(1995).
                                                                                                                                                                                                                                                                    small intestine and colon.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a substrate analog.";
                                                                                                                                                                                                                                                                                                                                    PARTIAL PROTEIN SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              soluble form.
                                                                                                                                                                              PubMed=1677636;
                                                                                                                                                                                                                                                                                                                                                           TISSUE=Kidney;
                                                                                                                                                                                                                             Maroux S.;
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NUCLEOTIDE SEQUENCE OF 2-67.
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     This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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PubMed=14719797; DOI=10.1515/BC.2003.172;
PubMed=14719797; DOI=10.1515/BC.2003.172;
Base J., Weber A., Hoffmann T., Stork J., Wermann M., Wagner L.,
Aust S., Gerhartz B., Demuth H.-U.;
"Characterisation of human dipeptidyl peptidase IV expressed in Pichia pastoris. A structural and mechanistic comparison between the recombinant human and the purified porcine enzyme.";
Biol. Chem. 384:1553-1563(2003).
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AC P22411; Q866G2;
DT 01-AUG-1991 (Rel. 19, Created)
DT 13-SEP-2004 (Rel. 45, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DF Dipeptidal peptidase 4 (EC 3.4.14.5) (Dipeptidal peptidase IV) (DPP DE IV) (T-Cell activation antiqen CD26) (Contains: Dipeptidyl peptidase 4 DE IV) (P-Cell activation antiqen CD26) (Contains: Dipeptidyl peptidase B DE IV) (DPP D
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Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
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AABGOGG.1; JOINED; Genomic_DNA,
BABGOGGG.1; JOINED; Genomic_DNA,
AABGOGGG.1; JOINED; Genomic_DNA,
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AAB60646.1; JOINED; G
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U13710; AAB60646.1;
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Best Local Similarity 100.
Matches 8; Conservative
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PIR; 1.5
PDB; 10RW; X-ray; ..,
PROPS; S09.003; -.

A InterPro; IPR002469; Peptidase_S9.
DR InterPro; IPR001375; Peptidase_S9.
DR InterPro; IPR001375; Peptidase_S9.
DR Pfam; PP00326; Peptidase_S9; 1.
DR Pfam; PP00326; Peptidase_S9; 1.
DR Pfam; PR00326; Peptidase_S9; 1.
DR PROSITE; PS00708; PRO ENDOPEP_SRR; 1.
DR PROSITE; PS00708; PROSITE PROSI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       soluble form.
--- prm: The soluble form (SDPP) derives from the membrane form (MDPP) by proteolytic processing.
---- SIMILARITY: Belongs to the peptidase S9B family. DPPIV subfamily.
                                                                                                                                                                                                                                                                                               MEDLINE=91273813; PubMed=1675855;
Seidl R., Mann K., Schaeffer W.;
"N-terminal amino-acid sequence of pig kidney dipeptidyl peptidase IV
solubilized by autolysis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Type II membrane protein. Also exists in a
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Charge relay system (By similarity).
Charge relay system (By similarity).
N-linked (GloNAc. .).
N-linked (GloNAc. .).
N-linked (GloNAc. .) (By similarity).
                                                                               "Assignment of the dipeptidylpeptidase IV (DPP4) gene to pig chromosome 15q21.";
                         Thomsen P.D., Qvist H., Marklund L., Andersson L., Sjostrom
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biol. Chem. Hoppe-Seyler 372:213-214(1991).
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EMBL, X73276; CAA51717.1; -; mRNA.
PIR, 147134; 147134.
PDB; 10RV; X-ray; A/B/C/D=39-766.
PDB; 10RW; X-ray; A/B/C/D=39-766.
SMR; P22411; 39-766.
MEDLINE=94093209; PubMed=7903569;
                                                                                                                                                                       Mamm. Genome 4:604-607(1993).
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DPP4 RAT
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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  | (GlCNAc. . .) (By similarit | (GlCNAc. . .) |
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GO; GO:0003824; F:catalytic activity; IEA.
GO; GO:0004274; F:catalytic activity; IEA.
GO; GO:0004274; F:prolyl oligopeptidase IV activity; IEA.
GO; GO:0004287; F:prolyl oligopeptidase activity; IEA.
GO; GO:0006508; F:prolyl oligopeptidase activity; IEA.
GO; GO:0006508; F:prolyl oligopeptidase activity; IEA.
InterPro; IPR00317; Peptidase_S9.
InterPro; IPR00317; Peptidase_S9.
InterPro; IPR00319; Ser estre.
Pfam; PF00310; DPPIV N, I.
Pfam; PF00310; PP0 ENDORFP SER; I.
PROSTIE; PS00708; PPO ENDORFP SER; I.
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6.7;
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Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; AC0080631; AAX93179.1; -; Genomic_DNA.
SMR; Q53TN1; 39-766.
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Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases
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Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases
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88279 MW, SFB4A2C6662D6117 CRC64;
                                                                                                                                                                                                                                                                     32 Missing (in Ref. 2).
88242 MW; 8800D520BAEA856D CRC64;
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein DPP4.
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Beet Local Similarity 100.v.
Be-Local Similarity 6, Conservative
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Q53TN1;
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SEQUENCE 766 AA; 882
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Matches 8; Conserva'
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NUCLEOTIDE SEQUENCE.
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766 AA;
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CONFLICT
SEQUENCE
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MEDLINE-52190188; PubMed=1347701; Ogata S., Misumi Y., Tsuji E., Takami N., Oda K., Ikehara Y.; Ogata S., Misumi Y., Tsuji E., Takami N., Oda K., Ikehara Y.; Idantification of the active site residues in dipeptidyl peptidase IV affinity labeling and site-directed mutagenesis."; Biochemistry 31:25882-2587(1992).
                                                                                                                                                                      01-ARR-1990 (Rel. 14, Created)
01-FEB-2005 (Rel. 46, Last sequence update)
11-SEP-2005 (Rel. 48, Last annotation update)
Dipeptidal peptidase 4 (EC 3.4.14.5) (Dipeptidyl peptidase IV) (DPP
IV) (T-cell activation antigen CD26) (GP110 glycoprotein) (Bile canaliculus domain-specific membrane glycoprotein) (Contains: Dipeptidal peptidase 4 membrane form (Dipeptidyl peptidase IV membrane form); Dipeptidyl peptidase 4 soluble form (Dipeptidyl peptidase IV membrane soluble form); Dipeptidyl peptidase 4 soluble form (Dipeptidyl peptidase IV 60 kDa soluble form (Dipeptidyl)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLECTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.
MEDLINE=89123496; PubMed=2563382;
Ogata S., Misumi Y., Ikehara Y.;
Primary structure of rat liver dipeptidyl peptidase IV deduced from its cDNA and identification of the NH2-terminal signal sequence as the membrane-anchoring domain.";
                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEIN SEQUENCE OF 28-58, AND TISSUE SPECIFICITY.
MEDLINE=90228896; PubMed=1970322;
McCaughan G.W., Wickson J.E., Creswick P.F., Gorrell M.D.;
"Identification of the bile canalicular cell surface molecule GP110
the ectopeptidase dipeptidyl peptidase IV: an analysis by tissue
distribution, purification and N-terminal amino acid sequence.";
Hepatology 11:534-544(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Iwaki-Egawa S., Watanabe Y., Fujimoto Y.;
"N-terminal amino acid sequence of the 60-kDa protein of rat kidney
dipeptidyl peptidase IV.";
Biol. Chem. Hoppe-Seyler 374:973-975(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [5]
SEQUENCE OF 281-302, AND MUTAGENESIS OF GLY-629; TRP-630; SER-631; TRY-632 AND GLY-633.
TISSUE-Kidney; PubMed=7905271;
MEDLINE=94128239; PubMed=7905271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
MEDLINE-88068516; PubMed=3479775;
Hong W., Doyle D.;
loning for a bile canaliculus domain-specific membrane glycoprotein of rat hepatocytes.";
Proc. Natl. Acad. Sci. U.S.A. 84:7962-7966(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE OF 1-40.
MOBLINES #89034185; PubMed=3182821;
Hong W.J., Doyle D.; Doyle D.; Membrane orientation of rat gp110 as studied by in vitro
                                                                                                                                      767 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN SEQUENCE OF 624-648
                                                                                                                                                                                                                                                                                                                                                                                   Name=Dpp4; Synonyma=Cd26;
                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
                                                                                                                                         STANDARD;
                                   213 ALWWSPNG 220
σ
2 ALWWSPNG
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                          -!- TISSUE SPECIFICITY: Expressed in bile ducts and other epithelial brush borders (small intestine, Kidney, colon, pancreatic duct); acinar structures in salivary glands; endothelial structures and T cell areas in thymus; spleen and lymph node.
                             Hong W., Doyle D.;
"Molecular dissection of the NH2-terminal signal/anchor sequence of
"at dispetidy! peptidase IV.";
J. Call Biol. 111:323-328 (1990).
-!- FUNCTION: Removes N-terminal dispetides sequentially from
polypeptides having unsubstituted N-termini provided that the
ponlymate residue is proline.
-!- CATALYTIC ACTIVITY. Release of an N-terminal dispetide, Xaa-Yaa-|-
Zaa, from a polypeptide, preferentially when Yaa is Pro, provided
Zaa is neither Pro nor hydroxyproline.
                                                                                                                                                                                                                                                                                                                                   by proteolytic processing.
SIMILARITY: Belongs to the peptidase S9B family. DPPIV subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (By similarity).
                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam, PF001326; Peptidase S9; 1.
PROSITE, PS00708; PRO ENDOPEP SER; 1.
Aminopeptidase; Direct protein sequencing; Glycoprotein; Hydrolase; Protease; Serine protease; Signal anchor; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Charge relay system (By similarity).
N-linked (GlcNAc. .) (By similarity).
By similarity.
By similarity.
By similarity.
By similarity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytoplasmic (Potential).
Signal-anchor for type II membrane protein (Potential).
Extracellular (Potential).
               MEDLINE=90338089; PubMed=1974258; DOI=10.1083/jcb.111.2.323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0005624; C:membrane fraction; IDA.
GO; GO:0005625; C:soluble fraction; IDA.
GO; GO:0004274; P:sproteolygis and peptidase IV activity;
GO; GO:0006508; P:proteolygis and peptidolysis; TAS.
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Ensembl; ENSRNOG00000030763; Rattus norvegicus.
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InterPro; IPR001375; Peptidase S9.
InterPro; IPR001469; Peptidase S9.
InterPro; IPR001469; Peptidase S9B.
Pfam; PF00930; DPPIV_N; I.
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EMBL; J02997; AAA41272.1; -; mRNA.
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HSSP; P27487; 1PFQ.
SMR; P14740; 37-766.
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NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN-ATCC 2001 / CBS 138;

STRAIN-ATCC 2001 / CBS 138;

Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,

Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,

Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,

Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,

Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,

Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,

Boistame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,

Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,

Kerrest A., Kosul R., Lemaire M., Lesur I., Ma L., Muller H.,

Nicaud J.-M., Nikolski M., Oztas S., Ozter-Kalogeropoulos O.,

Swennen D., Tekaia F., Wesolowski-Louvel M., Westhoff E., Wirth B.,

Zeniou-Meyer M., Zivanovic Y., Bolotin-Pukuhara M., Thierry A.,

Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,

"Hencker P., Souchet J.-L.;

"Hencker P., Scarpelli C., Gaillardin C., Weissenbach J.,

"Hencker P., Souchet J.-L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sannotation update)
Similar to sp|P18962 Saccharomyces cerevisiae YHR028c DAP2 dipeptidyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OrderediocusNames=CAGL0J00583g;
Candida glabrata (Yeset) (Torullopsis glabrata).
Eukaryota; Pungi, Ascomycota, Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 53; DB 1; Length 767;
Pred. No. 6.7;
                                                 No effect on activity.
                                                               Reduced activity.
Reduced activity.
Reduced activity.
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EMBL, CA380956, CAG60684.1; -; Genomic_DNA.

GO; GO:0016177; F:aminopeptidase activity; IEA.

GO; GO:0004177; F:aminopeptidase activity; IEA.

GO; GO:0004274; F:dipeptidyl-peptidase IV activity; IEA.

GO; GO:0016787; F:hydrolase activity; IEA.

GO; GO:0006508; F:prolyl oligopeptidase activity; IEA.

GO; GO:0006508; P:proteclysis and peptidolysis; IEA.
                                                                                                                                                                                                                                                                                                C -> V (in Ref. 2).
V -> D (in Ref. 2).
L -> F (in Ref. 2).
R -> Q (in Ref. 2).
ED947174F1F3E440 CRC64;
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Reduced activity.
Reduced activity.
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G->A: Reduced activy
G->R: Reduced activy
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Y->F: No effect on a
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InterPro; IPR001375, Peptidase S9.
InterPro; IPR002469, Peptidase S9B.
InterPro; IPR000379; Ser_estrs.
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Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
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      OOC KARARA KARAR
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Tremellomycetidae, Tremellales, Tremellaceae, Filobasidiella.
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Bukaryota, Fungi, Basidiomycota, Hymenomycetes; Heterobasidiomycetes;
                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fung B., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M., Wickes B.L., Fu J., Davis R.W.; Cryptococcus neoformans serotype D sequencing."; Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.

-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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      Pfam; PF00930; DPPIV N; 1.
Pfam; PF00126; Peptidase S9; 1.
PROSITE; PS00708; PRO ENDOPEP_SER; 1.
Aminopeptidase; Complete protecome; Hydrolase; Transmembrane.
SEQUENCE 817 AA; 93991 MW; 9789F01F44F967FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, AAEYO100066; EAL17310.1; -; Genomic_DNA.

GO; GO:0010824; F:catalytic activity; IEA.

GO; GO:0003824; F:catalytic activity; IEA.

GO; GO:0003824; F:catalytic activity; IEA.

GO; GO:0004274; F:dipeptidyl-peptidase IV activity; IEA.

GO; GO:0004274; F:dipeptidyl-peptidase IV activity; IEA.

GO; GO:0004274; F:dipeptidyl-peptidase IV activity; IEA.

GO; GO:0004274; F:dipeptidase_S9.

R InterPro; IPR001375; Peptidase_S9.

R InterPro; IPR00379; Ser_estrs.

R InterPro; IPR00379; Ser_estrs.

R Pfam; PF00930; DPPIV N; I.

R Pfam; PF00316; PRO ENDOPEP SRR; UNKNOWN I.

W Hydrolase; Hypothetical proteIn; Transmembrane.
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                                                                                                                                                                                         Score 53; DB 2; Length 817;
Pred. No. 7.2;
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Dipeptidyl-peptidase and tripeptidyl-peptidase, putative.
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein.
ORFNames=CNBN1370;
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                                                                                                                                                                                                                         100.0%; Pred. No. 7.2
ive 0; Mismatches
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                                                                                                                                                                                             81.5%;
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Q5K721 CRYNE PRELIMINARY;
Q5K721;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QSSHI3;
QSSHI3;
                                                                                                                                                            Query Match
Best Local Similarity 100.
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247 ALWWSPNG 254
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STRAIN=B-3501A;
                                                                                                                                                                                                                                                                                                                   2 ALWWSPNG 9
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Best Local Similarity
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OSK721 CRY,
ID OSK722
AC OSK72
DT 10-MA
DT 10-MA
DE Dipep
GN ORFNA
OG CRYPA
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CRY
OSSH13-CRY
OSSH13-CRY
DD 13-SE
DT 
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STRAIN=ATCC 10895;
Pubmed=15001715; DOI=10.1126/science.1095781;
Dietrich F.S., Voegeli S., Brachat S., Lerch A., Gates K., Steiner S., Mohr C., Poehlmann R., Luedi P., Choi S., Wing R.A., Flavier A., Gaffiney T.D., Philippsen P.;
The Ashbya gossypii genome as a tool for mapping the ancient saccharomyces cerevisiae genome.";
                                                                                                                                                                                                                                                                                                                                                                                                     Loftus B.J., Fung E., Rondaglia P., Rowley D., Amedeo P., Bruno D., Vamathevan J., Miranda M., Anderson I.J., Fraser J.A., Allen J.E., Booket I.E., Brent M.R., Chiu R., Decring T.L., Donlin M.J., Houset I.A., For D. S., Grinberg V., Fu J., Fukushima M., Haas B.J., Huang J.C., Janbon G., Jones S.J.M., Koo H.L., Krzywinski M.I., Kwon-Chung K.J., Lengeler K.B., Mairia M.A., Marra R.B., Mathewson C.A., Mitchell T.G., Pertea M. Riggs F.R., Salzberg S.L., Schein J.E., Shvartsbeyn A., Shin H., Shumway M., Specht C.A., Wye N.H., Kronsted J.W., Lodge J.K., Heitman J., Davis R.W., Fraser C.M., Hyman R.W., "The genome of the basidiomycetous yeast and human pathogen
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                                                                                                                                             Loftus B., Amedeo P., Roncaglia P., Vamathevan J., Utterback T., Van Aken S., Fraser C.;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
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Eukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Eremothecium.
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R GO; GO:0016020; C:membrane; IEA.

GO; GO:0004274; F:aintopeptidase activity; IEA.

R GO; GO:0004274; F:dipeptidy1-peptidase IV activity; IEA.

R GO; GO:0016787; F:hydrolase activity; IEA.

R GO; GO:0016508; P:proteolysis and peptidolysis; IEA.

R GO; GO:0016508; P:proteolysis and peptidolysis; IEA.

R InterPro; IPR001375; Peptidase_S9.

R InterPro; IPR001375; Peptidase_S9.

R InterPro; IPR00340; Peptidase_S9.

R Pfam; PF000305; Peptidase_S9; I.

R PGOSITE; PS00708; PRO ENDOPEP_SER; UNKNOWN_I.

COMPLETE protecome; Hydrolase; Transmembrane.

SEQUENCE 883 AA; 99072 MW; 2866FFA3F5445FI CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81.5%; Score 53; DB 2;
88.9%; Pred. No. 7.8;
iive 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                     PubMed=15653466; DOI=10.1126/science.1103773;
                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cryptococcus neoformans.";
Science 307:1321-1324(2005).
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ID Q75C44 ASHGO PRELIMINARY;
AC Q75C44;
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NCBI_TaxID=214684;
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Dev. Dyn. 225:384-391(2002).
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ID 06
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Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schmeer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schmeer C.F., Bhat N.K.,
Hopking R.F., Jordan H., More T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
Brownstein M.J., Usdin T.B., Tonshiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McKennan P.J., Makernan R.J., Malek J.A., Gunazatne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
M. Schnerch A., Schain J.B., Jones S.J.M., Marra M.A.,
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus, Xenopus.
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MEDLINE-22341132; PubMed-12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 52; DB 2; Length 872;
Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                         GO:0016020; C:membrane; IEA.
GO:0004177; F:aminopeptidase activity; IEA.
GO:0004274; F:dipeptidy1-peptidase IV activity; IEA.
GO:0016787; F:proly1 oligopeptidase activity; IEA.
GO:0004287; F:proly1 oligopeptidase activity; IEA.
GO:0006508; P:proteolygis and peptidolysis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                        98529 MW; 4E7FEA3726EE1E07 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
MGC64382 protein.
Xenopus laevis (African clawed frog).
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roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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PROSITE; PS00708; PRO ENDOPED SER; 1.
Complete proteome; Hydrolase; Transmembrane.
SEQUENCE 872 AA; 98529 MW; 4E7FEA1776FE
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                           AE016816; AAS51299.1; -; Genomic DNA
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Interpro; IPR001375; Peptidase S9.
Interpro; IPR002469; Peptidase S9B.
Interpro; IPR00379; Ser estrs.
Pfam; PF00930; DPPIV_N; I.
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88.9%;
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       Science 304:304-307(2004)
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Best Local Similarity 88.9
Matches 8; Conservative
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66625 XENLA
C 066625 X
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AC 066625 X
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DE MGC64382
OC Amphibia
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MEDLINE=22608306; PubMed=12692562; DOI=10.1038/nbte820;
Ricka H., Ishikawa J., Hanamotto A., Shinose M., Kikuchi H., Shiba T., Sakaki Y., Hattori M., Omura S.;
"Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis.";
Nat. Biotechnol. 21:526-531(2003).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomyces avermitilis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=33903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75.4%; Score 49; DB 2; Length 404; 77.8%; Pred. No. 15; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                              Score 51; DB 2; Length 439;
Pred. No. 7.8;
                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                           Klein S., Strausberg R.; Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases. Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases. GO: GO: 001042020; C: emmbrane; IEA. GO; GO: 0004274; P: dipeptidyl-peptidase IV activity; IEA. GO; GO: 0006508; P: protecolysis and peptidolysis; IEA. InterPro; IPR002469; Peptidase_S9B. Pfam; PF00930; DPPIV N; 1. SEQUENCE 439 AA; 50314 MW; 14212078E30DBA18 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 98:12215-1220(2001).
EMBL. BA000030; BAC73197.1; -; Genomic_DNA.
Complete proteome; Hypothetical protein.
SEQUENCE 404 AA; 43046 MW; 76CA609577776838 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   082069 STRAW PRELIMINARY; PRT; 404 AA. 082069; Clarent Coll (TrEMBLrel. 24, Created) 01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   737 AA
                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                       78.5%;
80.0%;
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Q641D6;
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hes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     195 YALWWSTNAK 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 YALWWSPNGK 10
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01-JUN-2003 (TrEMBLre
Hypothetical protein.
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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SEQUENCE
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OKCFX2 YARLI
                     P70092 XENLA
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                                                                                                                                                                                                                                                                                MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Alusner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
Brownstein M.J., Usdin T.B., Trobhlyuki S., Carninci P., Frange C.,
A Brownstein M.J., Usdin T.B., Trobhlyuki S., Carninci P., Frange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Brownstein M.J., Wadin P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Halton B.K., Kurzhy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Halton B.K., Murany D.M., Green E.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Schautz J., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Salska U., Smailus D.E.,
Brohnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
Brohnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
Brohnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                    LOC397888 protein.
Name=LOC397888;
Renopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                        TISSUE=Kidney;
MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klain S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                           'Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75.4%; Score 49; DB 2; Length 737; 87.5%; Pred. No. 28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84184 MW; 1E08CF94EDFBCC4B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                         Xenopodinae, Xenopus, Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                     Dev. Dyn. 225:384-391(2002).
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Best Local Similarity 87.5-
France 7; Conservative
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195 YALWWSPD 202

1 YALWWSPN 8

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NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=CLIB 122 / E 150;
PubMedia1522952; DOI=10.1038/nature02579;
Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
Barnay A., Rangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.-M., Beyne B., Bleykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to tr|Q96VT7 Aspergillus niger Dipeptidyl aminopeptidase type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                      Vlasak R., Vilas U., Strobl B., Kreil G., "cDNA cloning and expression of secreted Xenopus laevis dipeptidyl aminopeptidase IV.";
                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus, Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OrderedLocusNames=YALIOBO2838g;
Yarrowia lipolytica (Candida lipolytica).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Dipodascaceae; Yarrowia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEROPS; SOO.003; -. GO, GO, C: membrane; IEA.
GO, GO:0004177; F: aminopeptidase activity; IEA.
GO, GO:0004274; F: dipeptidyl-peptidase IV activity; IEA.
GO, GO:00016787; F: hydrolase activity; IEA.
GO; GO:0004287; F: prorlyl Oligopeptidase activity; IEA.
GO; GO:0006508; P: proteolysis and peptidolysis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 748 AA; 85587 MW; 31CCF61B25104E5B CRC64;
                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75.4%; Score 49; DB 2;
87.5%; Pred. No. 28;
ive 1; Mismatches (
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    748 AA
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Pfam; PF00326; Peptidase S9; 1.
PROSITE; PS00708; PRO_ENDOPEP_SER; 1.
                                            01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequ
01-MAR-2004 (TrEMBLrel. 26, Last anno
Diopptidyl-peptidase IV (EC 3.4.14.5)
Xenopus laevis (African clawed frog).
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                                                                                                                                                                                                                                                                                                                                                                                                                              Eur. J. Blochem. 247:107-113(1997).
EMBL, Y08932; CAA70136.1; -; mRNA.
HSSP; P27487; IPPQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002471; Pept S9 AS.
InterPro; IPR001375; PeptIdase S9.
InterPro; IPR002469; Peptidase S9B.
InterPro; IPR000799; Ser_estrs.
                                                                                                                                                                                                                                                                                                                   TISSUE=Skin;
MEDLINE=97390076; PubMed=9249015;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87.5%;
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Q6CFX2;
P70092_XENLA PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 87.5
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                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                              NCBI_TaxID=8355;
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BA000012; BAB50329.1; -; Genomic\_DNA.

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RESULT 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kaneko T., Nakamura Y., Sato S., Agamizu E., Kato T., Sagamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashina K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti.";
           Hantraye F., Hennequin C., Jaunlaux N., Joyet P., Kachouri R., Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H., Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O., Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A., Swennen D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B., Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A., Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               demethylubiquinone-9 = S-adenosyl-L-homocysteine + ubiquinone-9.
-!- PATHWAY: Ubiquinone biosynthesis.
-!- SIMILARITY: Belongs to the methyltransferase superfamily.
Ubig/COQ3 family.
                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-MAY-2005 (Rel. 47, Last sequence update)
3-demethylubiquinone-9 3-methnyltransferase (EC 2.1.1.64) (3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase) (DHHB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name-ubig, OrderedLocusNames=mlr3442;
Malzobium loti (Mesorhizobium loti).
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 868;
                                                                                                                                                        EMBL; CR382128; CAG82658.1; -; Genomic_DNA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0004177; F:aminopeptidase activity; IEA.
GO; GO:000324; F:catcalytic activity; IEA.
GO; GO:000508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR001375; Peptidase_S9.
InterPro; IPR001375; Peptidase_S9B.
                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                    olete_protecme; Lipid degradation.
97775 MW; A6C4244DFC15F3F2 CRC64;
 Fabre E., Fairhead C., Ferry-Dumazet H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 3-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249 AA
                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                              75.4%; Score 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                      Pfam, PF00930; DPPIV N; 1.
Pfam; PF00326; Peptidae S9; 1.
Aminopeptidase; Complete proteo
SEQUENCE 868 AA, 97775 MW;
                                                                                                                                "Genome evolution in yeasts.";
                                                                                                                  Wincker P., Souciet J.-L.;
                                                                                                                                                                                                                                                                                                                                                                                            7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   314 ALWWSPDGQ 322
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             methyltransferase)
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Q98GB7;
28-FEB-2003 (
Despons L.,
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Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., Nicaud S., Jaffe D., Fisher S., Luffalla G., Dossat C., Sequrens B., Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S., Anthouard V., Jubin C., Cattolico L., Foulain M., Vacherie B., Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V., Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J., Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J., McEwan P., Bosak S., Lindblad-Toh K., Birren B., Nubbaum C., Kahn D., Robinson-Rechavi M., Lindblad-Toh K., Birren B., Nubbaum C., Kahn D., Robinson-Rechavi M., Hincker P., Lander E.S., Weissenbach J., Roest Crollius H., Wickenome duplication in the teleost fish Tetraodon nigroviridis reveals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                          Сарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tetraodon nigroviridis (Green puffer).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha; Tetraodontiformes;
Tetradontoidea, Tetraodontidae, Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
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                                                                                                                                                                                                                                                                                               Length 249;
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                                                                                                                                                                                                                                               249 AA; 27318 MW; F8216C9041F0AC5A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chromosome 3 SCAF14756, whole genome shotgun sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update) .
Last annotation update)
                                                                                                                                                                                      Complete proteome; Methyltransferase; Transferase;
Ubiquinone biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAAE01014756; CAG04973.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                 core 48; DB 1
red. No. 13;
Mismatches
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Nature 431:946-957(2004).
                                                                                                                                                                                                                                                                                                    Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                              SAM bd.
UbiG_mtfrase
                                                                                                                                                             TIGREAMS; TIGR01983; UbiG; 1.
                                                                                                                                                                                                                                                                                                    73.8%;
77.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORFNames=GSTENG00024844001;
                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 77.00
From 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q4S309 TETNG PRELIMINARY;
Q4S309;
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es 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              22 AEWWNPNGK 30
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                                                                                                                                       Pfam; PF02353; CMAS;
                                                                                                                                                                                                                                                                                                                                                                                                               2 ALWWSPNGK 10
HAMAP; MF_00472; -; 1
InterPro; IPR003333;
                                                                                 InterPro; IPR00051;
InterPro; IPR010233;
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Best Local S:
Matches 7,
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SEQUENCE REVISION.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa; Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The C.briggsae Sequencing Consortium;

The C.briggsae Sequencing Consortium;

Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.

-- CAUTION: The sequence shown here is derived from an english sequence shown here is derived from an preliminary data.

EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is good GO:00018024; CAES6836.1; -; Genomic_DNA.

R GO; GO:0001824; F:catalytic activity; IEA.

R GO; GO:0001829; P:proteolysis and peptidolysis; IEA.

InterPro; IPR002469; Peptidase_S9.

R InterPro; IPR002469; Ser_estrs.

R Pfam; PF00303; DPPIV, N; I.

P Pfam; PF00303; DPPIV, N; I.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetrandontoidea; Tetraodontidae; Tetraodon.
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome 13 SCAF14566, whole genome shotgun sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l protein.
794 AA; 90259 MW; D06C0095A5724EDE CRC64;
                                                                                                                                                            25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein CBG24661.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                  794 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     553 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 48; DB
Pred. No. 44;
1; Mismatches
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                                                                                                  PRT;
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Similarity 87.5%;
7; Conservative
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                                                                                           QE0370_CAEBR PRELIMINARY;
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Q4SKD2;
                                                                                                                                                                                                                                                                                                                               Caenorhabditis briggsae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |||||||||
245 ALWWSPSG 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=6238;
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                                                                TARABARA BERKERA BERKA BERKA BERKERA BERKA B
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Okazaki Y., Furuno M., Kagukawa T., Adachi J., Bono H., Kondo S., Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals the early vertebrate proto-karyotype.";
Nature 431:946-957(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires, Glires, Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-1992 (Rel. 24, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
13-SED-2006 (Rel. 48, Last senotation update)
13-SED-2006 (Rel. 48, Last annotation update)
Dipeptidyl peptidase 4 (EC 3.4.14.5) (Dipeptidyl peptidase IV) (Treal activation antigen CD26) (Thymocyte-activating molecule)
(THAM) (Contains: Dipeptidyl peptidase 4 membrane form (Dipeptidyl peptidase IV membrane form); Dipeptidyl peptidase IV soluble form)
(Dipeptidyl peptidase IV soluble form))

Name-DDP4; Synonymas-Cd26;
Mus musculus (Mouse)
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                                                                                                                                                                                    Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FBS-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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MEDLINE=95092780; PubMed=1999781;
Bernard A.-M., Nattel M.-G., Pierres M., Marguet D.;
Structure of the mouse dipeptidyl peptidase IV (CD26) gene.";
Biochemistry 33:15204-15214(1994).
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MEDLINE=92129288; PubMed=1370813;
Marguet D.A., Bernard A.-M., Vivier I., Darmoul D., Naquet P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
STRAIN=CS7BL/6J; TISSUE=Kidney;
MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 553;
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Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                          553 AA; 63057 MW; 0F7BA4D3C73E2048 CRC64;
                                                                                                                                                                                                                                                                                                                                                       CAAE01014566; CAF98900.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
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75.0%;
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                                                                                                                                                                                                                                                                                                                       preliminary data.
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                                                                                                                                                        NUCLEOTIDE SEQUENCE
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JOINED, Genomic\_DNA.

AAA82213.1;

EMBL;

EMBL;

JOINED, Genomic\_DNA

U12618; AAA82213.1; JOINED; Genomic\_DNA U12619; AAA82213.1; JOINED; Genomic\_DNA

U12617; AAA82213.1 U12618; AAA82213.1

EMBL; EMBL;

U12616; AAA82213.1

AK085370; BAC39434.1; -; mRNA. BC022183; AAH22183.1; -; mRNA.

EMBL; EMBL; EMBL; HSSP;

HSSP; P27487; 1PFQ. SMR; P28843; 37-759.

Genomic\_DNA.
IINED; Genomic\_DNA.
IINED; Genomic\_DNA.
IINED; Genomic\_DNA.
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JOINED;

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AAA82213.1; JOINED; G AAA82213.1; JOINED; G AAA82213.1; JOINED; G AAA82213.1; JOINED; G AAA82213.1; JOINED; G

EMBL; EMBL; EMBL; EMBL;

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WICLEOTIDE SEQUENCE [LARGE SCALE MRNA].

WICLEOTIDE SEQUENCE [LARGE SCALE MRNA].

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Leschul S.F., Zeeberg B. Buctow K.H., Schaefer C.F., Bhat N.K.,

A Diatchehot L., Marushan K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchehot L., Marushan K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchehot L., Marushan K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Rohas S.A., McEwan P.J., McKernan K.J., Malek J.A., Glubs R.A.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

A Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Salaska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Salaska U., Smailus D.E.,

R. Generation and initial analysis of more than 15,000 full-length human
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Kanai A., Kawaih H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Kanai A., Kawaih H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Mangaya A., Kurochkin I.V., Lee Y., Lenhard B.L., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Maglott D.R., Maltais R., Obtido T., Pavan W.J., Pertea G., Pesole G.,
RA Ravasi T., Numata K., Okido T., Pavan W.J., Petrea G., Pesole G.,
RA Ravasi T., Reed D.C., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Wilming L.G., Wynshaw-Boris A., Yanagiaa R.D., Tomita M.,
RA Wilming L.G., Wynshaw-Boris A., Yanagiaaw M., Yang I., Yang L.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Saco K.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Hayashishi K., Sasaki D., Shibata K., Shinagawa A.,
Raunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Hayashizaki Y.,
RA Hayashizaki Y.,
RA Hanalysis of the mouse transcriptome based on functional annotation of
RI Nature 420:563-573(2002):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEIN SEQUENCE OF 1-20.
MEDLINE=91302787; PubMed=1712807;
Vivier I., Marguet D.A., Naquet P., Bonicel J., Black D., Li C.X.-Y.,
Vivier I., Marguet D.A., Naquet P., Bonicel J., Black D., Li C.X.-Y.,
Bernard A.-M., Gorvel J.-P., Pierres M.;
"Evidence that thymocyte-activating molecule is mouse CD26 (dipeptidy)
peptidase IV).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Gaps
                                                                                                                                                                                                                                                                                          (By similarity).
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similarity)
                                                                                                                                                                                                                                                                          Bimilarity)
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                                                                                                                                                                                                                                                              Extracellular (Potential).
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Charge relay system
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           207 ALWWSPN 213
                                                                                                                                                                                                                                                                                                                                                               760 AA;
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J. Immunol. 147:447-454 (1991).

-!- FUNCTION: Removes N-terminal dipeptides sequentially from polypeptides having unsubstituted N-termini provided that the penultimate residue is prolline.

-!- CATALYTIC ACTIVITY: Release of an N-terminal dipeptide, Xaa-Yaa-|- Zaa-, from a polypeptide, preferentially when Yaa is Pro, provided Zaa is neither Pro nor hydroxyproline.

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EMBL; X58384; CAA41274.1; -; mRNA

removed

soluble form. PTM: The soluble form (SDPP) derives from the membrane form (MDPP)

SUBUNIT: Homodimer. SUBCELLULAR LOCATION: Type II membrane protein. Also exists in a

by proteolytic processing. SIMILARITY: Belongs to the peptidase S9B family. DPPIV subfamily.

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RESULT 31
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                                      DPP4 BOVIN STANDARD; PRT; 765 AA.

PB1425; Q8WMCB;

15-DEC-1998 (Rel. 37, Created)

16-DEC-1998 (Rel. 37, Last sequence update)

13-SEP-2005 (Rel. 48, Last sequence update)

13-SEP-2005 (Rel. 48, Last annotation update)

13-SEP-2005 (Rel. 49, Last sequence update)

14 C-cell activation antigen CD26) (Adenosine deaminase complexing protein) (ADCP-1) (Activation molecule 3) (ACT3) (WC10) [Contains: Dipeptidyl peptidase 4 membrane form (Dipeptidyl peptidase IV membrane form); Dipeptidyl peptidase IV membrane form); Dipeptidyl peptidase IV membrane form);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATALYTIC ACTIVITY: Release of an N-terminal dipeptide, Xaa-Yaa-|-Zaa-, from a polypeptide, preferentially when Yaa is Pro, provided Zaa is neither Pro nor hydroxyproline.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gliddon D.R., Howard C.J.; "CD26 is expressed on a restricted subpopulation of dendritic cells in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUB-T-cell;
MEDLINE=2146204; PubMed=11598101;
MEDLINE=214621A1.69.11.7190-7193.2001;
Lee S.-U., Ferens W., Davis W.C., Hamilton M.J., Park Y.-H., Fox L.K.,
Naessens J., Bohach G.A.;
"Identity of activation molecule 3 on superantigen-stimulated bovine cells is CD26.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- SUBCELLULAR LOCATION: Type II membrane protein. Also exists in a soluble form (By similarity).

-i- TISSUB SPECIFICITY: Intestinal epithelium, dendritic cells and several immune system tissues.
-i- PTM: The soluble form (SDPP) derives from the membrane form (MDPP) by proteolytic procesing (By similarity).
-i- SIMILARITY: Belongs to the peptidase S9B family. DPPIV subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98293306; PubMed=9629661; DOI=10.1016/S0305-0491(97)00327-1; Ben-Shooshan I., Parola A.H.; "The CP-I subunit of adenosine deaminase complexing protein from calf kidney is identical to human, mouse, and rat dipeptidyl peptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Comp. Biochem. Physiol. 119B:289-292(1998).
--- FUNCTION: Removes N-terminal dispeptides sequentially from
--- polypeptides having unsubstituted N-termini provided that the
penultimate residue is proline. Binds and regulates the activity
                                                                                                                                                                                                                                     Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                            TISSUE=Lymphocyte;
MEDINE=22067734; PubMed=12073152; DOI=10.1007/800251-002-0456-6;
MEDINE=22067734; Park Y.-H., Davis W.C., Hamilton M.J., Naesgens J.,
Bohach G.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22021197; PubMed=11981836;
DOI=10.1002/1521-4141(200205)32:5<1472::AID-IMMU1472>3.0.CO;2-Q;
                                                                                                                                                                                                                                                                                                                                                                                                         Molecular characterization of bovine CD26 upregulated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 1-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eur. J. Immunol. 32:1472-1481(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Infect. Immun. 69:7190-7193(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                       staphylococcal superantigen.";
Immunogenetics 54:216-220(2002)
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                                                                                                                                                                                                                   Name=DPP4; Synonyms=CD26;
Bos taurus (Bovine).
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                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                NCBI_TaxID=9913;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Charge relay system (By similarity).
N-linked (GLCNAC...) (By similarity).
By similarity.
By similarity.
By similarity.
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By similarity.
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28-FEB-2003 (Rel. 41, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Dipeptidyl peptidase 4 (EC 3.4.14.5) (Dipeptidyl peptidase IV) (DPP
Dipeptidyl peptidase 4 (EC 3.4.14.5) (Dipeptidyl peptidase IV)
IV) (T-cell activation antigen CD26) (Contains: Dipeptidyl peptidase
membrane form (Dipeptidyl peptidase IV) membrane form); Dipeptidyl
Name=DPPP4; Synonyms=CD26;
Felis silvestris catus (Cat).
Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Rammalia; Butheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
ROBI_TAXID=9685;
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                                                                                                                                                                                                                                                                                                                                                                  Dipeptidyl peptidase 4 membrane form. By Dipeptidyl peptidase 4 soluble form (By aimilarity). Cytoplasmic (Potential). Signal-anchor for type II membrane protein (Potential). Extracellular (Potential).
                                                                                                                                                                                                                                                 InterPro; IPR000379; Serestrs.
Pfam; PF00030; DPPIV N; 1.
Pfam; PF00326; Peptidase S9; 1.
PROSITE; PS00708; PRO ENDOREP SER; 1.
Aminopeptidase; Direct protein sequencing; Glycoprotein; Hydrolase; Brichase; Serine protease; Signal-anchor; Transmembrane.
CHAIN
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                                                                                                             EMBL; AF461806; AAL67836.1; -; mRNA.
EMBL; AY056834; AAL23628.1; -; mRNA.
                                                                                                                                                                                                       InterPro, IPR002471; Pept S9_AS.
InterPro, IPR001375; Peptidase_S9.
InterPro, IPR002469; Peptidase_S9B.
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                                                                                                                                                 HSSP; P27487; 1PFQ.
SMR; P81425; 38-764.
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212 ALWWSPKG 219
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                                                                                                                                                  Nishimura Y., Miyazawa T., Ikeda Y., Izumiya Y., Nakamura K., Sato E., Mikami T., Takahashi E.; Mikemi T., Takahashi E.; "Molecular cloning and sequencing of a cDNA encoding the feline T-cell activation antigen CD26 homologue."; Immunogenetics 50:366-368(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (By similarity). (By similarity). (By similarity). (Potential).
                                                                                                                                                                                                                                                                                                                                 by proteolytic processing (By similarity). SIMILARITY: Belongs to the peptidase S9B family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (By similarity).
(By similarity).
(By similarity).
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Dipeptidyl peptidase 4 soluble form (By
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Pfam; PF00930; DPP1V N; 1.
Pfam; PF00326; Peptidase_SP 1.
PROSITE; PS00708; PR0 ENDOPEP SER; 1.
Aminopeptidase; Glycoprotein; Hydrolase; Protease; Serine protease;
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similarity)
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Charge relay system (By similarity)
Charge relay system (By similarity)
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Signal-anchor for type II membrane
protein (Potential).
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                                       TISSUE=Peripheral blood;
MEDLINE=20094000; PubMed=10630304; DOI=10.1007/8002510050616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Extracellular (Potential).
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N-linked (GlCN
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HSSP; P27487; 1PFQ.
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InterPro; IPR001375; Peptidase_S9
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InterPro; IPR000379;
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Best Local Similarity
7; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              removed.
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Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S., Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavkiy L., Arachchi H.M., Barna N., Calvo S.E., Camarata J., Chang J., Chong J., Bricken J., Farco S., Ferreira P., FitzGerald M., Gage D., Galagan J., Androw J., Hagos B., Hall J., Horton L., Hulme W., Iliev I., Andrew D., Hagos B., Hall J., Horton L., Hulme W., Iliev I., Andrew C., Landers T., Levine R., Jones C., Kamal M., Kamat A., Karatas A., Karle C., Landers T., Levine R., Macdonald P., Major J., Manning J., Malbout R., MacLean C., Macdonald P., Major J., Manning J., Mathews C., Mauceli E., McCarthy M., Meldrim J., Meneus L., Nauga V., Murphy T., Naylor J., Nay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
X1-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Kluyveromyces lactis strain NRRL Y-1140 chromosome E of strain NRRL Y-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Kluyveromyces lactis (Yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     intred (FEB-2004) to the EMBL/GenBank/DDBJ databases. CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                       Gibberella zeae PH-1.
Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Hypocreomycetidae, Hypocreales, Nectriaceae, Gibberella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72.3%; Score 47; DB 2; Length 779; 77.8%; Pred. No. 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
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SEQUENCE 779 AA; 87757 MW; 3EC8D468C633F192 CRC64;
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                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   preliminary data.
779 AA.
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1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Fusarium graminearum genome sequence.";
Submitted (FEB-2004) to the EMBL/GenBank
PRT;
                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1140 of Kluyveromyces lactis.
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QGCNM1;
GIBZE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 77.8 es 7; Conservative
                                                                        13-SEP-2005 (TrEMBLrel. 13-SEP-2005 (TrEMBLrel.
                                                                                                                                                             (TrEMBLrel.
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                                                                                                                                                                                              Hypothetical protein.
ORFNames=FG10982.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=229533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=PH-1;
                                                                                                                                                             13-SEP-2005
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Conservative

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Gaps

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Length 765; Indels

DB 1;

Score 47; 72.3%; Score 47; 87.5%; Pred. No.

90; Mismatches

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Q4FNA2_9RICK
ID Q4FNA2_9RICK PRELIMINARY;
AC Q4FNA2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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es 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=CBG07598
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SEQUENCE 83
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Matches
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                                                                 STRAIN-CES 2359 / IFO 1267 / NURL Y-1140 / WM37;

Pubmed=1522559; DOI=10.1038/nature02579;

Dudon B., Sherman D., Fischer G., Durrens P., Casaregola S.,

Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla B.,

Lafontaine I., Balachin S., Backerich J.-M., Beyne E., Bleykasten C.,

Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,

Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,

Barnay S., Banchin S., Beckerich J.-M., Beyne E., Bleykasten C.,

Barnay S., Banchin S., Pairhead C., Ferry-Dumazet H., Groppi A.,

Hantraye F., Hennequin C., Jaunauw N., Joyet P., Kachouri R.,

Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,

Nicaud J.-M., Nikolski M., Oztas S., Ozter-Kalogeropoulos O.,

Pellenz S., Potier S., Richard G.-F., Strawb M.-L., Suleau A.,

Swennen D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,

Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,

Bouchler C., Caudachon B., Scarpelli C., Gaillardin C., Weissenbach J.,

"Gennen P., Souciet J.-L.;

"Gennen P., Souciet J.-L.;

"Gennen P., Souciet J.-L.;

"Gennen P., Souciet J.-L.;
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MEDINE=99065613; PubMed=9851916; DOI=10.1126/science.282.5396.2012;
TTP C elegans sequencing consortium;
"Genome sequence of the nematode C. elegans: a platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhadditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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0
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87.5%; Pred. No. 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11, CR382125; CAG99555.1; -; Genomic_DNA.
GO:0016020; C:membrane; IEA.
GO:0004177; F:aminopeptidase activity; IEA.
GO:0004274; F:dipeptidyl-peptidase IV activity; IEA.
GO:0016797; F:hydrolase activity; IEA.
GO:00162087; F:prolyl oligopeptidase activity; IEA.
GO:0006508; P:proteolysis and peptidolysis; IEA.
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Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR00247; Pept 59.AS.
InterPro; IPR001375; Peptidase S9.
InterPro; IPR001375; Peptidase S9.
InterPro; IPR000349; Ser estre.
Pfam; PF00330; DPPIV N; I.
Pfam; PF00326; Peptidase S9; 1.
PROSITE; PS00708; PRO ENDOPEP SER; 1.
Complete Protecome; Hydrolase; Transmembrane.
SEQUENCE 829 AA; 94226 MM; 733BB79B040C8CD9 CRC64;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
1-JAN-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein dpf-2.
Name-dpf-2; ORFNames-C27C12.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
                                                  NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
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Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q18253 CAEEL PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 430:35-44 (2004)
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STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 ALWWSPNG 9
NCBI_TaxID=28985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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CAEEL
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Q18253 C
  THE SECOND PROPERTY AND THE SE
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The C.briggsae Sequencing Consortium;
Submitted (SEF-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
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EMBL; CAACO1000032; CAE63236.1; -; Genomic_DNA.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0003824; F:catalytic activity; IEA.

GO; GO:0004274; F:catalytic activity; IEA.

R GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

R InterPro; IPR001375; Peptidase_S9B.

R InterPro; IPR003469; Peptidase_S9B.

R InterPro; IPR00379; Ser estrs.

R Pfam; PF00930; DPPIV N; I.

R Pfam; PF00930; DPPIV N; I.
R EMBL; Z69883; CAA93743.1; -; Genomic_DNA.

R HSSP, P27487; 1P50.

R HSSP, P27487; 1P50.

R Ensembl; C27C12.7; Caenorhabditis elegans.

R WormBase; WBGene00001055; dpf-2.

R WormBep; C27C12.7; CE05324.

R GO; GO:000620; C:membrane; IEA.

R GO; GO:000620; F:catalytic activity; IEA.

GO; GO:000620; F:catalytic activity; IEA.

GO; GO:000620; P:proteolysis and peptidolysis; IEA.

R GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

R InterPro; IPR001375; Peptidase_S9B.

R InterPro; IPR00139; Ser setrs.

R Pfam; PF00930; DPPIV N; I.

R Ffam; PF00930; DPPIV N; I.

R Complete proteone; Hypochetical protein.

R COMPLETE 829 AA; 94387 MW; B3F76F6DC12E44A5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 836;
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836 AA; 95596 MW; F09E922E48C5DBCF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OG1PC7.
CAEBR PRELIMINARY; PRT; 836 AA.
Q61PC7.
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein CBG07598.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72.3%; Score 47; DB 2; 66.7%; Pred. No. 66; ative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7
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Bukaryota; Fungi, Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                                                                                                                                 peptidase-encoding gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl, Acad. Sci. U.S.A. 100:8298-8303 (2003).

EMBL, BX294150, CAD76604.1; -; Genomic_DNA.

GO; GO:0003899; F:DNA-directed RNA polymerase activity; IEA.

GO; GO:0016987; F:sigma factor activity; IEA.

GO; GO:0001700; F:transcription factor activity; IEA.

GO; GO:0016740; F:transferase activity; IEA.

GO; GO:0016740; F:transferase activity; IEA.

GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100; Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T., Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R., Schlesner H., Amann R., Reinhardra K., Complete genome sequence of the marine planctomycete Pirellula strain 1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria, Planctomycetes, Planctomycetacia, Planctomycetales, Planctomycetaceae, Pirellula.
NCBI_TaxID=117;
                                                                                                                                                                                                                                                                                                                                                                     MEROPS, 509.006; --

R GO; GO: 0016020; C: membrane, IEA.

R GO; GO: 0016020; C: membrane, IEA.

R GO; GO: 00167274; F: Ripperiddyl-peptidase IV activity; IEA.

R GO; GO: 0016787; F: Ripdrolase activity; IEA.

R GO; GO: 0006508; P: proteolysis and peptidolysis; IEA.

R InterPro; IPR001375; MIP.

R InterPro; IPR001375; Peptidase_S9.

R InterPro; IPR000379; Ser_estrs.

R Pfam; PF003126; Peptidase_S9: 1.

R Pfam; PF003126; Peptidase_S9: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70.8%; Score 46; DB 2; Length 771; 70.0%; Pred. No. 88; 1. Indels tive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prolyl dipeptidyl peptidase.
8AB0CB33797B3FC6 CRC64;
                                                                                                                                                                                                                                                  Doumas A., Van den Broek P., Affolter M., Monod M.;
"Characterisation of the prolyl dipeptidyl peptidase-enc
(dpplv) from the koji mould Aspergillus oryzae.";
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
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Lucated)

Locatedia (TrEMBLrel. 26, Last sequence update)

Probable alternative sigma factor Algu.

OrderediocusNames-RB10049;

Rhodopirellula baltir
               01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Prolyl dipeptidyl peptidase precursor (EC 3.4.14.5)
                                                                                                                                                                                                                                               Van den Broek P., Affolter M., Monod M.;
                                                                                                                                                                                                                                                                                                                            EMBL; AJ002369; CAA05343.1; -; Genomic_DNA
HSSP; P27487; 1PFQ.
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                                                                                                                                                                                                                          SEQUENCE.
                                                                                                                          Asperdillus oryzae.
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                                                                                                                                                                            NCBI_TaxID=5062;
                                                                                                                                                                                                                              NUCLEOTIDE
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Eukaryota, Viridiplantae, Streptophyta; Embryophyta, Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                  STRAIN-HTCC1062;
Givannoni S.J., Tripp H.J., Givan S.A., Podar M., Vergin K.L.,
Baptista D., Bibbs L., Eads J., Richardson T.H., Noordweir M.,
Rappe M.S., Short J., Carrington J.C., Mathur E.J.;
"Genome Streamlining in a Cosmopolitan Oceanic Bacterium.";
Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; CP000004; AAZ1337.1; -; Genomic_DNA.
Methyltransferase; Transferase; Ubiquinone.
SEQUENCE 240 AA; 27681 MW; 259B6C800AAIE218 CRC64;
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                                                                              Name-ubig; ORFNames-SARil 0515;
Candidatus Pelagibacter ubique HTCC1062.
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
SARII cluster; Candidatus Pelagibacter.
NCBI_TaxID=335992;
                   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Probable 3-demethylubiquinone-9 3-O-methyltransferase RP622
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58780 MW; F8E7F8458BED7BC0 CRC64;
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Last annotation update)
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Pred. No.
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  13-SEP-2005 (TrEMBLrel. 31, Created)
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InterPro; IPRO06740; DUF604.
Pfam; PF04646; DUF604; 1.
SEQUENCE 509 AA; 58780 MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2003 (TrEMBLrel. 24,
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Q9LMM4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
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Best Local Similarity
Local 6; Conserve
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Name=F22L4.11;
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Query Match

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PRT;
                    HAMAP, MF_00472; -; 1.
InterPro; IPR003333; CMAS.
InterPro; IPR001601; Methyltransf.
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Q7T290;
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Les 6; Conservative
                                                                                                                                                                                                                                                                                Best Local Similarity 77.8
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                      22 AEWWSPTGK 30
PIR; E98295; E98295
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Q7T290_BRA
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NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

MEDLINE=21608551; PubMed=11743194; DOI=10.1126/science.1066803;

Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,

Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C.,

Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,

Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,

Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,

"Genome sequence of the plant pathogen and biotechnology agent

Agrobacterium tumefaciene C58.",

Science 294:2323-2328(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                         Gaps
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MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804;

Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
Rutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.
Shang S., Yoo H., Tao Y., Biddle P., Jung M., Kreeppan W., Perry M.,
Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 294:2323-2328(2001)
-|- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 3-
demethylubiquinone-9 = S-adenosyl-L-homocysteine + ubiquinone-9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  demethylubiquinone-9 = S-adenosyl-L-homocysteine + ubiquin
-!- PATHWAY: Ubiquinone biosynthesis.
-!- SIMILARITY: Belongs to the methyltransferase superfamily.
UbiG/COQ3 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NameaubiG; OrderedLocusNames=Atu3509, AGR L_2640;
Agrobacterium tumefaciene (strain C58 / ATCC 33970).
Bacteria, Proteobacteria, Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Agrobacterium.
                                                                                                                          69.2%; Score 45; DB 2; Length 217; 66.7%; Pred. No. 33; 1.ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
3-demethylubiquinone-9 3-methyltransferase (EC 2.1.1.64)
dihydroxy-5-hexaprenylbenzoate methyltransferase) (DHHB
GO; GO:0006352; P:transcription initiation; IEA.
InterPro; IPR007627; Sigma70_r2.
Pfam; PF04542; Sigma70_r2; 1.
Complete proteome.
SEQUENCE 217 AA; 25237 MW; E2IF5D752873AFFA CRC64;
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EMBL; AE008332; AAK89887.1; -; Genomic_DNA.
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                                                                                                                            Query Match
Best Local Similarity 66.7
Matches 6; Conservative
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Gaps
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 26, Last sequence update)
Hypothetical process 25:64214;
ORFNames=zgc:64214;
Brachydanio rerio (Zebrafish) (Danio rerio).
Brachydanio resto (Zebrafish) (Danio rerio).
Actinopterygii; Neopterygii; Teleostei; Ostarlophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Bristol N2;
MSDLINE-29069613; PubMed-9851916;
The C. elegans sequencing consortium;
"Genome sequence of the nematode C. elegans: a platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 45; DB 2; Length 320;
Pred. No. 50;
                                                                                                                                                                                                                                 Length 250;
                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WormPep; W07A8.1; CE20159.
InterPro; IPR005047; DUF286_Grecp_put.
Pfam; PF03383; DUF286; 1.
Complete protecome; Hypothetical protein.
SEQUENCE 320 AA; 36897 MW; 7B87D10281BB17D4 CRC64;
                                                                                                                                                                       250 AA; 27827 MW; 2448F6627D093B88 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ol-NOV-1999 (TrEMBLrel. 12, Created)
Ol-NOV-1999 (TrEMBLrel. 12, Last sequence update)
Ol-NOV-1999 (TrEMBLrel. 24, Last annotation update)
Hypotheitcal protein srxa-1.
Name=srxa-1; ORFNames=W07A8.1;
InterPro; IPR010033; UbiG_mtfrase.
InterPro; IPR010233; UbiG_mtfrase.
Pfam; PF02353; CMAS; 1.
TIGRFAMS; TIGR01983; UbiG; 1.
Complete protecome; Methyltransferase; Transferase;
Ubiquinone biosynthesis.
                                                                                                                                                                                                                           69.2%; Score 45; DB 1; 77.8%; Pred. No. 39; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           320 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       579 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69.2%; Sco. 100.0%; Pred. No. 50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      investigating biology.";
Science 283:2012-2018(1998).
EMBL: 282075; CAB04930.1; -; Genomic_DNA.
PIR; 126259; 126259.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ensembl; W07A8.1; Caenorhabditis elegans WormBase; WBGene00012318; W07A8.1.
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Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome assembly of Burkholderia cenocepacia
                                                                                                                                                                                                                                                                                                                                                                                         Larimer F., Land M.;
"Annotation of the draft genome assembly of Burkholderia cenocepacia
                                                                                                                                                                                      NOCENTIALIS424;
US DOE Joint Genome Institute (JGI-PGF);
US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
Hammon N., Israni S., Pitluck S., Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                   Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales,
Burkholderiaceae, Burkholderia, Burkholderia cepacia complex.
                                                                                                                                                                                                                                                                                                  Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Xanthine dehydrogenase (EC_1.17.1.4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     preliminary data.
EMBL; AAHL01000005; EAM20974.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                        STRAIN=HI2424;
US DOE Joint Genome Institute (JGI-ORNL);
                                                                                    Burkholderia cenocepacia HI2424.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORFNames=Bcen2424DRAFT
                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                        [2]
NUCLEOTIDE SEQUENCE.
                                                                                                                                      NCBI_TaxID=331272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oxidoreductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                    HI2424."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 44
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                                                                                                   Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Rlausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hasheh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tonahlyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Gardarane P.H.,
Richards S., Worley K.C., Hale S., Gardarane B.J., Lu X., Glubbs R.A.,
Whiting M., Maden A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakebley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
Generation and initial malysis of more than 15,000 full-length human
                                                                         TISSUE=Embryo;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 579;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZEIN; ZDB-GENE-040426-1407; zgc:64214.
GO; GO:0000151; C:ubiquitin ligase complex; IEA.
GO; GO:0046872; F:metal ion binding; IEA.
GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
GO; GO:0008270; F:ainc ion binding; IEA.
GO; GO:0016567; P:protein ubiquitination; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
TISSUE=Embryo;
Straumberg R.;
Submitted (UUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC054643; AAH54643.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PSS0119; ZF BBOX; 1.
PROSITE; PS00518; ZF RING 1; 1.
PROSITE; PS0099; ZF RING 2; 1.
Hypotherical protein.
SEQUENCE 579 AA; 65428 MW; 24B23B304EC10C80 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69.2%; Score 45; DB 2; llarity 87.5%; Pred. No. 94; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ensembl; ENSDARG00000007730; Danio rerio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001870; B302.
InterPro; IPR001879; Butyrophylin.
InterPro; IPR005874; PRY.
InterPro; IPR001877; SPRY receptor.
InterPro; IPR001815; Znf. Bbox.
InterPro; IPR001841; Znf. RNG.
Pfam; PF00642; SPRY, 1.
Pfam; PF00643; Zf.-B box; 1.
Pfam; PF00097; Zf.-B box; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR01406; BBOXZNFINGER
PRINTS; PR01407; BUTYPHLNCDUF
                                                                                                                                                                                                                                                                                                                                                                                                                                     sednences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00336; BBOX; 2
SMART; SM00589; PRY; 1.
SMART; SM00184; RING; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
7; Conserve
                                                       NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P38398; 1JM7
     Cyprinidae; Danio.
                NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA
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Gaps

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Score 45; DB 2; Length 787; Pred. No. 1.3e+02; 1; Mismatches 1; Indels

69.2%; 75.0%;

787 AA; 84911 MW; 0AAC94973B3395AA CRC64;

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Wood V. Gwilliam R., Rajandream M.A., Lyne M.H., Lyne R., Stewart A., Sgouros J.G., Peat N., Hayles J., Baker S.G., Babham D., Bowman S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Comor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D.E., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle B.J., Hunt S., Jagels K., James K.D., Jones L., Leather S., McDonald S., McLean J., Mooney P., Moule S., Mungall K.L., Murphy L.D., Niblett D., Odell C., Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch B., Rutherford K.M., Rutter S., Saunders D., Seeger K., Sharp S., Skelton J., Simmonds M.N., Squares S., Stewens K., Taylor R.G., Tlaylor R.G., Taylor R.G., Taylor R.G., Warren T., Whitehead S., Woodward J.R., Volckaert G., Aert R., Robben J., Grymonprez B.,
                                                                                                                                                                                 Q9P7E9; O13720;
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Putative dipeptidyl aminopeptidase C14C4.15c (EC 3.4.14.-).
ORFNames=SPAC14C4.15c, SPAPJ760.01c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=972;
MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
                                                                                                                                                                                                                                                                                                                                Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                853 AA
                                                                                                                                                                STANDARD;
                                            683 LWWNPGGK 690
3 LWWSPNGK 10
                                                                                                                                                                                                                                                                                                                                                                                                             Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4896
                                                                                                                                                                  SCHPO
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82 9BURK Q4LY82 9BURK PRELIMINARY; Q4LY82;

RESULT 43 Q4LY82 ID Q4 AC Q4

497 YALWWSGN 504

1 YALWWSPN 8

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Gaps

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1; Indels

322 AA.

Length 227;

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Benno Y.;
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, ABD22867; BAA74515.1; -; Genomic_DNA.
HSSP; P07985; 1CEO,
GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
InterPro; IPR001547; Glyco_hydro_5.
Pfam; PF00150; Cellulase; I.
SEQUENCE 322 AA; 37331 MW; 413F0A69652F5237 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ogata K., Aminov R.I., Matsui H., Tajima K., Nakamura M., Nagamine T.,
           Harrison M., Abu-Elmagd M., Grocott T., Yates C., Gavrilovic J., Wheeler G.N.;
Wheeler G.N.;
Whatrix metalloproteinase genes in Xenopus development.";
Dev. Dyn. 231:214-220(2004).
EMBL; AYS73379; AAT00546.1; -; mRNA.
InterPro. IRRO00585; Hemopexin.
Pfam: PF00045; Hemopexin.
SMART; SM00120; HX; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales; Planctomycetaceae; Pirellula.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales; Prevotellaceae; Prevotella
                                                                                                                                                                                                                NON TER 1 1 SEQUENCE 227 AA; 25910 MW; 6A03E9B0ECF111FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                          67.7%; Score 44; DB 2;
77.8%; Pred. No. 51;
tive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67.7%; Score 44; DB 2; 60.0%; Pred. No. 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prevotella ruminicola (Bacteroides ruminicola)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
  PubMed=15305302; DOI=10.1002/dvdy.20113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                          PROSITE; PS00024; HEMOPEXIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-2003 (TrEMBLrel. 25, 01-0CT-2003 (TrEMBLrel. 25, 01-0CT-2003 (TrEMBLrel. 25, Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q7UP27_RHOBA PRELIMINARY;
Q7UP27;
                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 77...
Rest Local 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9ZN63 PRERU PRELIMINARY;
Q9ZN63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OrderedLocusNames=RB7205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhodopirellula baltica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    250 YGAWWTPLGK 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 YALWWSPNGK 10
                                                                                                                                                                                                                                                                                                                                                                     2 ALWWSPNGK 10
                                                                                                                                                                                                                                                                                                                                                                                                           66 ALYWMPNGK 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
STRAIN=1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-JCM8958;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cellulase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RHOBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRERU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 47
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    STREETER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
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                                                                                                                                                                                                                                                                                                                                                 This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Duesterhoeft A., Fritzc C., Holzer E., Moestl D., Hilbert H., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Eger P., Zimmerann W., Wedler H., Wambutt R., Purnelle B., Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Ducas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P., "The genome sequence of Schizosaccharomyces pombe.", Nature 415:871-880(2022).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Charge relay system (By similarity).
Charge relay system (By similarity).
Charge relay system (By similarity).
N-linked (GloNAc. ) (Potential).
N-linked (GloNAc. ) (Potential).
N-linked (GloNAc. ) (Potential).
N-linked (GloNAc. ) (Potential).
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus, Xenopus.
                                                                                                                                                                                                                                                                                     -i- SUBCELLULAR LOCATION: Type II membrane protein. Lysosome-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AL162631; CAB83084.1; -; Genomic_DNA.
EMBL; Z98596; CAB11208.1; -; Genomic_DNA.
GenebB Spombe; SPAC14C4.15c; -.
InterPro; IPR001375; Peptidase_S9.
InterPro; IPR001379; Peptidase_S9.
InterPro; IPR00379; Ser_estrs.
Pfam; PF00300; DPPIV N; 1.
Pfam; PF00300; Peptidase_S9; 1.
Aminopeptidase; Complete proteome; Glycoprotein; Hydrolase;
Hypothetical protein; Protease; Serine protease; Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytoplasmic (Potential).
Signal-anchor for type II membrane protein (Potential)
Lumenal (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Potential)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69.2%; Score 45; DB 1; Length 853; 75.0%; Pred. No. 1.4e+02; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98342 MW; 38450BA50F8304B6 CRC64;
                                                                                                                                                                                                                                                                                                                           -1- SIMILARITY: Belongs to the peptidase S9B family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 227 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequenc
05-JUL-2004 (TrEMBLrel. 27, Last annotatimatrix metalloproteinase 14 (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OGPWO4 XENLA PRELIMINARY;
OGPWO4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane, Vacuole.
TOPO DOM 1 65
TRANSMEM 66 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               472
483
613
653 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=8355
                                                                                                                                                                                                                                                                                                              vacuoles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=MMP-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACT SITE
ACT SITE
ACT SITE
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383 AA.

Length 322;

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Calcium, Hydrolase, Metal-binding, Metalloprotease, Protease, Zinc. SEQUENCE 575 AA, 65810 MW, EA8C4A9E9BB60D34 CRC64;
                                                                                                                                                                                                                                                                                                       GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA-
GO; GO:0004222; F:metalloendopeptidase activity; IEA.
GO; GO:0008270; F:rainc ion binding; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
                                                                                                         Hasebe T., Shī Y.-B.;
"Xenopus laevis MTI-MMP.";
Submitred (MAY-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY633953; AAU94940.1; -; mRNA.
SMR; O5USC3; 105-275.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00546; CYSTEINE SWITCH; 1. PROSITE; PS00024; HEMOPEXIÑ; 1. PROSITE; PS00142; ZINC_PROTEASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interpro; IPR000585; Hemopexin.
Interpro; IPR001818; Pept MIOA MIL2B.
Interpro; IPR006025; Pept M T. BS.
Interpro; IPR006026; Peptidase_M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00045; Hemopexin; 4.
Pfam; PF00413; Peptidase_M10; 1.
Pfam; PF0333; Peptidase_M10_N; 1.
PRINTS; PR00138; MATRIXIN.
SMART; SM00120; HX; 4.
SMART; SM00235; ZnMc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 77.8
hes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=mmp24-prov;
NCBI_TaxID=8355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    initiative.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Leishmania major.
Eukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae, Leishmania.
                                                                                                                                                             'Complete genome sequence of the marine planctomycete Pirellula sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopus laevis (African clawed frog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
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0
    MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100; Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T., Ludwig W., Gade D., Beck A., Bozzyw K., Heitmann K., Rabus R., Schlener H., Aman, R., Reinhardt R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5
                                                                                                                                                                                                                                                                                                                                                                                                                            h Similarity 72.7%; Score 44; DB 2; Length 383; Similarity 72.7%; Pred. No. 88; 8; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67.7%; Score 44; DB 2; Length 476; 70.0%; Pred. No. 1.1e+02;
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                                                                                                                                                                                                  gtrain 1.";
Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
EMBL; BX294145; CAD75238.1; -; Genomic DNA.
Complete proteome; Hypothetical protein.
SEQUENCE 383 AA; 42610 MW; CAF119863344A439 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52325 MW; 4A1389B4B60C57EF CRC64;
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01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last annotation update)
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Last sequence update)
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Name=MMP-14;
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PROSITE; PS00678; WD REPEATS_1; 1.
PROSITE; PS50082; WD REPEATS_2; 4.
PROSITE; PS50294; WD REPEATS_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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ProDom; PD000018; WD40; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopodinae; Xenopus; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31,
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ID Q5USC3 XENLA PRELIMINARY;
AC Q5USC3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q4Q7R7_LEIMA PRELIMINARY;
Q4Q7R7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 67.7
Best Local Similarity 70.0
Matches 7; Conservative
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116 ALWWTPEDNGK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 ALWWSP--NGK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    135 YALQWSPSGR 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WD-40 repeat protein.
ORFNames=LmjF30.0410;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=5664;
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Gaps

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Length 575; 1; Indels

67.7%; Score 44; DB 2; I 77.8%; Pred. No. 1.38+02; tive 1; Mismatches 1;

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Klauenerg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klauener R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haleh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Perers G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopus Taevis (African clawed frog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IISSUE=Spleen;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                            25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Mmp24-prov protein.
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                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopodinae; Xenopus; Xenopus.
NC11_TaxID=8355;
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                                                                                                                                                                                                                                                                                                                                 25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                                                                 QEDCWB_XENLA PRELIMINARY;
                                          ||:| ||||
414 ALYWMPNGK 422
2 ALWWSPNGK 10
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MALQ HAEIN
P45176;
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Matches
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Richards S., Worley K.C., Hale S., García A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Heltron E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Shalska U., Smallus D.E., Schnerch A., Schein J.B., Oones S.J.M., Marra M.A., "Schein J.B., Oones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Embryo;
MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Rlausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheerz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Blosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gab L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Hypothetical protein.
Kenopus tropicalis (Western clawed frog) (Silurana tropicalis).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Annra; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
                                                                                                                                                                                       RNUCLEGIALD S. (STAIRED D.S.);
RA Klein S., Gerhard D.S.);
RL Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
BL Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
DR GO7078070 AAH77870.1; -; mRNA.
DR GO; GO:0006258; C: extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0006208; P: precedloapeptidase activity; IEA.
DR GO; GO:0006508; P: precedloapeptidase activity; IEA.
DR InterPro; IPR000626; Pept.M. A.
DR InterPro; IPR001818; Pept.M. A.
DR InterPro; IPR00451; Pept.M. A.
DR Fam; PF00413; Peptidase M.O; 1.
DR Pfam; PF00141; Peptidase M.O; 1.
DR Pfam; PF00141; Peptidase M.O; 1.
DR SWART; SM00120; HX; 4.
DR SWART; SM00120; HX; 4.
DR SWART; SM00120; HX; 4.
DR PROSITE; PS00014; PROPEXIN; 1.
DR PROSITE; PS000142; ZINC_PROTEASE; UNKNOWN 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN 1.
CROUENCE 576 AA; 65601 MW; F083528DFZDC35F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67.7%; Score 44; DB 2; Length 576; 77.8%; Pred. No. 1.3e+02; ive 1; Mismatches 1; Indels
                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          578 AA.
                                                                                                                                          cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 XENTR
QSBL52 XENTR PRELIMINARY;
QSBL52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 77.0-
Ti Conservative
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                                                                                                                                          and mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 51
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Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=95550630; PubMed=7542800;
Relischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Relischmann R.D., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
MCKenney K., Sutton G.G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Venter J.C., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R SMR; G5BL52; 105-275.

R GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.

R GO; GO:000422; F:metalloendopeptidase activity; IEA.

R GO; GO:000820; F:amctalloendopeptidase activity; IEA.

R GO; GO:0008508; P:proteolysis and peptidolysis; IEA.

R InterPro; IPR000585; Hemopexin.

R InterPro; IPR000685; Pept_M Zn BS.

R InterPro; IPR000625; Pept_M Zn BS.

R InterPro; IPR006025; Pept_M Zn BS.

R InterPro; IPR00413; Peptidase_M.

Pfam; PF00413; Peptidase_M.

R Pfam; PF03933; Peptidase_M.

R Pfam; PF03933; Peptidase_M.).
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Pasteurellaceae; Haemophilus.
NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67.7%; Score 44; DB 2; Length 578
77.8%; Pred. No. 1.4e+02;
tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00546; CYSTEINE SWITCH; 1.
PROSITE; PS00024; HEMOPEXIN; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Calcium; Hydrolase; Hypothetical protein; Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Klein S., Gerhard D.S.;
Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; BC090600; AAH90600.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
4-alpha-glucanotransferase (EC 2.4.1.25) (Amylomaltase)
(Disproportionating enzyme) (D-enzyme).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Metalloprotease, Protease, Zinc.
SEQUENCE 578 AA, 65838 MW, F7BC45C7EA1FA96E CRC64;
                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           699 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name≃maîQ; OrderedLocusNames=HI1356.
Haemophilus influenzae.
                                                                                                                                                                                                                                                        and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 77.8
Les 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0138; MATRI
SMART; SM00120; HX; 4.
SMART; SM00235; ZnMC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            417 ALYWMPNGK 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 ALWWSPNGK 10
                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Embryo;
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removed

TIGR;

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NUCLEOTIDE SEQUENCE.
STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE-22608306; PubMed=12692562; DOI=10.1038/nbt820;
Iteda H. Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T., Sakaki Y., Hattori M., Omura S.;
"Complete genome sequence and comparative analysis of the industrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=WB C6;
Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D., Olsen G.J., Sogin M.L.;
"Draft sequence of the Glardia lamblia genome.";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=MA-4680 / ATCC 31267 / NOTMB 12804 / NRLL 8165;
MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
Omura S., Ikeda H., Ishikawa J., Hanamoco A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H.. Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hatcroriganism Streptomyces
avermitilis deducing the ability of producing secondary
                                                                                                                                                                                                        Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 44; DB 2; Length 123-Pred. No. 3.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              microorganism Streptomyces avermitilis.";
Nat. Biotechnol. 21:526-531 (2003).
BMBL. BA000030; BAC69913.1; -; Genomic_DNA.
GO; GO:0005488; F: binding; IEA.
InterPro; IPR002114; HPr_SerP_S.
InterPro; IPR011990; TPR-like_helical.
Complete proteome; Hypothetical protein.
SEQUENCE 1256 AA; 134840 MW; 73578BS72F0F7C4C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     preliminary data.
EMBL; AACB01000099; EAA38489.1; -; Genomic_DNA.
SEQUENCE 1271 AA; 142786 MW; 712CA9D7223B2490 CRC64;
                                                                           Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1271 AA
                                     1256 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.78;
85.78;
                                                                           01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-MAR-2004 (TrEMBLrel. 26, Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, GLP 169 4270 455, Giardia lamblia ATCC 50803.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q7QTZ9 GIALA PRELIMINARY;
Q7QTZ9;
                                 Q82L10_STRAW PRELIMINARY;
                                                                                                                                                                                        Streptomyces avermitilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 85.7
Matches 6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1002 LWWSPSG 1008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1]NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          on.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=184922;
                                                                                                                                                                                                                                                         NCBI_TaxID=33903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 LWWSPNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        metabolites.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                 STRAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GIALA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q7QTZ9
                 Q82L10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                  This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                          Science 269:496-512(1995).
-!- CATALYTIC ACTIVITY: Transfers a segment of a 1,4-alpha-D-glucan to a new position in an acceptor, which may be glucose or a 1,4-alpha-D-glucan.
"Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PUCLEOTIDE SEQUENCE.
PubMed=15968074; DOI=10.1128/JB.187.13.4627-4636.2005;
Harrison A., Dyer D.W., Gillaspy A., Ray W.C., Mungur R., Carson M.B. Zhong H., Gipson J., Gipson M., Johnson L.S., Lewis L., Bakaletz L.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genomic sequence of an otitis media isolate of nontypeable
Haemophilus influenzae: comparative study with H. influenzae serotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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0
                                                                                                                          -1- SUBCELLUTAR LOCATION: Cytoplasmic (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003385; Glyco_hydro_77.
Pfam; Pr02446; Glyco_hydro_77; 1.
TIGRPAMS; TIGR00217; malQi_1.
Carbohydrate metabolism; Complete proteome; Glycosyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria, Proteobacteria, Gammaproteobacteria, Pasteurellales,
Pasteurellaceae, Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67.7%; Score 44; DB 2; Length 699; 60.0%; Pred. No. 1.7e+02; ive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 67.7%; Score 44; DB 1; Length 699; Best Local Similarity 60.0%; Pred. No. 1.7e+02; Matches 6; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome; Glycosyltransferase, Transferase.
SEQUENCE 699 AA; 80147 MW; 32B8DDB72F06A0C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                699 AA; 80252 MW; 80D6E1D51EC2E1E9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                699 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; CP000057; AAX88581.1; -; Genomic_DNA.
InterPro; IPR003385; Glyco hydro_77.
Pfam: PF02446; Glyco_hydro_77; 1.
TIGRRPAMS; TIGR00217; malQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4-alpha-glucanotransferase (EC 2.4.1.25).
Name=malO; OrderedLocusNames=NTHI1810;
                                                                                                                                                                                                                                                                                                                   EMBL, U32815; AAC23003.1; -; Genomic_DNA.
PIR; H64118; H64118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haemophilus influenzae (strain 86-028NP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . 187:4627-4636(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q4QK66_HAEI8 PRELIMINARY;
Q4QK66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       466 FRLWWIPKGK 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        466 FRLWWIPKGK 475
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                                                                                                                                                                                                                                                                                                                                                                    HI1356;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transferase
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RESULT 53 **Q4QK6**6

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Gaps

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Length 1256;

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Name=MMP-14;
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QGQLX0 CANFA
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PubMed=16020728; DOI=10.1126/science.1112680;
Ivens A.C., Peacock C.S., Worthey E.A., Murphy L., Aggarwal G.,
Berriman M., Sisk E., Rajandream M.A., Adlem E., Aert R., Anupama A.,
Apostolou Z., Attipoe P., Bason N., Bauser C., Beck A., Beverley S.M.,
Blanchetin G., Borzym K., Bothe G., Bruschi C.V., Collins M.,
Cadag E., Ciarloni L., Clayton C., Coulson R.M., Cronin A., Cruz A.K.,
Davies R.M., De Gaudenzi J., Dobson D.E., Duesterhoeft A.,
Fazelina G., Fosker N., Frasch A.C., Fraser A., Fuchs M., Gabel C.,
Goble A., Goffeau A., Harris D., Hertz-Fowler C., Hilbert H., Horn D.,
Huang Y., Klages S., Knights A., Wabe M., Larke N., Litvin L.,
Lord A., Louie T., Marra M., Masuy D., Matthews K., Michaeli S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=ATCC30001;
MEDLINE=99270317; PubMed=10340492; DOI=10.1016/S0166-6851(99)00017-1;
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                                                                                                                            Gaps
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NCBI_TaxID=5664;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Trichomonas vaginalis possesses a gene encoding the essential spliceosomal component, PRP8 ";
Mol. Biochem. Parsaitol. 99:275-278 (1999).
EMBL, AFILS849; ABJ2088.1; -; Genomic DNA.
GO, GO:0008180; C:signalosome complex; IEA.
InterPro; IRR000555; Mov34 MPN PAD1.
FPGM; PR01398; Mov34; I.
SMART; SM00222; JAB MPN; 1.
SMART; SM00222; JAB MPN; 1.
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85.7%; Pred. No. 5.8e+02;
tive 0; Mismatches 1; Indels
                                   Score 44; DB 2; Length 1271;
Pred. No. 3.1e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trichomonas vaginalis.
Eukaryota, Parabasalides, Trichomonada, Trichomonadida;
Trichomonadidae, Trichomonadinae, Trichomonas.
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
U5 snRNA-associated splicing factor.
ORFNames=LMJ_1325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Pre-mRNA processing 8 protein homolog PRP8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 2320 AA.
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                                                                                                                            1; Mismatches
                                   67.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fast N.M., Doolittle W.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74_LEIMA
Q4FW74_LEIMA PRELIMINARY;
Q4FW74;
9 TRIVA
Q9XYM9 TRIVA PRELIMINARY;
Q9XYM9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1524 YTLWWSP 1530
                                                                                                                                                                                                                                                                                                 386 FALWWSP 392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=5722;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=PRP8;
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099XYM9
TRI 1D 009XXM
AC 099XYM
DT 01-NO
DT 01-
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Mottram J.C., Muller-Auer S., Munden H., Nelson S., Norbertczak H., Oliver K., O'Neil S., Pentony M., Pohl T.M., Price C., Purnelle B., Quail M.A., Rabbinowitsch E., Reinhardt R., Rieger M., Rinta J., Schben J., Robertson L., Ruiz J.C., Rutter S., Saunders D., Schafer M., Schein J., Schwartz D.C., Seeger K., Seyler A., Sharp S., Shin H., Sivam D., Squares R., Squares S., Tosato V., Vogt C., Volckaert G., Wanbutt R., Warren T., Wedler H., Woodward J., Zimmermann W., Smith D.F., Blackwell J.M., Stuart K.D., Barrell B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Canis familiaris (Dog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Carnivora, Fissipedia, Canidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
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                                                                                                                                                                                                                                          Myler P.J., "The Genome of the Kinetoplastid Parasite, Leishmania major.", "The Genome of the Kinetoplastid Parasite, Leishmania major.",
                                                                                                                                                                                                                                                                                                                                                                                                           67.7%; Score 44; DB 2; Length 2427; 85.7%; Pred. No. 6.1e+02; Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66.2%; Score 43; DB 2; Length 148; 77.8%; Pred. No. 47; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                Science 309:436-442(2005).
EMBL; CP000081; AAZ14619.1; -; Genomic DNA.
SEQUENCE 2427 AA; 277492 MW; AAAD82891F4E5ECF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carter S.D., Barnes A., Clegg P.D.;
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF097633; AAC64975.1; -; mRNA.
HSSP; P08253; 1CK7.
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Last annotation update)
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Last annotation update)
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Ensembl, ENSCAFG0000011197; Canis familiaris.
InterPro, IPR000585; Hemopexin.
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OGOLXO.
OGOLXO.
OS-JUL-2004 (TEMBLEL: 27, Created)
OS-JUL-2004 (TEMBLEL: 27, Last sequenc)
OS-JUL-2004 (TEMBLE: 27, Last sequenc)
OS-JUL-2004 (TEMBLE: 27, Last annotat
Matrix metalloproteinase 14 (Fragment)
Canis familiaris (Dog).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00045; Hemopexin; 3.
SMART; SM00120; HX; 3.
                                                                                                                                                                                                                                                                                                                                                                                   Cuery Match
Best Local Similarity 85.70,
Canage 6; Conservative
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097657_CANFA PRELIMINARY;
097657;
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hes 7; Conservative
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1608 FALWWSP 1614
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47 ALFWMPNGK 55
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This Swiss-Proc entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

Cazalet C., Rusniok C., Brueggemann H., Zidane N., Magnier A., Ma L.,

Tichit M., Jarraud S., Bouchier C., Vandenesch F., Kunst F.,

Etichit M., Jarraud S., Bouchier C., Vandenesch F., Kunst F.,

Etichit M., Jarraud S., Bouchier C., Vandenesch F., Kunst F.,

Etichit M., Jarraud S., Bouchier C., Vandenesch F., Kunst F.,

Etichit M., Jarraud S., Bouchier C., Vandenesch F., Kunst F.,

Nat. Genet 36:1165-1173(2004).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-MAY-2005 (Rel. 47, Created)
10-MAY-2005 (Rel. 47, Last sequence update)
10-MAY-2005 (Rel. 47, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Leucyl/phenylalanyl-tRNA--protein transferase (BC 2.3.2.6) (L/F-
transferase) (Leucyltransferase) (Phenyalanyltransferase).
Name-ast, OrderedLocusNames=1ppl/32;
Legionella pneumophila (Gtrain Paris).
Bacteria, Proteobacteria, Gammaproteobacteria; Legionellales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66.2%; Score 43; DB 2; Length 148; 77.8%; Pred. No. 47;
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                                                                                                                                 Groeters S., Alldinger S., Baumgaertner W.;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AYE34615, AAS48101.1; -; mRNA.
Ensembl; ENSCAFG00000011197; Canis familiaris.
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Acyltransferase; Complete proteome; Transferase.
SEQUENCE 222 AA; 25474 MW; BBB70BE39AF87BCE CRC64;
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-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the L/F-transferase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     148 AA; 17414 MW; EC12EEB584E23289 CRC64;
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๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚	1 US-08-850-293-5 Sequence 2 US-09-949-016-9753 Sequence 2 US-09-489-039A-10840 Sequence 2 US-09-248-796A-19233 Sequence	2 US-09-228-986-114 Sequence	2 US-09-248-796A-16626 Sequence	2 US-09-079-592-11 Sequence	2 US-09-130-103M-031 Sequence 031, App Sequence 4160, Ap	1 US-08-447-464-5 Sequence 5, Appli	1 US-08-716-679-5 Sequence 5, Appli	2 US-09-543-681A-5145 Sequence 5145, Ap	2 US-108-301-332-60 Sequence 60, App. 1	2 03-03-24-36-2 Sequence 36512. A	2 US-09-270-767-51729 Sequence 51729, A	2 US-09-538-092-792 Sequence 792, App	1 US-08-321-670-3 Sequence 3, Appli	2 US-09-270-767-32523 Sequence 32523, A	2 US-09-270-767-47740 Sequence 47740, A	A US-US-488-14080 SEQUENCE 14080 A	4 PCI-0891-00899-I4 Sequence 14, Appl	2 03-03-303-310D-070 35444600 370, App. 2 113-03-270-767-31765 Semience 31765. A	2 CO-CONT CO-CONT CONT CO-CONT CONT CO-CONT CO-C	1 US-07-914-281-8 Sequence 8, Appli	1 US-08-393-246-8 Sequence 8, Appli	1 US-08-525-058A-8 Sequence 8, Appli	1 US-08-483-151-4 Sequence 4, Appli	1 US-08-696-731-8 Sequence 8, Appli	2 US-09-042-531-8 Sequence 8, Appli	2 US-09-602-787A-424 Sequence 424, App	2 US-09-252-991A-24883 Sequence 24883, A	1 US-08-294-872-2 Sequence 2, Appli	4 PCT-US95-09823-2 Sequence 2, Appli	2 US-09-595-8578-25 Sequence 25, Appl	2 US-09-949-016-10547 Sequence 10547, A	2 US-09-489-039A-11073 Sequence 11073, A	2 US-US-101-111-1115-111 SEGUENCE 111 AINT	2 11S-09-301-518D-878 Semence 878, App	2 US-09-303-518D-882 Sequence 882, App	2 US-09-303-518D-884 Sequence 884, App	1 US-08-470-350B-2 Sequence 2, Appli	2 US-US-101SA-IO SEQUENCE IO APPL	2 US-US-US-450-50 Segrented 50, April 2 178-00-504-500-40 Segrented 49, April 2	2 US-09-903-456-46 Sequence 46, Appl	2 US-09-624-670-45 Sequence 45, Appl	2 US-09-903-456-42 Sequence 42, Appl	2 US-09-624-670-41 Sequence 41, Appl	2 US-09-903-456-48 Sequence 2 US-09-624-670-47 Segmence	2 US-09-903-456-54 Sequence 54, Appl	2 US-09-624-670-53 Sequence 53, Appl	2 US-09-903-456-44 Sequence 44, Appl	2 US-US-524-57U-43 Sequence 43, Appl 2 HS-09-901-456-32 Sequence 32, Appl	2 US-09-624-670-31 Sequence 31, Appl	2 US-09-903-456-87 Sequence 87, Appl	2 US-09-903-456-57 Sequence 57, Appl	2 US-09-624-670-56 Sequence 56, Appl	2 US-09-903-456-52 Sequence 52, Appl	2 US-09-624-670-51 Sequence	2 US-09-605-703B-2850 Sequence	2 US-U9-9U3-4-56-31 Sequence	2 US-09-624-6/0-30 Sequence	4 pCT-US95-07744A-6 Sequence	1 US-08-362-739-7 Sequence	2 US-08-914-350A-7 Sequence 7, Appli
๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚	1 US-08-850-293-5 Sequence 2 US-09-949-016-9753 Sequence 2 US-09-489-039A-10840 Sequence 2 US-09-248-796A-19233 Sequence	2 US-09-228-986-114 Sequence	2 US-09-248-796A-16626 Sequence	2 US-09-079-592-11 Sequence	2 US-09-130-103M-031 Sequence 031, App Sequence 4160, Ap	1 US-08-447-464-5 Sequence 5, Appli	1 US-08-716-679-5 Sequence 5, Appli	2 US-09-543-681A-5145 Sequence 5145, Ap	2 US-108-391-391-00 Sequence 60, App. 1	2 03-03-20-20-20-20-20-20-20-20-20-20-20-20-20-	2 US-09-270-767-51729 Sequence 51729, A	2 US-09-538-092-792 Sequence 792, App	1 US-08-321-670-3 Sequence 3, Appli	2 US-09-270-767-32523 Sequence 32523, A	2 US-09-270-767-47740 Sequence 47740, A	US-US-488-1-0054A-14080 SEQUENCE 14-000 A	4 PCI-0891-00899-14 Sequence 14, App.	2 03-03-303-310D-070 35444600 370, App. 2 113-03-270-767-31765 Semience 31765. A	2 CO-CONT CO-CONT CONT CO-CONT CONT CO-CONT CO-C	1 US-07-914-281-8 Sequence 8, Appli	1 US-08-393-246-8 Sequence 8, Appli	1 US-08-525-058A-8 Sequence 8, Appli	1 US-08-483-151-4 Sequence 4, Appli	1 US-08-696-731-8 Sequence 8, Appli	2 US-09-042-531-8 Sequence 8, Appli	2 US-09-602-787A-424 Sequence 424, App	2 US-09-252-991A-24883 Sequence 24883, A	1 US-08-294-872-2 Sequence 2, Appli	4 PCT-US95-09823-2 Sequence 2, Appli	2 US-09-595-8578-25 Sequence 25, Appl	2 US-09-949-016-10547 Sequence 10547, A	2 US-09-489-039A-11073 Sequence 11073, A	2 US-US-101-111-1115-111 SEGUENCE 111 AINT	2 11S-09-301-518D-878 Semence 878, App	2 US-09-303-518D-882 Sequence 882, App	2 US-09-303-518D-884 Sequence 884, App	290 1 US-08-470-350B-2 Sequence 2, Appli	559 Z US-109-592-ZUDAN-10 Sequence 10, Appl	2 US-US-US-450-50 Segrented 50, April 2 178-00-504-500-49 Segrented 49, April	2 US-09-903-456-46 Sequence 46, Appl	2 US-09-624-670-45 Sequence 45, Appl	2 US-09-903-456-42 Sequence 42, Appl	2 US-09-624-670-41 Sequence 41, Appl	2 US-09-903-456-48 Sequence 2 US-09-624-670-47 Segmence	2 US-09-903-456-54 Sequence 54, Appl	2 US-09-624-670-53 Sequence 53, Appl	2 US-09-903-456-44 Sequence 44, Appl	2 US-US-524-57U-43 Sequence 43, Appl 2 HS-09-901-456-32 Sequence 32, Appl	2 US-09-624-670-31 Sequence 31, Appl	2 US-09-903-456-87 Sequence 87, Appl	2 US-09-903-456-57 Sequence 57, Appl	2 US-09-624-670-56 Sequence 56, Appl	2 US-09-903-456-52 Sequence 52, Appl	2 US-09-624-670-51 Sequence	2 US-09-605-703B-2850 Sequence	2 US-U9-9U3-4-56-31 Sequence	2 US-09-624-6/0-30 Sequence	4 pCT-US95-07744A-6 Sequence	1 US-08-362-739-7 Sequence	2 US-08-914-350A-7 Sequence 7, Appli
	9 508 1 US-08-850-293-5 Sequence 9 533 2 US-09-949-1016-9753 Sequence 9 557 2 US-09-489-039A-10840 Sequence 9 698 2 US-09-248-796A-19233 Sequence	9 762 2 US-09-228-986-114 Sequence	9 766 2 US-09-248-796A-16626 Sequence	9 931 2 US-09-079-592-11 Sequence	9 11/8 2 US-09-430-103A-831 Sequence 031, App. 4 91 2 US-09-513-999C-4160 Sequence 4160, Ap	4 93 1 US-08-447-464-5 Sequence 5, Appli	4 93 1 US-08-716-679-5 Sequence 5, Appli	4 106 2 US-09-543-681A-5145 Sequence 5145, Ap	4 131 Z US-UG-961-39Z-90 SEGMICENCE 60, Appl. 1131 Z 1131-09-961-39Z-60 SEGMICENCE 60, Appl. 1	4 131 2 03-03-04-342-00 044-04-04-04-04-04-04-04-04-04-04-04-04-	4 146 2 US-09-270-767-51729 Sequence 51729, A	4 181 2 US-09-538-092-792 Sequence 792, App	4 245 1 US-08-321-670-3 Sequence 3, Appli	4 249 2 US-09-270-767-32523 Sequence 32523, A	4 249 2 US-09-270-767-47140 Sequence 47/40, A	4 ZVU Z US-UV-48V-10XA-14V8U SEQUENCE 14 DVV A	4 35/ 4 PCI-LOSI-LOUGYS-LI4 SEGUESICE II, APPI 103 3 IIC_103_373_518D_874 SEGUESICE R76 DRN	4 595 & US-U9-303-3120D-010 Sequence 31765 B	4 400 2 102-03-03-04-04-03 Commence 11:03:03 D	4 405 1 US-07-914-281-8 Sequence 8, Appli	4 405 1 US-08-39-246-8 Sequence 8, Appli	4 405 1 US-08-525-058A-8 Sequence 8, Appli	4 405 1 US-08-483-151-4 Sequence 4, Appli	4 405 1 US-08-696-731-8 Sequence 8, Appli	4 405 2 US-09-042-531-8 Sequence 8, Appli	4 426 2 US-09-602-787A-424 Sequence 424, App	4 464 2 US-09-252-991A-24883 Sequence 24883, A	4 533 1 US-08-294-872-2 Sequence 2, Appli	4 533 4 PCT-US95-09823-2 Sequence 2, Appli	4 584 2 US-09-595-8578-25 Sequence 25, Appl	.4 588 2 US-09-949-016-10547 Sequence 10547, A	4 743 2 US-09-489-039A-11073 Sequence 11073, A	4 848 2 US-US-US-US-144 SEGUENTE 31, APPL 4 841 1 118-108-108-144 SEGUENTE 880 Bro	4 888 11S-09-303-518D-878 Sequence 878 ADD	4 922 2 US-09-303-518D-882 Sequence 882, App	4 922 2 US-09-303-518D-884 Sequence 884, App	.4 1290 1 US-08-470-350B-2 Sequence 2, Appli	4 3559 Z US-09-10-054-10 Sequence 10, Appr	6 1/8 2 US-09-905-430-30 Sequence 49. App.		6 182 2 US-09-624-670-45 Sequence 45, Appl	.6 238 2 US-09-903-456-42 Sequence 42, Appl	.6 238 2 US-09-624-670-41 Sequence 41, Appl	.6 241 2 US-09-903-456 Sequence	6 265 2 US-09-903-456-54 Sequence 54, Appl	.6 265 2 US-09-624-670-53 Sequence 53, Appl	.6 278 2 US-09-903-456-44 Sequence 44, Appl	.6 2/8 2 US-US-624-6/U-43 Sequence 43, App. 6 279 2 IIS-US-903-456-32 Sequence 32. App.	6 279 2 US-09-624-670-31 Sequence 31, Appl			.6 282 2 US-09-624-670-56 Sequence 56, Appl	.6 302 2 US-09-903-456-52 Sequence 52, Appl	.6 302 2 US-09-624-670-51 Sequence	.6 306 2 US-09-605-703B-2850 Sequence	.6 318 2 US-09-9U3-458-31 sequence	.6 318 2 US-09-624-6/0-30 Sequence	.6 628 4 PCT-US95-07744A-6 Sequence	.8 60 1 US-08-362-739-7 Sequence	.8 60 2 US-08-32-73-7 Sequence 7, Appli
사용용 소문 등인 교문 통령령 시력 통신 부탁 등인 당당 중앙 등입 등 다른 다양 시작 시작 시작 입업 입업 지수가 의미국 목욕 목욕 목욕을 목욕을 모음을 하는 것 같은 한 것 같다.	7 56.9 508 1 US-08-850-293-5 Sequence 7 56.9 533 2 US-09-949-016-9753 Sequence 7 56.9 567 2 US-09-489-039A-10840 Sequence 7 56.9 698 2 US-09-248-796A-19233 Sequence	7 56.9 762 2 US-09-228-986-114 Sequence	7 56.9 766 2 US-09-248-796A-16626 Sequence	7 56.9 931 2 US-09-079-592-11 Sequence	7 35.9 11/8 2 US-09-438-123A Sequence 031, APP 6 55.4 91 2 US-09-513-999C-4160 Sequence 4160, Ap	5 55.4 93 1 US-08-447-464-5 Sequence 5, Appli	6 55.4 93 1 US-08-716-679-5 Sequence 5, Appli	55.4 106 2 US-09-543-68145 Sequence 5145, Ap	5 55.4 131 2 105-00-901-202-60 Sequence 60. April 15 105-00-901-202-60 Sequence 60. April 1	5 53.4 131 2 03-02-22-00 0-04-00-00-04 05-0-0	6 55.4 146 2 US-09-270-767-51729 Sequence 51729, A	6 55.4 181 2 US-09-538-092-792 Seguence 792, App	6 55.4 245 1 US-08-321-670-3 Sequence 3, Appli	6 55.4 249 2 US-09-270-767-32523 Sequence 32523, A	55.4 249 2 US-09-2/0-67-47/740 Sequence 4/740, A	6 DS-4 ZVO & US-10448V-1044-14408V SEGUETICE 14408V, A	6 55.4 35/14 FLIOSAL-114 SEGUENCE 14, Appt.	6 35.4 354 2 US-09-303-3160-0)	6 553.4 400 & 03-09-12/0-12/0-13/0-13/0-13/0-13/0-13/0-13/0-13/0-13	5 55 4 405 1 US-07-1914-281-8 Sequence 8, Appli	6 55.4 405 1 US-08-393-246-8 Sequence 8, Appli	6 55,4 405 1 US-08-525-058A-8 Sequence 8, Appli	6 55.4 405 1 US-08-483-151-4 Sequence 4, Appli	6 55.4 405 1 US-08-696-731-8 Sequence 8, Appli	6 55.4 405 2 US-09-042-531-8 Sequence 8, Appli	6 55.4 426 2 US-09-602-787A-424 Sequence 424, App	6 55.4 464 2 US-09-252-991A-24883 Sequence 24883, A	6 55.4 533 1 US-08-294-872-2 Sequence 2, Appli	6 55.4 533 4 PCT-US95-09823-2 Sequence 2, Appli	6 55.4 584 2 US-09-595-857B-25 Sequence 25, Appl	6 55.4 588 2 US-09-949-016-10547 Sequence 10547, A	6 55.4 743 2 US-09-489-039A-11073 Sequence 11073, A	0 05).4 044 2 0.05-04-1412-141 3-044-0110-0-141 APPLA	6 53.4 ARR 2 115-109-301-518D Sequence 878, App	6 55.4 922 2 US-09-303-518D-882 Sequence 882, App	6 55.4 922 2 US-09-303-518D-884 Sequence 884, App	6 55.4 1290 1 US-08-470-350B-2 Sequence 2, Appli	36 55.4 3559 Z US-709-694-10 SEGUENCE TO, APPL	5.5 54.6 1/8 2 02.09-90-30 Sequence 30, April	5.5 5.4 6 182 2 US-09-903-456-46 Secuence 46, Appl	5.5 54.6 182 2 US-09-624-670-45 Sequence 45, Appl	5.5 54.6 238 2 US-09-903-456-42 Sequence 42, Appl	5.5 54.6 238 2 US-09-624-670-41 Sequence 41, Appl	5.5 54.6 24. 2 US-09-903-456-46 Sequence 5 5 5 4 6 24.1 2 HS-09-624-670-47 Sequence	5.5 54.6 265 2 US-09-903-456-54 Sequence 54, Appl	5.5 54.6 265 2 US-09-624-670-53 Sequence 53, Appl	5.5 54.6 278 2 US-09-03-456-44 Sequence 44, Appl.	5.5 54.6 2/8 2 US-09-1644-0-13 Sequence 13, Appl.	5.5 54.6 279 2 US-09-624-670-31 Sequence 31, Appl	5.5 54.6 2.80 2 US-09-903-456-87 Sequence 87, Appl	5.5 54.6 2.82 2 US-09-903-456-57 Sections 57, Appl	5.5 54.6 282 2 US-09-624-670-56 Sequence 56, Appl	5.5 54.6 302 2 US-09-903-456-52 Sequence 52, Appl	5.5 54.6 302 2 US-09-624-670-51 Sequence	5.5 54.6 306 2 US-09-605-703B-2850 Sequence	5.5 54.6 318 2 US-UY-YU3-456-31 sequence	5.5 54.6 318 2 US-09-624-6/U-30 Sequence 5 5 5 54 6 628 1 US-08-261-822A-6 Sequence	5.5 54.6 628 4 PCT-US95-07744A-6 Sequence	35 53.8 60 1 US-08-362-739-7 Sequence	5 53.8 60 1 02.08-08-914-350A-7 Sequence 7, Appli

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2 US-09-270-767-58810 Sequence 56 US-09-621-976-703 Sequence 70 US-09-275-252A-3 Sequence 22 US-09-275-252A-25 Sequence 22 US-09-513-999C-7437 Sequence 16 US-09-513-999C-7437 Sequence 17 US-09-513-995C-7437 Sequence 16 US-09-270-767-35267 Sequence 50 US-	2 US-09-902-540-15615 Sequence 1.2 US-09-384-302A-17 Sequence 1.2 US-09-384-502A-17 Sequence 2.2 US-09-252-991A-26680 Sequence 2.2 US-09-252-991A-26680 Sequence 2.2 US-09-252-991A-26680 Sequence 2.3 US-09-252-9	2 US-09-252-991A-12892 Sequence 1. 2 US-09-275-252A-1 Sequence 1. 2 US-09-275-252A-1 Sequence 1. 2 US-09-275-252A-1 Sequence 1. 2 US-09-275-252A-1 Sequence 1.	2 US-U3-10-104-2677 Sequence 267 2 US-09-252-991A-29639 Sequence 297 2 US-09-583-110-4684 Sequence 466	2 US-09-543-68LA-4219 Sequence 422 2 US-09-107-433-4633 Sequence 465 2 US-09-270-767-31656 Sequence 31	2 US-09-902-540-9964 Sequence 99 2 US-09-570-856B-23 Sequence 23 2 US-09-570-856B-24 Sequence 24	2 US-09-248-796A-17262 Sequence 17. 2 US-09-270-767-33317 Sequence 33. 2 US-09-270-767-43455 Sequence 43.	1 US-08-886-765-2 Sequence 2, 2 US-09-115-660-2 Sequence 2, 2 US-09-902-540-15456 Sequence 15	2 US-09-893-737-142 Sequence 14 2 US-09-252-991A-32410 Sequence 32 2 US-09-902-540-14926 Sequence 14	2 US-09-949-016-7903 Sequence 79 2 US-08-469-260A-40 Sequence 40 2 US-08-488-446-40 Sequence 40	2 US-08-46/-344A-40 Sequence 40 2 US-08-424-550B-40 Sequence 40 2 US-09-543-681A-6189 Sequence 61	2 US-09-270-767-44050 Sequence 44 2 US-09-248-796A-17346 Sequence 17 2 US-09-902-540-10405 Sequence 10	1 US-08-712-072C-5 Sequence 5, 2 US-10-087-013-7 Sequence 7, 2 US-10-087-013-10500 Sequence 7, 2 US-10-073-10500 Sequence 7, 2	2 US-09-222-991A-31608 Sequence 20 2 US-09-252-991A-31608 Sequence 20 2 US-09-252-991A-20780 Sequence 20	1 US-08-458-970A-2 Sequence 2, 2 US-09-082-270-2 Sequence 2,	2 US-09-248-796A-17341 Sequence 17 2 US-09-902-540-10171 Sequence 10	2 US-03-343-016-3-31 Sequence 49 2 US-09-328-352-4953 Sequence 49 1 US-08-712-072C-2 Sequence 2-	2 US-09-252-991A-23397 Sequence 23	2 US-09-198-452A-831 Sequence 83 2 US-09-438-185A-784 Sequence 78	2 US-09-248-7968-17146 Sequence 17 2 US-10-104-047-2209 Sequence 22	1 US-08-818-514-6 Sequence 6, 2 US-09-115-934A-6 Sequence 6,	2 US-09-611-175-6 Sequence 6, 2 US-09-489-039A-11840 Sequence 11	2 US-09-902-540-16052 Sequence 16 2 US-09-605-703B-1400 Sequence 14	2 US-09-605-703B-1426 Sequence 1426, 2 US-09-605-703B-1428 Sequence 1428, 2 US-09-489-039A-9142 Sequence 9142,
3 53 2 US-09-270-767-58810 Sequence 56 3 54 2 US-09-621-976-7003 Sequence 70 3 58 2 US-09-621-976-703 Sequence 70 3 58 2 US-09-275-252A-25 Sequence 23 59 2 US-09-275-252A-25 Sequence 24 05 2 US-09-513-999C-7437 Sequence 16 3 62 2 US-09-513-999C-7437 Sequence 16 3 64 1 US-08-274-655-15 Sequence 16 3 72 2 US-09-270-767-35267 Sequence 50 3 72 2 US-09-270-767-35267 Sequence 50 3 72 2 US-09-270-767-50484 Sequence 50 3 50 50 50 50 50 50 50 50 50 50 50 50 50	3     72     2     US-09-902-540-15615     Sequence 11       3     90     2     US-09-384-302A-17     Sequence 1-       3     92     2     US-09-902-540-10408     Sequence 1-       3     112     2     US-09-252-991A-26083     Sequence 2-       3     145     2     US-09-252-991A-22680     Sequence 2-	3 149 2 US-09-252-991A-18802 Sequence 13 158 2 US-09-252-991A-27898 Sequence 1. 3 160 2 US-09-275-252A-1 Sequence 1. 3 160 2 US-09-275-252A-1 Sequence 1. 3 160 2 US-09-275-252A-1 Sequence 1. 3 160 2 US-09-175-252A-1	182 2 US-09-252-991A-29639 Sequence 29639 Sequence 2991A-29639 Sequence 2993 182 2 US-09-583-110-4684 Sequence 466	3 184 2 US-09-543-68419 Sequence 42. 3 185 2 US-09-107-4633 Sequence 46. 3 190 2 US-09-270-767-31656 Sequence 31.	3 192 2 US-09-902-540-9964 Sequence 99 3 194 2 US-09-570-856B-23 Sequence 23 3 194 2 US-09-570-856B-24 Sequence 24	3 197 2 US-09-248-796A-17262 Sequence 17. 3 217 2 US-09-270-767-33317 Sequence 33. 3 218 2 US-09-270-767-43455 Sequence 43.	3 225 1 US-08-886-765-2 Sequence 2, 3 225 2 US-09-115-660-2 Sequence 2, 3 225 2 US-09-902-540-15456 Sequence 15	3 228 2 US-09-893-737-142 Sequence 14 3 229 2 US-09-252-991A-32410 Sequence 32 3 234 2 US-09-902-540-14926 Sequence 14	3 235 2 US-09-949-016-7903 Sequence 79 3 245 2 US-08-469-260A-40 Sequence 40 3 245 2 US-08-46-40 Sequence 40	3 245 2 US-08-467-44464-40 Sequence 40 33 245 2 US-08-424-5508-40 Sequence 40 3 256 2 US-09-543-681A-6189 Sequence 61	3 264 2 US-09-270-767-44050 Sequence 44 3 266 2 US-09-248-7968-17346 Sequence 17 3 280 2 US-09-902-540-10405 Sequence 10	3 285 1 US-08-712-072C-5 Sequence 5, 3 294 2 US-10-087-013-7 Sequence 7,	3 322 2 US-09-252-991A-15000 Sequence 20 3 345 2 US-09-252-991A-20780 Sequence 20 3 345 2 US-09-252-991A-20780 Sequence 20	3 355 1 US-08-458-970A-2 Sequence 2, 3 355 2 US-09-082-270-2 Sequence 2,	3 366 2 US-09-248-796A-17341 Sequence 17 3 392 2 US-09-902-540-10171 Sequence 10	3 402 US-09-328-352-4953 Coducing 5 3 402 US-09-328-352-4953 Sequence 49 3 402 I IR-08-712-072C-2	3 427 2 US-09-252-991A-23397 Sequence 23 427 2 US-09-252-991A-29948 Sequence 29	3 431 2 US-09-198-452A-831 Sequence 83 3 435 2 US-09-438-185A-784 Sequence 78	3 440 2 US-09-248-796A-17146 Sequence 17 3 445 2 US-10-104-047-2209 Sequence 22	3 450 1 US-08-818-514-6 Sequence 6, 3 450 2 US-09-115-934A-6 Sequence 6,	3 450 2 US-09-611-175-6 Sequence 6, 3 460 2 US-09-489-039A-11840 Sequence 11	3 470 2 US-09-902-540-16052 Sequence 16 472 2 US-09-605-703B-1400 Sequence 14	.3 472 2 US-09-605-703B-1426 Sequence 1426, .3 472 2 US-09-605-703B-1428 Sequence 1428, .3 532 2 US-09-489-039A-9142 Sequence 9142,
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33 50.8 415 2 US-09-538-092-708 33 50.8 425 1 US-08-109-0802A-58 33 50.8 425 1 US-08-109-0802A-58 33 50.8 425 2 US-08-477-346-58 33 50.8 425 2 US-08-477-072A-58 33 50.8 425 2 US-08-477-072A-58 33 50.8 425 2 US-09-538-092-1288 33 50.8 425 2 US-09-542-735E-17 33 50.8 425 2 US-09-542-735E-17 33 50.8 426 2 US-09-644-735E-17 33 50.8 426 2 US-09-643-94 33 50.8 432 2 US-09-443-041A-20 33 50.8 432 2 US-09-443-041A-20 33 50.8 432 2 US-09-673-395A-194		33 50.8 546 2 US-09-909-064-250 Sequence 250 33 50.8 546 2 US-09-909-064-250 Sequence 250 33 50.8 546 2 US-09-906-618-250 Sequence 250 33 50.8 546 2 US-09-906-646-250 Sequence 250 33 50.8 546 2 US-09-906-646-250 Sequence 250 34 50.8 546 2 US-09-906-646-250 Sequence 250 35 50.8 546 2 US-09-906-646-250 Sequence 250 36 50.8 546 2 US-09-906-646-250 Sequence 250 37 50.8 546 2 US-09-906-646-250 Sequence 250 38 50.8 546 2 US-09-906-646-250 Sequence 250 39 50.8 62 20339 ALIGNMENTS ALIGNMENTS ALIGNMENTON: POLYMORPHISMS IN KNOWN GENES ASSOCIATED LE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USING PAPLICATION NUMBER: 60/241,755 OR FILING DATE: 2000-10-3 OR APPLICATION NUMBER: 60/241,755 OR FILING DATE: 2000-10-03 OR PILING DATE: 2000-10-03	; SEQ ID NO 8330 ; LENGTH: 547 ; TENGTH: 547 ; ORGANISM: Human US-09-949-016-8330 Query Match Best Local Similarity 100.0%; Pred. No. 0.015; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 YALWWSPNGK 10 Db 217 YALWWSPNGK 226
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US-09-248-796A-26 US-09-252-991A-28 US-09-107-433-446 US-09-1107-433-446 US-09-134-000C-65 US-09-134-000C-65 US-09-198-452A-89 US-09-198-452A-89 US-09-252-991A-23 US-08-464-45 US-08-875-272-6	US-08-679-493A-21 US-09-489-039A-11 US-09-489-039A-11 US-09-252-991A-19 US-09-252-991A-20 US-09-252-991A-20 US-09-252-991A-20 US-09-252-991A-20 US-09-902-540-124 US-09-902-540-136-10 US-09-303-518D-70 US-09-303-518D-70 US-09-303-518D-70 US-09-303-518D-70 US-09-303-518D-70 US-09-303-518D-70 US-09-303-518D-70 US-09-303-518D-70 US-09-303-518D-70 US-09-303-518D-70 US-09-303-518D-70 US-09-303-518D-70 US-09-303-518D-70	18-09-540-26-3796 18-09-248-796A-23710 28-09-248-796A-23710 28-09-349-016-11599 28-08-09-349-016-11599 28-08-09-348-796A-13 28-09-248-796A-19874 28-08-48-796A-19874 28-08-48-796A-19874 28-08-48-796A-19874 28-08-48-796A-19874 28-08-48-70-10-10-10-10-10-10-10-10-10-10-10-10-10	US-0 US-0 US-0 US-0 US-0 US-0 US-0 US-0
144 8 8 150 150 167 167 167 172 8 172 8 193 8 193	88 88 88 88 88 88 88 88 88 88 88 88 88	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8

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APPLICANT: Zimmermann, Rainer; Park, John E.;
APPLICANT: Retrig, Wolfgang; Old, Lloyd J.
TITLE OF INVENTION: ISOLATED DIMERIC FIBROBLAST ACTIVATION
TITLE OF INVENTION: PROTEIN ALPHA, AND USES THEREOF
NUMBER OF SEQUENCES:
CORRESPONDENCE : 10
CORRESPONDENCE : LODDESS:
ADDRESSE: Felfe & Lynch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 65; DB 1; Length 760; 100.0%; Pred. No. 0.021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIE: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 2.0 MB storage
COMPUTER: IBM P8/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordberfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,391
CLASSIFICATION 5430
PRIOR APPLICATION DATA:
APPLICATION NATA:
APPLICATION NUMBER: 08/619,280
                       FILING DATE: 1B-MARCH-1996

FILING DATE: 1B-MARCH-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NAMER: 08/230,491

FILING DATE: 20-APRIL-1994

ATTORNEY/AGENT INFORMATION:
NAME: HANSON, NO. 5767242man D.
REGISTRATION NUMBER: 30,946

REGISTRATION NUMBER: 30,946

RETERENCE/DOCKET NUMBER: 30,946

RELEPOMMUNICATION INFORMATION:
TELEPOMMUNICATION INFORMATION:
TELEPOMMUNICATION INFORMATION:
TELEPOMMUNICATION INFORMATION:
TELEPOMMUNICATION SEQ 1D NO: 2:
SEQUENCE FRARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 18-MACH-1996
APPLICATION NUMBER: 08/230,491
FILING DATE: 20-APRIL-1994
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Hanson, No. 5965373man D. REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-940-391-2
; Sequence 2, Application US/08940391
; Patent No. 5965373
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TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 805 Third Avenue CITY: New York City STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                 760 amino acida
CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      210 YALWWSPNGK 219
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                                                                                                                                                                                                                                                                                                                                                                                                amino acid
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Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                FOPOLOGY:
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APPLICANT: Zimmermann, Rainer; Park, John E.;

APPLICANT: Estige Wolfgang; Old, Lloyd J.

TITLE OF INVENTION: ISOLATED DIMERIC FIBROBLAST ACTIVATION PROTEIN

TITLE OF INVENTION: ALPHA, AND USES THEREOF

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Felie & Lynch

STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                 GENERAL INFORMATION:
APPLICANT: Rettig, Wolfgang J.; Scanlan, Matthew J.;
APPLICANT: Garin-Chea, Pilar; Old, Lloyd J.
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE CODING FOR TITLE OF INVENTION: FIBROBLAST ACTIVATION PROTEIN AND USES TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 760; 0.021;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE 3.5 inch 1.2 MB STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT - ASC II
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/230,491A
FILING DATE: 20-APRIL-1994
CLASSIFICATION: NO. 5587299man D.
RADELSTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 330
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 2.0 MB
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                                                                                                                                                                                                                                           TITLE OF INVINER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: FELFE & LYNCH
cTDRET: 805 THIRD AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08619280A Patent No. 5767242
                                                                    Sequence 2, Application US/08230491A
Patent No. 5587299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                        NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 760 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                       10022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 10; Conservative
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OPERATING SYSTEM:
SOFTWARE: Wordper
                                                                                                                                                                                                                                                                                                                                                   CITY: NEW YORK STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-230-491A-2
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                              RESULT 2
US-08-230-491A-2
                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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RESULT 5

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81.5%; Score 53; DB 4; Length 593; 100.0%; Pred. No. 1.4;
TITLE OF INVENTION: PROLYL PEPTIDASES AND. METHODS OF USE FILE REFERENCE: 235.00190101
CURRENT APPLICATION NUMBER: US/09/518,550
CURRENT FILING DATE: 2000-03-03;
PRIOR APPLICATION NUMBER: 60/123,148
PRIOR PILING DATE: 1999-03-05
PRIOR PILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 26
LENGTH: 761
                                                                                                                                                                                                                                                                                                                                                                              92.3%; Score 60; DB 2; Length 761; 90.0%; Pred. No. 0.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Morimoto, Chikao
APPLICANT: Schlossman, Stuart F.
APPLICANT: Schlossman, Stuart F.
APPLICANT: Tanaka, Toshiaki
TITLE OF INVENTION: HUMAN CD26 AND METHODS FOR USE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIREBI: Cas Franklin Street
CITY: Boston
COUNTRY: Boston
COUNTRY: 0210-2804

ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 180 F5/2 Model 502 or 55X
OPERATING SYSTEM: 1BM P.C. DOS (Version 3.30)
SOFTWARE: MORDERFECT (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07923
FILING DATE: 19930819
CLASSIFICATION NUMBER: 07/934,162
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: 07/934,162
FILING DATE: 06-FEB-1992
APPLICATION NUMBER: 07/832,211
FILING DATE: 06-FEB-1992
APPLICATION NUMBER: 07/832,211
REGISTRATION NUMBER: 34,819
REGISTRATION NUMBER: 07/832,211
TELEPOMONICATION NUMBER: 00530/055002
TELECOMONICATION INPORMATION:
TELEPOMONICATION INPORMATION:
TELEPOMONICATION NUMBER: 00530/055002
                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CT-US93-07923-11
Sequence 11, Application PC/TUS9307923
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 200154
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                     Query Match 92.3
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 YALWWSPNGK 10
                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Mus musculus
US-09-518-550-26
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09265606;
Patent No. 6846910
GENERAL INFORMATION:
APPLICANT: Zimmermann, Rainer; Park, John E.;
APPLICANT: Zimmermann, Rainer; Park, John E.;
APPLICANT: Zimmermann, Rainer; Park, John E.;
APPLICANT: ALIMERATION: ISOLATED DIMERIC FIBROBLAST ACTIVATION PROTEIN
TITLE OF INVENTION: ALPHA, AND USES THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STRTE: New York City
COUNTRY: USA
                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                               100.0%; Score 65; DB 1; Length 760; 100.0%; Pred. No. 0.021;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 2.0 MB
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                 0; Mismatches
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CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 18-MARCH-1996
PILING DATE: 20-APRL-1994
ATTONNEY AGENT INFORMATION:
NAME: HANSON, NO. 6846910man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: 10,946
REFERENCE/DOCKET NUMBER: LUD 5330.1
TELECHONE: (212) 689-9200
TELECHONE: (212) 898-3884
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 760 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-265-606-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265,606
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 26, Application US/09518550
Patent No. 6875851
GENERAL INFORMATION:
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APPLICANT: POTEMPA, Jan
APPLICANT: BANBULA, Agnieszka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 10; Conservative
                                                                    Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                        210 YALWWSPNGK 219
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US-09-518-550-26
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                          US-08-940-391-2
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PATENT NO. 336.72.

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rettig, Wolfgang J.; Scanlan, Matthew J.;
APPLICANT: Garin-Chesa Pilar; Old, Lloyd J.
ITILE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE CODING FOR TITLE OF INVENTION: FIBROBLAST ACTIVATION PROTEIN 'AND USES TITLE OF INVENTION: THEREOF NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: FELFE & LYNCH

' ADDRESSEE: FELFE & LYNCH

' TOTAL OF SECULIARIES AND AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 759;
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MEDIUM TYPE: DISKETTE 3.5 inch 1.2 MB STORAGE
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
CORREATING SYSTEM: PC-DOS
SOFTWARE: WREDPERRECT - ASC II
APPLICATION DATE:
APPLICATION NUMBER: US/08/230,491A
FILING DATE: 20-APRIL-1994
                                                                                                                                                                                   OPERATING SYSTEM: 1EM F.C. DOS (VETSIC)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07923
FILING DATE: 19930819
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934,162
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: 07/832,211
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: FERSET, JANIS K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00530/055002
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  00530/055002
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NTTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5587299man D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08230491A Patent No. 5587299
                                                                                                                                 MEDIUM TYPE: 3.5" Diskette, 1
COMPUTER: IBM PS/2 Model 50Z
OPERATING SYSTEM: IBM P.C. DC
225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (617) 542-5070
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10022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                             Massachusetts
                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" Di
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                                                               COUNTRY: U.S.A.
ZIP: 02110-2804
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COUNTRY:
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         0; Indels
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GENERAL INFORMATION:
APPLICANT: Morimoco, Chikao
APPLICANT: Morimoco, Chikao
APPLICANT: Tanaka, Toshiaki
TITLE OF INVENTION: HUMAN CD26 AND METHODS FOR USE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
                                                                                                                                                                                            Sequence 3, Application PC/TUS9307923
GENERAL INFORMATION:
APPLICANT: Morimoto, Chikao
APPLICANT: Tanaka, Toshiaki
TITLE OF INVENTION: HUMAN CD26 AND METHODS FOR USE
NUMBER OF SEQUENCES: 16
CORRESPONDENCES:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READBLE PRAM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
COMPUTER: IBM PS/2 Model 502 or 55SX
COPENATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07923
FILING DATE: 19930819
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934,162
APPLICATION NUMBER: 07/934,162
APPLICATION NUMBER: 07/932,211
FILING DATE: 21-AUG-1992
ATPONNEY/AGENT INFORMATION:
ANNEY AGENT INFORMATION:
         0; Mismatches
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (617) 542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Fraser, Janis K. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100
Matches 8; Conservative
         8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Boston
STATE: Massachusetts
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                                                                                               213 ALWWSPNG 220
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                                                  2 ALWWSPNG 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
PCT-US93-07923-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
           Matches
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Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-940-391-3
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US-09-794-236-1
               S-08-940-391-3
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                                                                                                                                                                                                                                                                             RESULT 11
US-0B-619-280A-3
; Sequence 3, Application US/08619280A
; Patent No. 5767242
; GENERAL INFORMATION:
; APPLICANT: Zimmermann, Rainer; Park, John E.;
; APPLICANT: Simmermann, Rainer; Park, John E.;
; TITLE OF INVENTION: ISOLATED DIMERIC FIBROBLAST ACTIVATION PROTEIN
; TITLE OF INVENTION: ALPHA, AND USES THEREOF
; NUMBER OF SEQUENCES:
; ADDRESSEE: Felfe & Lynch
; STATE: New York City
; STATE: New York
                                                                                                                                                                                        Gaps
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                                                                                                                                                           DB 1; Length 766;
1.8;
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                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Prec. ...
                                                                                                                                                                                        0; Mismatches
REGISTRATION NUMBER: 30,946
REPRENCE/DOCKET NUMBER: LUD 330
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEPAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 3:
SEGUENCE CHARACTERISTICS:
EBGUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                             Query Match 81.5
Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                         TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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                                                                                                                                    US-08-230-491A-3
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Sequence 1, Application US/08940191
PEREMALINIA CALLONIC ZEMENTARION SET SEQUENCE 1, Application US/08940191
PEREMALINIA OF INVESTION ENCLAY DIMERIC FIREOGRAPHICANT ZEMENTARION ENCLANGE AND USES THEREOF TITLE OF INVESTION ENCLAYS DIMERIC FIREOGRAPHICANT ZEMENTARION ENCLANGE AND USES THEREOF CORRESPONDED TO THE APPLICANT APPLICAN
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Sequence 3, Application US/09265606; Sequence 3, Application US/09265606; Patent No. 6846910
| GENERAL INFORMATION:
| APPLICANT: Zimmermann, Rainer; Park, John E.;
| APPLICANT: Ettig, Wolfgang; Old, Lloyd J. ITLE OF INVENTION: ISOLATED DIMERIC FIBROBLAST ACTIVATION PROTEIN TITLE OF INVENTION: ALPHA, AND USES THEREOF NUMBER OF SEQUENCES: 10
| CORRESPONDENCE ADDRESS: ADDRESS: Felfe & Lynch STREET: 805 Third Avenue CITY: New York City STATE: New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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APPLICANT: POTENTA, James
TITLE OF INVENTION: PROLYL PEPTIDASES AND METHODS OF USE
FILE REFERENCE: 235.00190101
CURRENT APPLICATION NUMBER: US/09/518,550
CURRENT PILLING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: 60/123,148
PRIOR PILING DATE: 2000-03-05
PRIOR APPLICATION NUMBER: PCT/US00/05551
PRIOR PILING DATE: 2000-03-05
NUMBER OF SEQ ID NOS: 48
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                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 10022
COMPUTER REALABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 2.0 MB storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: _ PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/619,280
FILING DATE: 18-MARCH-1996
APPLICATION NUMBER: 08/230,491
FILING DATE: 20-APRIL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Hanson, No. 6846910man D. REGISTRATION NUMBER: 30,946 REFERENCE/DOCKET NUMBER: LUD 5330.1 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265,606
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   766 amino acids
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Best Local Similarity 100.
Matches 8; Conservative
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Patent No. 6586198

Patent No. 6586198

Patent No. 6586198

APPLICANT: Vanderbilt University
APPLICANT: Brown, Nancy J.
TITLE OF INVENTION: INDICATION UNIVERSES AND DIAGNOSTIC TESTS FOR ANGIOTENSIN CONVERTINTING OF INVENTION: INHIBITOR AND VASOPEPTIOASE INHIBITOR ASSOCIATED ANGIOEDEMA FILE REFERENCE: Atty Docket No. 6586198 1242/48/2

CURRENT APPLICATION NUMBER: 60/244,524

PRIOR APPLICATION NUMBER: 60/244,524

PRIOR APPLICATION NUMBER: 60/244,524

PRIOR APPLICATION NUMBER: 60/244,524

PRIOR SEQ ID NOS: 10

SOFTWARE: Patent In version 3.1
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Sequence 6146, Application US/09949016

Patent No. 6812339

Patent No. 6812339

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR PILING DATE: 2000-10-03

SOFTWARE FASTSEQ for Windows Version 4.0

SEQ ID NOS: 207012

SOFTWARE FASTSEQ for Windows Version 4.0
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              Score 53; DB 2; Length 766;
Pred. No. 1.8;
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                                                           0; Indels
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81.5%; Sc.
100.0%; Pre
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Best Local Similarity 100.
Matches 8; Conservative
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Best Local Similarity 100.
Matches 8; Conservative
                   Query Match
Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                                                                      213 ALWWSPNG 220
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 ALWWSPNG 9
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-949-016-6146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 6
LENGTH: 766
                                                                                                                                                                                                                           RESULT 14
US-10-002-593-6
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APPLICANT: Kimberly Brown
APPLICANT: Kimberly Brown
APPLICANT: Kimberly Brown
APPLICANT: Michael W. Rey
APPLICANT: Michael W. Rey
APPLICANT: Michael W. Rey
APPLICANT: Alan Klotz
APPLICANT: Tony Byun
TITLE OF INVENTION: Polypeptidase Activity And Nucleic Acids Encoding Same
TITLE OF INVENTION: Aminopeptidase Activity And Nucleic Acids Encoding Same
TITLE OF INVENTION: Aminopeptidase Activity And Nucleic Acids Encoding Same
FILE REFERENCE: 5254.200-US
CURRENT APPLICATION NUMBER: 08/857,884
PRIOR FILING DATE: 1997-05-15
PRIOR PLING DATE: 1997-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 771
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                          Indels
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APPLICANT: Nestec S.A.
APPLICANT: Mond, Michel
APPLICANT: Mond, Michel
APPLICANT: Affolter, Micheal
APPLICANT: Affolter, Micheal
APPLICANT: Van Den Broek, Peter
TITLE OF INVENTION: CLONING OF THE
TITLE OF INVENTION: ASPERGILLUS ORYZAE
TITLE OF INVENTION: ASPERGILLUS ORYZAE
FILE REPRENCE: 8265-298
CURRENT FILIATION NUMBER: US/09/462,284
CURRENT FILIATION DATE: 2000-01-03
NUMBER OF SEQ ID NOS: 9
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Pred. No. 24;
3; Mismatches C
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Pred. No. 24;
3; Mismatches
Best Local Similarity 100.0%; Pred. No. 1.8; Matches 8; Conservative 0; Mismatches
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; Sequence 2, Application US/09079592B
Patent No. 6664092
; GENERAL INFORMATION:
                                                                                                                                                                                                                               Sequence 2, Application US/09462284
Patent No. 6309868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70.8%;
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Best Local Similarity 70.0%;
Matches 7; Conservative
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US-09-079-592-2
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Best Local Similarity 70.0
Matches 7; Conservative
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205 YALWFSPDGE 214
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                                                                                                            222 ALWWSPNG 229
                                                                     2 ALWWSPNG 9
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ORGANISM: Fungus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Fas
SEQ ID NO 2
LENGTH: 771
                                                                                                                                                                                      RESULT 20
US-09-462-284-2
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Patent No. 6887679
GENERAL INPORMATION:
TITLE OF INVENTION:
INTILE OF INVENTION AND VASOPEPTIDASE INHIBITOR ASSOCIATED ANGIOEDEMA
FILE REPERENCE: Atry Docket No. 6887679 1242/48/2
CURRENT APPLICATION NUMBER: US/10/423,714
PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PALENTIN VERSION 3.1
SEQ ID NO 6
LENGTH: 766
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Sequence 10450, Application US/09949016

Sequence 10450, Application US/09949016

SENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE OF INVENTION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-10-20
PRIOR PELING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FeatSEQ for Windows Version 4.0
SEQ ID NO 10450
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                                                                                                                                                              Score 53; DB 2; Length 766;
Pred. No. 1.8;
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                                                                                                                                                                                                              0; Indels
                                                                                                                                                              Query Match 81.5%; Score 53; DB Best Local Similarity 100.0%; Pred. No. 1.8 Matches 8; Conservative 0; Mismatches
  SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 27
LENGTH: 766
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Matches 8; Conservative
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                                                                                             ) ORGANISM: Homo sapiens
US-09-518-550-27
                                                                                                                                                                                                                                                                                                         213 ALWWSPNG 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                            2 ALWWSPNG 9
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                                                                            TYPE: PRT
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Gaps
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Patent No. 6114159
GENERAL INFORMATION:
APPLICANT: WILL, Horst
APPLICANT: WILLAND, Bernd
TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
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                                                               Score 44; DB 1; Length 323;
Pred. No. 20;
1; Mismatches 3; Indels
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/704,711A

FILING DATE: 20-NOV-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: WO PCT/DE95/00357

FILING DATE: 17-MAR-1995

PRIOR APPLICATION NUMBER: DE 4438838.1

FILING DATE: 21-OCT-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE 4409663.1

FILING DATE: 17-MAR-1994

ATTORNEY/AGENT INFORMATION:

NAME: GRANADOS, PRITICIA D.

REFERENCE/POCKET NUMBER: 33,683

REFERENCE/POCKET NUMBER: 33,683

REFERENCE/POCKET NUMBER: 26083/124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 43; DB 2;
Pred. No. 53;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STARE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                 Query Match
Best Local Similarity 60.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 904136
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 579 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOley & La
; MOLECULE TYPE: peptide US-08-838-543-4
                                                                                                                                                           1 YALWWSPNGK 10
                                                                                                                                                                                                     90 FRLWWIPKGK 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-704-711A-1
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                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Blater, Steven C.
APPLICANT: Wiegand, Roger C.
APPLICANT: References and Uses Thereof
CURRENT APPLICATION NUMBER: 60/217,883
FRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 11805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 45; DB 2; Length 574;
Pred. No. 25;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTY: UNITED STATES OF AMERICA

ZIF: 19898
COMPUTER READBLE FORM:
MEDIUM TYPE: 3.50 INCH DISKETTE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD FOR WINDOWS 95
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1007 MARKET STREET
CITY: WILMINGTON
CONTACT
CITY: DELAWRDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/08838543
Patent No. 5994623
GENERAL INFORMATION:
APPLICANT: REBBERS, ENNO
APPLICANT: BROGLIE, KAREN E.
TITLE OF INVENTION: CORN 4-(-GLUCANOTRANSFERASE
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DUFONT DE NEMOURS AND COMPANY
                                                                                                                                   Sequence 11805, Application US/09902540 Patent No. 6833447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: MAJARIAN, WILLIAM R.
REGIGTRATION NUMBER: P-41,173
REFERENCE/DOCKET NUMBER: BB-1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-92-4926
TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 323 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Myxococcus xanthus US-09-902-540-11805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 85.7
Matches 6; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 WWSPNGK 10
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Sequence 1, Application US/08448489
; Sequence 1, Application US/08448489
; Patent No. 6184022
; GENERAL INFORMATION:
    APPLICANT: SEIKI, Motoharu
    APPLICANT: SHINGAMA, Akira
    APPLICANT: SHINGAMA, Akira
    TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
    FILLE REFERENCE: 55-290F
    CURRENT APPLICATION NUMBER: US/08/448,489
    CURRENT PILING DATE: 1995-06-07
    NUMBER OF SEQ ID NOS: 19
    SOFTWARE: PatentIN Ver. 2.0
    SEQ ID NO 1
    LENGTH: 582
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Pred. No. 53;
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                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
FILING APPLICATION 435
PRIOR APPLICATION A15
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
BAPPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
BRIOR APPLICATION DATA:
APPLICATION NUMBER:
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APPLICATION NUMBER:
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BRIOR APPLICATION DATA:
ATTOMNOMBER:
AT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALIONARIA GRANADOS, PERTICIA D.
REGISTRATION NUMBER: 33,683
REPERBNCE/POCKET NUMBER: 26083/124
TELECOMMUNICATION INFORMATION:
TELEFAX: (202)672-5399
TELEFAX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 582 anino acids
                      COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release
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Best Local Similarity 77.5
Best Local Similarity 77.5
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US-08-448-489-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: Si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
Washington
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                             Sequence 1, Application US/09521220
| Patent No. 6399348
| GENERAL INFORMATION:
| APPLICANT: WILL, Horst
| HINZMANN, Bernd
| TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08704711A
Patent No. 6114159
GENERAL INFORMATION:
APPLICANT: WILL, Horst
APPLICANT: HINZWANN, Bernd
TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
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Pred. No. 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/521,220
FILING DATE: 00-Mar-2000
CLASSIFICATION: cUnknown>
                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: GRANDOS, Patticia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 26083/124
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/704,711
FILING DATE: «Unknown»
APPLICATION NUMBER: DE 4438838.1
FILING DATE: 21-0CT-1994
APPLICATION NUMBER: DE 4409663.1
FILING DATE: 17-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: bingle sequence: studies sequence description: Sequence description: Seq ID NO: 1: US-09-521-220-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-OCT-1994
17-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                             STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 904136
TELEX: 904136
INFORMATION FOR SEQ 1D NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 579 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
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77.8%;
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                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 77.8
Matches 7; Conservative
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415 ALFWMPNGK 423
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US-08-704-711A-2
         US-09-521-220-1
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TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,
TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
TITLE OF INVENTION: OF USING SAME
FILE REFERENCE: 6073.US.P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66.2%; Score 43; DB 2; Length 582;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/521,220
FILING DATE: 08-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 43; DB 2;
Pred. No. 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 26083/124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/704,711
FILING DATE: «Unknown»
APPLICATION NUMBER: DE 4438838.1
FILING DATE: 21-0CT-1994
APPLICATION NUMBER: DE 4409663.1
FILING DATE: 17-MAR-1994
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CURRENT APPLICATION NUMBER: US/09/391,104
CURRENT FILING DATE: 1999-09-07
PRIOR APPLICATION NUMBER: US 08/814,394
PRIOR FILING DATE: 1997-03-11
PRIOR FILING DATE: 35
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE DESCRIPTION: SEQ ID NO: 2
                                                                                                                                                                                                                                             21-OCT-1994
17-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                      , Patricia D.
                                                                                                                                                                                                                        CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 28, Application US/09391104
Patent No. 6399371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 582 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
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Magnuson, Scott R.
Morgan, Douglas W.
                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                  ZIP: 20007-5109
COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 77.8'
'... 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: GRANADOS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 418 ALFWMPNGK 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
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TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
METALLOPROTEASES, THEIR PRODUCTION AND USE
                                                                               APPLICANT: de Saint-Vis, Blandine Marie
APPLICANT: de Saint-Vis, Erancois
APPLICANT: Caux, Christophe
APPLICANT: Lebecque, Serge J.E.
TITLE OF INVENTION: Mammalian Proteinases; Related Reagents
TITLE OF INVENTION: and Methods
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Por-
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/211,704A
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ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/005,263
FILING DATE: 09-JAN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                    : 901 California Avenue
Palo Alto
California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             not relevant
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TYPE: amino acid
STRANDEDNESS: not releva
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Best Local Similarity 77.8
Matches 7; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 582 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
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418 ALFWMPNGK 426
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Patent No. 6399348
GENERAL INFORMATION:
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                                                                                 US-09-211-704A-9
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CITY: Pa
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APPLICANT: SEIKI, Motoharu
APPLICANT: SATO, Hiroshi
APPLICANT: SATO, Hiroshi
APPLICANT: SHINGAWA, Akira
APPLICANT: SHINGAWA, Akira
TITLE OF INVENTION: NOVEL METALLOPROFEINASE AND ENCODING DNA THEREFOR
CURRENT APPLICATION NUMBER: US/09/689,730
CURRENT FILING DATE: 1000-10-13
PRIOR APPLICATION NUMBER: US/08/448,489
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 1
LENGTH: 582
                                                                                                                                                      Sequence 84, Application US/09919497;
Sequence 8773883;
GENERAL INFORMATION:
APPLICANT: MALTELE, GEOTGE L.
TITLE OF INVENTENT ENCHOUSTIC CLASSIFICATION OF ENDOMETRIAL CANCER;
FILE REFERENCE: B0801/7225
CURRENT APPLICATION NUMBER: US/09/919,497
CURRENT PILING DATE: 2001-07-31
PRIOR PILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 100
SOFTWARE: Patentin version 3.0
SEQ ID NO 84
LENGTH: 582
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                 Gaps
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Pred. No. 53;
1; Mismatches 1; Indels
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               Indels
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Pred. No. 53;
1; Mismatches
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Parent No. 6747137
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09689730 Patent No. 6825024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66.2%;
77.8%;
77.8%;
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Best Local Similarity 77.6
English 77.6
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Best Local Similarity 77.8
Matches 7; Conservative
Best Local Similarity 77.8
Matches 7; Conservative
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418 ALFWMPNGK 426
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418 ALFWMPNGK 426
                                                                    418 ALFWMPNGK 426
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ORGANISM: Homo sapiens
US-09-919-497-84
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ORGANISM: Homo sapiens
                                                2 ALWWSPNGK 10
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US-09-248-796A-18040
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US-09-919-497-84
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US-09-689-730-1
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TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN.
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196-132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR PAPLICATION NUMBER: US 60/074,725
PRIOR PAPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 1840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 702, Application US/09198452A
Fatent No. 6559294
GENERAL INFORMATION:
APPLICANT: Griffais, R.
TITLE OF INVENITON: thereof and uses thereof, in particular for the diagnosis, prever
TITLE OF INVENITON: thereof and uses thereof, in particular for the diagnosis, prever
TITLE OF INVENITON: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NOS: 6849
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Patent No. 6747137

GENERAL INFORMATION:
TITLE OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANTITLE OF INVENTION: UNCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
PRIOR FILING DATE: 1998-08-13
PRIOR FILING DATE: 1998-08-13
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Pred. No. 45;
1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                            66.2%;
100.0%;
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ORGANISM: Chlamydia pneumoniae
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Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 6; Conservative
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US-09-198-452A-702
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LENGTH: 396
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Gaps
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Pred. No. 59;
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APPLICANT: Stephens, Richard
APPLICANT: Mitchell, Wayne
APPLICANT: Mitchell, Wayne
APPLICANT: Mitchell, Wayne
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
FILE REFERENCE: 018941-000411US
CURRENT PELING NUMBER: US/09/438,185A
CURRENT FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: US 60/108,279
PRIOR APPLICATION NUMBER: US 60/128,606
PRIOR FILING DATE: 1999-04-08
                                                                                                                                                                                                                                                                                                                                                                        Length 443;
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Pred. No. 58;
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                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                           , NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...443
; SEQUENCE DESCRIPTION: SEQ ID NO: 7119:
US-09-107-532A-7119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 1074
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
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                TELECOMMUNICATION INFORMATION TELEPHONE: (781)893-5007
                                                                         INFORMATION FOR SEQ ID NO: 7119: SEQUENCE CHARACTERISTICS: LENGTH: 443 amino acids TYPE: amino acid
                                                         (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Chlamydia pneumoniae
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70.0%;
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66.7%;
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Best Local Similarity 66.7-
5. Conservative
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Best Local Similarity 70.0
Matches 7; Conservative
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                                                                                                                                                                                                                                                       FEATURE:
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APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: UNCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NOS: 8344
LENGTH: 400
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                    Gaps
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                                                         Length 396,
                                                                                                  0; Indels
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CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                               ed. No. 51;
Mismatches
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FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 42;
Pred. No.
                                                             Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM RYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-107-532A-7119
; Sequence 7119, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                             US-09-543-681A-5821
; Sequence 5821, Application US/09543681A
; Patent No. 6605709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 100 Beaver Street
CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64.6%;
                                                             64.6%;
71.4%;
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US-09-543-681A-5821
; ORGANISM: Candida albicans
US-09-248-796A-19923
                                                           Query Match
Best Local Similarity 71.4
Matches 5; Conservative
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Best Local Similarity
Matches 6; Conserv
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sequence 5, Application US/09976674

sequence 5, Application US/09976674

parent No. 6844180

GENERAL INFORMATION:

APPLICANT: Oliver, Pierre

APPLICANT: Alinenya, Karen

APPLICANT: Alinenya, Karen

APPLICANT: Application NOVEL SERINE PROTEASE GENES RELATED TO DPPIV

FILE REFERENCE: 70669

CURRENT APPLICATION NUMBER: US/09/976,674

CURRENT APPLICATION NUMBER: US 60/240,117

PRIOR APPLICATION NUMBER: US 60/240,117

PRIOR FILING DATE: 2000-10-12

NUMBER OF SEQ ID NOS: 61

SOFTWARE: Patentin version 3.1

SEQ ID NO 5

LENGTH: 796
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       APPLICANT: TILDOULEY, CACTELLIRE P., AUGULICANT: GULUNIAJAN, Rajagopal; Tang, Y. Tom;
APPLICANT: Gururajan, Rajagopal; Tang, Y. Tom;
APPLICANT: Hernandez, Roberto; Buggan, Brendan M.
TITLE OF INVENTION: PROTEASES
FILE REFERENCE: PI-0212 USN
CURRENT APPLICATION NUMBER: US/10/363,937
CURRENT APPLICATION NUMBER: US/021/28161
PRIOR APPLICATION NUMBER: US 60/231,039
PRIOR APPLICATION NUMBER: US 60/231,039
PRIOR PILING DATE: 2000-09-08
PRIOR PILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/234,850
PRIOR PILING DATE: 2000-09-15
PRIOR PILING DATE: 2000-09-22
PRIOR PILING DATE: 2000-09-22
PRIOR PILING DATE: 2000-09-29
PRIOR PILING DATE: 2000-10-1
PRIOR APPLICATION NUMBER: US 60/239,658
PRIOR PILING DATE: 2000-10-1
NUMBER OF SEQ ID NOS: 34
SEQ ID NO 4
SEQ ID NO 4
LENGTH: 743
Tribouley, Catherine M.; Khan, Farrah A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6927056 2923874CD1
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Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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ORGANISM: Homo sapiens
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US-09-976-674-5
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Sequence 41, Application US/09976674

PREEDL INFORMATION:
APPLICANT: Q1, Steven
APPLICANT: Akinsanya, Karen
APPLICANT: Akinsanya, Karen
APPLICANT: Akinsanya, Karen
APPLICANT: Unien, Jean-Louis
TILLE OP INVENTION: NOVEL SERINE PROTEASE GENES RELATED TO DPPIV
FILE REPERENCE: 70669
CURRENT PILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,117
PRIOR FILING DATE: 2000-10-12
NUMBER: OF SEQ ID NOS: 61
SOFTWARE: Patentin version 3.1
SEQ ID NO 41
LENGTH: 706
  APPLICANT: Junien, Jean-Louis
TITLE OF INVENTION: NOVEL SERINE PROTEASE GENES RELATED TO DPPIV
FILE REPERENCE: 70669
CURRENT APPLICATION NUMBER: US/09/976,674
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,117
PRIOR APPLICATION NUMBER: US 60/240,117
PRIOR PILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 61
SSQ ID NO 43
LENGTH: 691
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95;
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APPLICANT: Gandhi, Ameena R.; Nguyen, Danniel B.;
APPLICANT: Hafalia, April U.A.; Kearney, Liam;
APPLICANT: Lu, Yan; Lee, Ernestine A.;
APPLICANT: Chawla, Narinder K.; Das, Debopriya;
APPLICANT: Arvizu, Chandra S.; Yao, Monique G.;
APPLICANT: Kallick, Deborah A.; Elliott, Vicki S.;
APPLICANT: Rallick, Deborah A.; Elliott, Vicki S.;
APPLICANT: Reddy, Roopa; Burford, Neil;
APPLICANT: Baughn, Mariah R.; Lal, Preeti G.;
APPLICANT: Baughn, Markiah R.; Lal, Preeti G.;
APPLICANT: Ramkumar, Jayalaxmi; Yang, Junming;
                                                                                                                                                                                                                                                                                                                                                                Score 42; DB Pred. No. 93; 2; Mismatches
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Pred. No.
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Patent No. 6927056
GENERAL INFORMATION:
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66.7%;
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66.7%;
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Best Local Similarity 66.7
Matches 6; Conservative
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151 AHWWSPDGE 159
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ORGANISM: Homo sapiens
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CORGANISM: Homo sapiens
US-09-976-674-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 40
US-09-976-674-41
                                                                                                                                                                                                                                                                                                                 US-09-976-674-43
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US-10-363-937-4
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LENGTH: 818
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US-10-401-436-3
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APPLICANT: Estell, David A.
TITLE OF INVENTION: Proteases From Gram-Positive Organisms
FILE REFERENCE: GC382-US
CURRENT APPLICATION NUMBER: US/10/402,312
CURRENT FILING DATE: 2003-03-26
PRIOR APPLICATION NUMBER: EFF 97305237.7
PRIOR APPLICATION NUMBER: EF 97305237.7
PRIOR PILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 818;
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Patent No. 6849440
GENERAL INFORMATION:
TITLE OF INVENTION: Proteases From Gram-Positive Organisms FILE REFERENCE: G0382-US
CURRENT APPLICATION NUMBER: US/10/401,437
CURRENT FILING DATE: 2003-03-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                le+02;
2; Indels
                                                GENERAL INFORMATION:
APPLICANT: Escell, David A.
TITLE OF INVENTION: Proceases From Gram-Positive Organisms
FILE REFERENCE: GC382-US
CURRENT PELING NUMBER: US/09/462,845
CURRENT FILING DATE: 2000-01-13
PRIOR APPLICATION NUMBER: PCT/US98/14647
PRIOR PILING DATE: 1998-07-14
PRIOR FILING DATE: 1998-07-14
PRIOR FILING DATE: 1998-07-15
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Pred. No. 1.1e+02
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 818
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Patent No. 6833261
       Sequence 3, Application US/09462845
Patent No. 6723550
                                                                                                                                                                                                                                                                                                                                                                         64.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT; ORGANISM: Bacillus subtilis
US-10-402-312-3
                                                                                                                                                                                                                                                                                                                    , ORGANISM: Bacillus subtilis
US-09-462-845-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 75.0
Matches 6; Conservative
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Matches 6; Conserv
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US-09-462-845-3
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; Sequence 3, Application US/10401436
; Patent No. 6911333
; GENERAL INFORMATION:
APPLICANT: Estell, David A.
TITLE OF INVENTION: Proteases From Gram-Positive Organisms
FILE REFERENCE: GC382-US
CURRENT APPLICATION NUMBER: US/10/401,436
CURRENT FILING DATE: 2003-03-26
PRIOR APPLICATION NUMBER: PCT/US98/14647
PRIOR APPLICATION NUMBER: PCT/US98/14647
; PRIOR PILING DATE: 1998-07-14
; PRIOR FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3;
LENGTH: 818
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TITLE OF INVENTION: Proteases From Gram-Positive Organisms FILE REFERENCE: GC382-US
CURRENT APPLICATION NUMBER: US/10/402,067
CURRENT FILING DATE: 2003-03-26
PRIOR APPLICATION NUMBER: PCT/US98/14647
PRIOR PILING DATE: 1998-07-14
PRIOR FILING DATE: 1998-07-15
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                                                                                                                                                                                                                                                                                                                      0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 3.0
PRIOR APPLICATION NUMBER: PCT/US98/14647
PRIOR FILING DATE: 1998-07-14
PRIOR APPLICATION NUMBER: EP 97305237.7
PRIOR FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                  Pred. No
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Patent No. 6881562
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT; ORGANISM: Bacillus subtilis
US-10-402-067-3
                                                                                                                                                                                                          ORGANISM: Bacillus subtilis
                                                                                                                                                                                                                                                                                                                      6; Conservative
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Matches 6; Conser
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Best Local Similarity
Matches 6; Conserv
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Gaps
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Sequence 3, Application US/08704711A

PAPLICANT: WILL, HOSE

APPLICANT: HINDANN, Bernd

TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSES: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STREET: D.C.
                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                          Query Match 63.1%; Score 41; DB 2; Length 564; Best Local Similarity 62.5%; Pred. No. 1.1e+02; Matches 5; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                          1.1e+02;
...heg 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUW TYPE: FORM:

MEDIUW TYPE: FORM:

MEDIUW TYPE: FORDABLE

COMPUTER: IBM PC COMPATIBLE

OPERATION SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/704,711A

FILING DATE: 20-NOV-1996

CLASSITEATION NUMBER: WO PCT/DE95/00357

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE 4438838.1

FILING DATE: 17-MAR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE 4409663.1

FILING DATE: 17-MAR-1994

ATTORNEY/AGENT INFORMATION:

NAME: GRANAMADS, PARTIAICA

NAME: GRANAMATION NUMBER: 33,683

REFERENCE/DOCKET NUMBER: 26083/124

TELECOMMUNICATION NUMBER: 33,683

REFERENCE/DOCKET NUMBER: 26083/124
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REGISTRATION NUMBER: 367081K
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEPRAX: (650)8651200
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 564 amino acids
                                                                                                                                                                                                                      not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 904136
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (202) 672-5300
(202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 669 amino acids
                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                           364 AIWWEPTG 371
                                                                                                                                                                                                                                                                                                                                                                                                                   2 ALWWSPNG 9
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                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
                                                                                                                                                                                                                                                                                        US-09-211-704A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 50
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US-09-248-796A-19283

Sequence 19281

Sequence 19283

Sequence 19283

Sequence 19283

Sequence 19283

Sequence 19283

Sequence 19283

Septemble 10 674713

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

FORE REPERBENCE: 107196.132

CURRENT APPLICATION NUMBER: US 60/096,409

PRIOR PELING DATE: 1998-08-13

PRIOR FILING DATE: 1998-08-13

PRIOR FILING DATE: 1998-08-13

SEQ ID NO 19283

SEQ ID NO 19283

LENGTH: 320
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                                                                       Gaps
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Patent No. 6271014
GENERAL INFORMATION:
APPLICANT: General Francois
APPLICANT: Fossiez, Francois
APPLICANT: Cossiez, Francois
APPLICANT: Cabecque, Serge J.E.
TITLE OF INVENTION: Mammalian Proteinases; Related Reagents
TITLE OF INVENTION: and Methods
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63.1%; Score 41; DB 2; Length 320; 77.8%; Pred. No. 59; tive 0; Mismatches 2; Indels
                        64.6%; Score 42; DB 2; Length 818; 75.0%; Pred. No. 1.1e+02;
                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/211,704A
                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: DNAX Research Institute
901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/005,263
FILING DATE: 09-JAN-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
        Query Match
Best Local Similarity 75.0-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178 YCLDWSPNG 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 901 Califo
CITY: Palo Alto
STATE: California
                                                                                                               2 ALWWSPNG 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-248-796A-19283
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Jequence 29, Application US/09391104
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62.5%;
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62.5%;
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                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 62.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                          CRGANISM: Homo sapiens US-09-391-104-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                469 AIWWEPTG 476
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90 VWWSANGR 97
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US-09-902-540-10963
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                                                                                                                                                                                                                                                      APPLICANT: WILL, Horst
APPLICANT: WILL, Horst
TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
METALLOPROTEASES, THEIR PRODUCTION AND USE
                                                               ö
                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63.1%; Score 41; DB 2; Length 669;
62.5%; Pred. No. 1.3e+02;
ive 1; Mismatches 2; Indels
                               DB 2; Length 669;
                      Score 41; DB 2; Leus-
Pred. No. 1.3e+02;
----hes 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/704,711
FILING DATE: cunknown>
APPLICATION NUMBER: DE 4438838.1
FILING DATE: 21-0C7-1994
APPLICATION NUMBER: DE 4409663.1
FILING DATE: 17-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 26083/124
TELECOMMUNICATION INFORMATION:
                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/521,220
FILING DATE: 08-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 3: US-09-521-220-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: «Unknown»
21-OCT-1994
17-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                               RESULT 51
US-09-521-220-3
; Sequence 3, Application US/09521220
; Patent No. 6399348
; GENERAL INFORMATION:
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 904136
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                63.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
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Best Local Similarity 62.5
Matches 5; Conservative
                                Query Match 63.1
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                               469 AIWWEPTG 476
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                                                                                                2 ALWWSPNG 9
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 US-08-704-711A-3
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RESULT 52

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APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Steven C.
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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APPLICANT: Abbott Laboratories
APPLICANT: Falduto, Michael T.
APPLICANT: Falduto, Michael T.
APPLICANT: Morgan, Soct R.
APPLICANT: Morgan, Douglas W.
TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,
TITLE OF INVENTION: PROTEINS ENCOBED THEREFROM AND METHODS
TITLE OF INVENTION: OF USING SAME
FILE REFERENCE: 6073.US.Pl
CURRENT APPLICATION NUMBER: US/09/391,104
CURRENT FILING DATE: 1999-09-07
PRIOR PILING DATE: 1997-03-11
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.3e+02;
2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
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45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 40; DB;
Pred. No. 45;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 1.36
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10963, Application US/09902540 Patent No. 6833447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 10963
LENGTH: 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12, Application US/09449218D Patent No. 6395511
GENERAL INFORMATION:
APPLICANT: Brunkow, Mary E.
APPLICANT: Galas, David J.
APPLICANT: Kovacevich, Brian
APPLICANT: Mulligan, John T.
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APPLICANT: Galas, David J.
APPLICANT: Galas, David J.
APPLICANT: Mulligan, John T.
APPLICANT: Mulligan, John T.
APPLICANT: Mulligan, John T.
APPLICANT: Wan Ness, Jeffrey
APPLICANT: Van Ness, Jeffrey
APPLICANT: Winkler, David G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INCREASING
TITLE OF INVENTION: BONE MINERALIZATION
FILE REPERENCE: 240083.508
CURRENT APPLICATION NUMBER: US/09/449,218D
CURRENT FILING DATE: 1999-11-24
                                                                                                                                                                                                     Length 211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 211;
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                                                                                                                                                                                                                                              Indels
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Pred. No. 54;
0; Mismatches
                                                                                                                                                                                                       Score 40; DB 2;
Pred. No. 54;
0; Mismatches
FILE REFERENCE: 240083.508D4
CURRENT APPLICATION NUMBER: US/09/668,037A
CURRENT FILING DATE: 2000-09-21
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 12
LENGTH: 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14, Application US/09449218D Patent No. 6395511
GENERAL INFORMATION:
                                                                                                                                                                                                           61.5%;
83.3%;
                                                                                                                                                                                          Query Match
Best Local Similarity 83..2
Best Local Si Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 61.5
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) ORGANISM: Mus musculus US-09-668-021-12
                                                                                                                                  TYPE: PRT ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 WWRPNG 127
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US-09-668-037A-12
Sequence 12, Application US/09668037A
Fatent No. 6495736
GENERAL INFORMATION:
APPLICANT: Brunkow, Mary E.
APPLICANT: Galas, David J.
APPLICANT: Muligan, John T.
APPLICANT: Wan Ness, Jeffrey
APPLICANT: Wan Ness, Jeffrey
APPLICANT: Wan Ness, Jeffrey
APPLICANT: Wan Ness, Jeffrey
APPLICANT: Winklex, David G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Brunkow, Mary E.
APPLICANT: Galas, David J.
APPLICANT: Kovacevich, Brian
APPLICANT: Muligan, John T.
APPLICANT: Paeper, Bryan W.
APPLICANT: Paeper, Bryan W.
APPLICANT: Winkler, David G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INCREASING BONE TITLE OF INVENTION: MINERALIZATION FILE REFERENCE: 240083 508D1
FILE REFERENCE: 240083 508D1
CURRENT APPLICATION NUMBER: US/09/668,529A
CURRENT FILING DATE: 2000-09-21
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FaetSEQ for Windows Version 3.0
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                   APPLICANT: Van Ness, Joffrey
APPLICANT: Winkler, David G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INCREASING
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INCREASING
TITLE OF INVENTION: BONDE MINERALIZATION
FILE REFERENCE: 240083.508
CURRENT PELLING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 12
LENGTH: 211
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Pred. No. 54;
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83.3%; Pred. No. 54;
ive 0; Mismatches
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83.3%;
         Paeper, Bryan W.
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Matches 5, Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
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; ORGANISM: Mus musculus
US-09-668-529A-12
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US-09-449-218D-12
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APPLICANT: Winkler, David G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INCREASING BONE
TITLE OF INVENTION: MINERALIZATION
FILE REFERENCE: 240083.508D4
CURRENT APPLICATION NUMBER: US/09/668,037A
CURRENT APPLICATION NUMBER: US/09/668,037A
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FASELSEQ for Windows Version 3.0
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APPLICANT: Winkler, David G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INCREASING BONE
TITLE OF INVENTION: MINERALIZATION
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Pred. No. 55;
0; Mismatches 1; Indel
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CURRENT APPLICATION NUMBER: US/09/668,529A
CURRENT FILING DATE: 2000-09-21
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 14
LENGTH: 213
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 14
LENGTH: 213
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Sequence 14, Application US/09668037A
Patent No. 6495736
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APPLICANT: Brunkow, Mary E.
APPLICANT: Galas, David J.
APPLICANT: Kovacevich, Brian
APPLICANT: Mulligan, John T.
APPLICANT: Paeper, Bryan W.
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83.3%;
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Mulligan, John T.
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; ORGANISM: Rattus norvegicus
US-09-668-529A-14
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; ORGANISM: Rattus norvegicus
US-09-449-218D-14
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Best Local Similarity 83.3%;
Matches 5; Conservative
; ORGANISM: Rattus norvegicus US-09-668-037A-14
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Search completed: March 11, 2006, 12:27:17 Job time: 27.3684 secs

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Sequence 19475, A
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US-10-369-493-7066
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US-10-36-949-2301
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US-10-45-919-494
US-10-45-918-7
US-10-45-918-7
US-10-47-918-7
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                           GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
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US-09-864-761-46651
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US-10-177-293-136
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US-10-723-860-4171
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60.0 333 4 US-10-631-581-20 Sequence 20, Ap 60.0 338 4 US-10-437-963-136543 Sequence 136543 60.0 360 4 US-10-437-963-136589 Sequence 136593 60.0 371 4 US-10-425-114-39491 Sequence 59599, 60.0 371 4 US-10-425-114-39491 Sequence 39491, 60.0 465 4 US-10-369-493-22543 Sequence 2575, 60.0 545 4 US-10-369-493-22543 Sequence 25843, 60.0 545 4 US-10-424-599-26864 Sequence 25843, 60.0 545 4 US-10-424-599-188553 Sequence 137672 60.0 657 4 US-10-437-963-115-188553 Sequence 137672 60.0 657 4 US-10-369-493-19349 Sequence 137672 60.0 657 4 US-10-369-493-181621 Sequence 137873 60.0 1018 4 US-10-398-122-13 Sequence 13583 60.0 1064 5 US-10-398-122-13 Sequence 137876 60.0 1018 4 US-10-399-122-13 Sequence 137676 60.0 1064 5 US-10-332-923-8191 Sequence 8191, 60.0 1064 5 US-10-732-923-8191 Sequence 8291, 60.0 1072 5 US-10-732-923-8294 Sequence 8291, 60.0 1072 5 US-10-732-923-8294 Sequence 1357, 60.0 1234 5 US-10-732-923-8211 Sequence 1357, 60.0 1234 5 US-10-732-923-8219 Sequence 1357, 60.0 10.0 5 US-10-732-923-8219 Sequence 1357, 60.0 1234 5 US-10-732-923-8219 Sequence 1357, 60.0 1357	1366 5 US-10-741-600-1355 Sequence 12551 4 US-10-741-600-1355 Sequence 12552 4 US-10-741-600-1355 Sequence 12553 4 US-10-367-559-243 Sequence 12552 4 US-10-367-559-243 Sequence 2268 4 US-10-367-559-243 Sequence 2268 4 US-10-367-559-243 Sequence 2268 4 US-10-367-568-243 Sequence 2268 4 US-10-367-658-243 Sequence 2268 4 US-10-367-658-243 Sequence 2269 4 US-10-450-459-25562 Sequence 2269 4 US-10-450-459-25562 Sequence 2269 4 US-10-425-115-282084 Sequence 2269 4 US-10-425-125-4683 Sequence 2269 4 US-10-425-125-4683 Sequence 2269 4 US-10-425-125-4683 Sequence 2269 4 US-10-425-125-68261 Sequence 2269 4 US-10-425-125-68261 Sequence 2269 4 US-10-425-125-68261 Sequence 2269 4 US-10-425-125-68261 Sequence 2260 4 US-10-425-4837 Sequence 2260 4 US-10-425-5848 Sequence 2260 4 US-10-425	3 58.5 44/ 4 US-10-139-930-10964 Sequence 1.08 58.5 479 4 US-10-139-940-2 Sequence 2.09 58.5 484 4 US-10-132-744A-2

4425-114-69534 Sequence 4425-114-60716 Sequence 4425-114-60716 Sequence 425-114-60716 Sequence 425-114-60716 Sequence 425-114-60716 Sequence 442-124-6022 Sequence 442-1224-51252 Sequence 4437-962-12529 Sequence 4437-962-1254-5178 Sequence 4437-962-1254-5178 Sequence 4437-962-1254-5178 Sequence 4437-962-1254-5178 Sequence 4437-962-11653 Sequence 444-599-184579 Sequence 444-599-18418 Sequence 445-116-13418 Sequence 445-116-	466 36 55.4 125 4 US-10-425-1115-284941 Sequence 233310, 468 36 55.4 128 4 US-10-435-1115-284941 Sequence 284941, 468 36 55.4 130 4 US-10-437-963-140418 Sequence 140418, 469 36 55.4 131 3 US-09-908-322-60 Sequence 60, Appl 471 36 55.4 131 3 US-09-783-931-60 Sequence 60, Appl 471 36 55.4 139 4 US-10-001-857-186 Sequence 186, Appl	36 55.4 140 4 US-10-424-599-154193 Sequence 3 55.4 144 3 US-09-860-232A-20 Sequence 3 55.4 147 4 US-10-424-599-225582 Sequence 2	36 55.4 156 4 US-10-437-963-170096 Sequence 36 55.4 170 4 US-10-425-115-257739 Sequence	36 55.4 171 5 US-10-450-763-53099 Sequence 36 55.4 209 4 US-10-424-599-158741 Sequence	36 55.4 211 4 US-10-425-115-221741 Sequence	36 55 4 215 4 US-10-425-114-49985 Sequence	36 55.4 226 4 US-10-369-493-9488 Sequence	36 55.4 239 4 US-10-424-599-158739 Sequence	36 55.4 257 3 US-09-860-232A-19 Sequence 36 55.4 264 4 US-10-425-115-252657 Sequence	36 55.4 278 4 US-10-437-963-143721 Sequence	36 55.4 285 4 US-10-424-599-184021 Sequence 1 36 55.4 285 4 US-10-424-599-234482 Sequence 2	36 55.4 303 6 US-11-097-143-22833 Sequence 2	36 55.4 365 4 US-11-09/-143-2091 Sequence 2 55.4 365 4 US-10-369-493-22931 Sequence 2	36 55.4 395 4 US-10-369-493-19604 Sequence 1	36 55.4 405 3 US-09-863-475A-8 Sequence	36 55.4 405 4 US-10-234-041-11 Sequence 1	36 55.4 417 4 US-10-437-963-150752 Sequence 1	36 55.4 426 3 US-09-738-626-6036 sequence 36 55.4 426 4 US-10-627-476-424 Sequence		ALIGNMENTS		RESULT 1	US-10-774-242-4 ; Sequence 4, Application US/10774242	; Publication No. US20040203102A1	, APPLICANT: McKee, Patrick A	; APPLICANT: Lee, Kyung N. ; APPLICANT: Jackson, Kenneth W.	; APPLICANT: Christiansen, Victoria J.	FILE REFERENCE: 5820.646	; CURRENT APPLICATION NUMBER: US/10/774,242 : CURRENT FILING DATE: 2004-02-06	PRIOR APPLICATION NUMBER: 60/445,774	; PRIOR FILING DATE: 2003-02-07; NUMBER OF SEQ ID NOS: 11	; SOFTWARE: PatentIn version 3.1	; SEQ ID NO 4 ; LENGTH: 10	; TYPE: PRT		100.0%; Score 65;	cal Similarity 100.0%; Pred. No. 0.0093;	servative 0; Mismatches 0; indels 0; Gaps	Oy 1 YALWWSPNGK 10	Db 1 YALWWSPNGK 10		RESULT 2
37 56.9 452 4 US-10- 37 56.9 492 4 US-10- 37 56.9 492 4 US-10- 37 56.9 492 4 US-10- 37 56.9 508 3 US-10- 38 56.9 508 3 US-10- 39 56.9 608 4 US-10- 39 56.9 608 4 US-10- 39 55.4 4 US-10- 30 55.4 4 US-10- 31 100 1 4 US-10-	Sequence 69534, A Sequence 52, Appl Sequence 191788, Sequence 60716, A Sequence 2, Appli Sequence 2, Appli	Sequence 2, Appl Sequence 20, Appl Sequence 5, Appli	Sequence 24, Appl Sequence 192, App	Sequence 125529, Semience 56178. A	Sequence 501.8, A Sequence 60328, A	Sequence 2, Appli Sequence 184579,	Sequence 211037,	Sequence 103334,	Sequence 61163, A Sequence 153848,	Sequence 174708,	Seguence 29376, A Seguence 114. App	Sequence 114, App	Sequence 6623, Ap Sequence 11397, A	Sequence 6622, Ap	Sequence 107258, Sequence 25761, A	Sequence 22397, A	Sequence 11, Appi Sequence 8775, Ap	Sequence 8184, Ap	Sequence 8300, Ap	Sequence 8/82, Ap Sequence 28, Appl	Sequence 15002, A Sequence 15001, A	Sequence 47967, A	Sequence 31355, A Sequence 30418, A	Sequence 357495,	Sequence 190399,	Sequence 213643, Sequence 283372,	Sequence 752, App	Sequence 193437, Sequence 195168,	Sequence 103, App	Sequence 172055,	Sequence 160178, Sequence 183, App	Sequence 183, App	Sequence 48, Appi Sequence 242928,	Sequence 48, Appl	Sequence 254370, Sequence 264523,	Sequence 302871,	Sequence 198514,	Sequence 46, Appl Sequence 46, Appl	Sequence 242450,	261,	2469	56727
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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APPLICANT: Rettig, Wolfgang; Old, Lloyd J.
TITLE OF INVENTION: ISOLATED DIMERIC FIBROBLAST ACTIVATION PROTEIN
TITLE OF INVENTION: ALPHA, AND USES THEREOF
CORRESPONDENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.84 INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.67 INFORMATION: EXPRESSED IN ADULT LIVER; SIGNAL = 0.69 INFORMATION: EXPRESSED IN BONE MARKOW, SIGNAL = 0.79 INFORMATION: SWISSPROT HIT: P27487, EVALUE 4.00e-17
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ZID. 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 2.0 MB storage
AMEDIUM TYPE: Diskette, 3.5 inch, 2.0 MB storage
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Pred. No. 0.043;
                                                                                                                        Sequence 29292, Application US/10029386 Publication No. US20030194704A1 GENERAL INFORMATION:
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Patent No. US20020034789A1
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illarity 100.0%;
Conservative 0;
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805 Third Avenue
ew York City
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APPLICATION NUMBER: U
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7 YALWWSPNGK 16
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 10; Conserv
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COTHER INFORMATION
COTHER INFORMATION
US-10-029-386-29292
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                                             PATENT NO. US2002004876311
GENERAL INFORMATION:
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST HUMAN HIT: AU136648.1, EVALUE 1.00e-25 SWISSPROT HIT: P27487, EVALUE 2.00e-16
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EXPRESSED IN ADULT LIVER, SIGNAL = 0.65
EXPRESSED IN PLACENTA, SIGNAL = 0.62
EXPRESSED IN FETAL LIVER, SIGNAL = 0.62
EXPRESSED IN BONE MARROW, SIGNAL = 0.65
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
EQ ID NO 46651
                                                                                                                                                                                                                                                  FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
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ATION NUMBER: PCT/US01/00667
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PPLICATION NUMBER: PCT/US01/00669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/USO1/0066
PRIOR APPLICATION NUMBER: PCT/USO1/0066
PRIOR APPLICATION NUMBER: PCT/USO1/0066
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
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PPLICATION NUMBER: US 60/236,359
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APPLICATION NUMBER: US 09/608,408
                                                                                                                                                                                                                                                                                                                                                                                                             LING DATE: 2000-05-26
PLICATION NUMBER: US 09/632,366
                        Sequence 46651, Application US/09864761
Patent No. US20020048763A1
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Best Local Similarity 100.
Matches 10; Conservative
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ORGANISM: Homo sapiens
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COTHER INFORMATION:
US-09-864-761-46651
  US-09-864-761-46651
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Hanson, No. US20020034789Alman D.

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APPLICANT: Thibodeau, Stephen N.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, TITLE OF INVENTION: THERAPY OF COLON CANCER
FILER REFRENCE: MPMOL-02PPRNM
CURRENT APPLICATION NUMBER: US 60/339,971
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR PILING DATE: 2000-12-10
PRIOR PILING DATE: 2000-12-10
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2005-03-05
PRIOR DATE: 2005-03-05
PRIOR FILING DATE: 2
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APPLICANT: Ginsburg, Wendy M.
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Zlotnik, Wendy M.
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma Modulators
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
CURRENT APPLICATION NUMBER: US/10/723,860
CURRENT FILING DATE: 2003-11-26
NUMBER OF SEQ ID NOS: 8393
SOFTWARE: Patentin version 3.2
SEQ ID NO 4171
LENGTH: 760
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                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4171, Application US/10723860
Publication No. US20040253606A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                          Sequence 55, Application US/10301822 Publication No. US20030148410A1 GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
                                            210 YALWWSPNGK 219
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US-10-301-822-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens
US-10-723-860-4171
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APPLICANT: Wonshan, John
APPLICANT: Hoersch, Sebastian
APPLICANT: Hoersch, Sebastian
APPLICANT: Meyers, Rachel B.
APPLICANT: Bast Jr., Robert C.
APPLICANT: Bast Jr., Robert C.
APPLICANT: Purit John
APPLICANT: Purit, Lajos
APPLICANT: Purit, Lajos
APPLICANT: Sahin, Aysegul
APPLICANT: Sahin, Aysegul
APPLICANT: Mills, Gordon B.
APPLICANT: Mills, Gordon B.
APPLICANT: Mills, Gordon B.
APPLICANT: Mills, Gordon B.
APPLICANT: MILLS OF INVENTION: COMPOSITION, AND THERAPY OF BREAST CANCER
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CURRENT APPLICATION NUMBER: US/10/177,293
CURRENT FILID DATE: 2002-06-21
CURRENT FILID DATE: 2002-06-21
PRIOR APPLICATION NUMBER: US 60/299,887
PRIOR PILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: US 60/306,501
PRIOR PILING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: US 60/306,501
PRIOR FILING DATE: 2001-06-27
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2001-09-35
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 506
LENGTH: 760
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REGISTRATION NUMBER: 30,946
REPERENCE/DOCKET NUMBER: LUD 5330.1
FELECOMMUNICATION: TELECOMMUNICATION:
TELEPHONE: (212) 688-9200
FELFAX: (212) 838-3884
INFORMATION FOR SEG ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 760 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 136, Application US/10177293
Publication No. US20030124128A1
GENERAL INFORMATION:
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Kamatkar, Shubhangi
Mertens, Maureen
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Best Local Similarity 100.
Matches 10; Conservative
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Wang, Youzhen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             210 YALWWSPNGK 219
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; ORGANISM: Homo sapiens
US-10-177-293-136
                                                                                                                                                                                                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
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Best Local Similarity
Matches 10; Conserv
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CURRENT APPLICATION NUMBER: US/10/072,012
CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: 60/265,102
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-31
PRIOR PILING DATE: 2001-01-31
PRIOR PILING DATE: 2001-01-31
PRIOR FILING DATE: 2001-01-31
PRIOR FILING DATE: 2001-01-31
PRIOR FILING DATE: 2001-01-31
PRIOR FILING DATE: 2001-01-31
PRIOR PILING DATE: 2001-01-31
PRIOR PILING DATE: 2001-01-31
PRIOR PILING DATE: 2001-02-31
PRIOR PLICATION NUMBER: 60/266,767
PRIOR FILING DATE: 2001-02-07
PRIOR PLICATION NUMBER: 60/266,767

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84.6%; Score 55; DB 4; Length 504; 88.9%; Pred. No. 8;
INVENTION: Proteins and Nucleic Acids Encoding Same
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APPLICANT: Cookeon, William Osmond Charles Michael
APPLICANT: Allen, Maxine
APPLICANT: Allen, Maxine
TITLE CANT: Lench, Nick
TITLE OF INVENTION: Enzyme and SNP marker for disease
FILE REFERENCE: 16721-002US1
CURRENT PELICATION NUMBER: US/10/476,264
CURRENT FILING DATE: 2003-10-24
PRIOR APPLICATION NUMBER: PCT/GB02/01887
PRIOR PILING DATE: 2001-04-24
PRIOR PILING DATE: 2001-04-24
PRIOR PILING DATE: 2001-04-24
PRIOR PILING DATE: 2001-04-24
PRIOR FILING DATE: 2001-10-12
PRIOR PELING DATE: 2001-10-12
PRIOR PELING DATE: 2001-10-12
PRIOR FILING DATE: 2001-10-12
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ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 88.9
Matches 8; Conservative
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APPLICANT: Wolf, Beni B.
APPLICANT: Wu, Thomas D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND TITLE OF INVENTION: TREATMENT OF TUMOR FILE REFERENCE: PSO36R-US
CURRENT APPLICATION NUMBER: US/10/884,070A
CURRENT FILING DATE: 2004-07-02
PRIOR APPLICATION NUMBER: US 60/484,959
NUMBER OF SEQ ID NOS: 14
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Anderson, David W.
Rastelli, Luca
Miller, Charles E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gerlach, Valerie
Taupier Jr, Raymond J
Gusev, Vladimir Y.
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Patturajan, Meera
Shimkets, Richard
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                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ashkenazi, Avi J.
APPLICANT: Cairns, Belinda
APPLICANT: Dowd, Patrick
APPLICANT: Frantz, Gretchen
APPLICANT: French, Dorothy
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Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                          210 YALWWSPNGK 219
                                            1 YALWWSPNGK 10
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ORGANISM: Homo sapiens
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RESULT 13
US-10-002-593-6
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APPLICANT: Zimmermann, Rainer; Park, John B.;
APPLICANT: Rettig, Wolfgang; Old, Lloyd J.
TITLE OF INVENTION: ISOLATED DIMERIC FIBROBLAST ACTIVATION PROTEIN
TITLE OF INVENTION: ALPHA, AND USES THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: New York City
CITY: New York City
COUNTRY: USA
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100.0%; Pred. No. 22;
cive 0; Mismatches 0; Indels
                                                   81.5%; Score 53; DB 5; Length 48; 100.0%; Pred. No. 1.9; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 2.0 MB storage
COMPUTER: 1BM PS/2
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US/08/619,280
FILING DATE: 18-MARCH-1996
APPLICATION NUMBER: 08/230,491
FILING DATE: 20-APRIL-1994
ATTORNEY AGENT INFORMATION:
NAME: Hanson, No. US20020034789Alman D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: JUD 5330.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212),689-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265,606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-993-959-1
; Sequence 1, Application US/09993959
; Publication No. US20030165489A1
; GENERAL INFORMATION
; APPLICANT: Grouzmann, Eric
; APPLICANT: Lacroix, Jean-Silvain
                                                                                                                                                                                                                                                                          Sequence 3, Application US/09265606; Patent No. US20020034789A1
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
                                                       Query Match
Best Local Similarity 100.
Matches 8; Conservative
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; ORGANISM: Homo sapiens
US-10-476-264-127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-265-606-3
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Sequence 6, Application US/10002593

Foguence 6, Application US/10002593

Publication No. US20020137120A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Vanderbilt University
APPLICANT: Brown, Nancy J.
TITLE OF INVENTION: BIOLOGICAL MARKERS AND DIAGNOSTIC TESTS FOR ANGIOTENSIN CONVERTING
TITLE OF INVENTION: INHIBITOR AND VASOPEPTIDASE INHIBITOR ASSOCIATED ANGIOEDEMA.
FILE REFERENCE: Arty Docket No. US20020137120A1 1242/48/2
CURRENT APPLICATION NUMBER: US/10/002,593
CURRENT FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 10

SOFTWARE: Patentin version 3.1
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APPLICANT: Monod, Michel
TITLE OF INVENTION: Method of Treating Rhinitis and Sinusitis
FILE REFERENCE: 81985/2716823
CURRENT APPLICANN WIMBER: US/09/993,959
CURRENT PILING DATE: 2001-11-27
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 766
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; Sequence 7, Application US/10165603
; Publication No. US20030021792A1
; GENERAL INFORMATION:
; APPLICANT: Roben, Paul M.
; APPLICANT: Stevens, Anthony C.
; TITLE OF INVENTION: TISSUE-SPECIFIC ENDOTHELIAL MEMBRANE
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: TPTECH OULA
; CURRENT APPLICATION NUMBER: US/10/165,603
; CURRENT PILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/297,021
; PRIOR FILING DATE: 2001-06-08
; PRIOR FILING DATE: 2001-06-08
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 100.
Matches 8; Conservative
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Best Local Similarity 100.
Matches 8; Conservative
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213 ALWWSPNG 220
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213 ALWWSPNG 220
                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
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SEQ ID NO 6
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PRIOR APPLICATION DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2000-15
PRIOR PELING DATE: 2001-11-13
PRIOR PELING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-13
PRIOR PILING DATE: 2001-11-21
PRIOR PELING DATE: 2001-11-29
PRIOR PILING DATE: 2001-11-29
PRIOR PELING DATE: 2001-11-29
PRIOR PELING DATE: 2001-11-29
PRIOR PELING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: US 60/340,376
PRIOR PILING DATE: 2002-11-09
PRIOR PELING DATE: 2002-10-08
PRIOR PELING DATE: 2002-01-08
PRIOR PELING DATE: 2002-02-08
PRIOR PELING DATE: 2002-02-13
PRIOR FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: US 60/340,376
PRIOR FILING DATE: 2001-12-14
PRIOR FILING DATE: 2002-12-14
PRIOR PELICATION NUMBER: US 60/347,211
PRIOR FILING DATE: 2002-01-08
PRIOR FILING DATE: 2002-01-10
PRIOR FILING DATE: 2002-01-10
PRIOR FILING DATE: 2002-02-03
PRIOR FILING DATE: 2002-02-03
PRIOR FILING DATE: 2002-02-13
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FITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions ar
FITLE OF INVENTION: Methods of Screening for Modulators of Cancer
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CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT FILING DATE: 2002-11-13
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Publication No. US20030222350A1
PEDLICATION:
APPLICANT: Afar, Daniel
APPLICANT: Afar, Daniel
APPLICANT: Graces, Wendy M.
APPLICANT: Gineberg, Wendy M.
APPLICANT: Gineberg, Wendy M.
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Murray, Richard
Watson, Susan R.
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Hevezi, Peter A.
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Best Local Similarity 100.
Matches 8; Conservative
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CORGANISM: Homo sapiens
US-10-295-027-590
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Brown, Nancy J.

TITLE OF INVENTION: BIOLOGICAL MARKERS AND DIAGNOSTIC TESTS FOR ANGIOTENSIN CONVENTILE OF INVENTION: BIOLOGICAL MARKERS AND DIAGNOSTIC TESTS FOR ANGIOEDEMA TITLE OF INVENTION: INHIBITOR AND VASOPEPTIDASE INHIBITOR ASSOCIATED ANGIOEDEMA CURRENT APPLICATION NUMBER: US/10/423,714

FILE REFERENCE: ALLY DOCKEL NS/10/423,714

CURRENT APPLICATION NUMBER: US/10/423,714

PRIOR PILING DATE: 2003-04-25

PRIOR FILING DATE: 2000-10-31

NUMBER OF SEQ ID NOS: 10

SOFTWARE: Patentin Version 3.1
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APPLICANT: Wateson, Susan R.
APPLICANT: Wateson, Susan R.
APPLICANT: Wateson, Susan R.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
FILE REFERENCE: 018501-012500US
CURRENT APPLICATION NUMBER: US/10/295,027
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22;
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                                                                                                                                      81.5%; Score 53; DB 100.0%; Pred. No. 22; ive 0; Mismatches
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PRIOR FILING DATE: 2000-09-15
PRIOR PILING DATE: 2000-09-15
PRIOR PLILING DATE: 2001-11-13
PRIOR PLILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR PILING DATE: 2001-11-15
PRIOR PAPLICATION NUMBER: US 60/335,464
PRIOR FILING DATE: 2001-11-15
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0. US20030232350A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/10423714
Publication No. US20030180828A1
GENERAL INFORMATION:
APPLICANT: Vanderbilt University
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APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Gish, Kurt C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glynne, Richard
Hevezi, Peter A.
                                                                                                                                      Query Match 81.5
Best Local Similarity 100.
Matches 8; Conservative
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Best Local Similarity 100.
Matches 8; Conservative
               ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-165-603-7
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213 ALWWSPNG 220
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; ORGANISM: Homo sapiens
US-10-423-714-6
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Publication No. US2
GENERAL INFORMATION
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Publication No. US20050123910A1
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Publication No. US20040146516A1
GENERAL INFORMATION:
APPLICANT: Utah Ventures
TITLE OF INVENTION: Lumen-Exposed Molecules and Methods Targeted Delivery
FILE REFERENCE: 27110-715
CURRENT PILING DATE: 2004-03-05
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin version 3.1
SEQ ID NO 41
LENGTH: 766
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22;
                                                                               DB 4; Length 766;
22;
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US-10-552-459-18

US-10-552-459-18

Sequence 18, Application US/10952459

Publication No. US20050074805A1

GENERAL INFORMATION:
APPLICANT: Kochan, Jarema Peter
APPLICANT: Roainski, Mitchell Lee
TITLE OF INVENTION: Specific Markers for Diabetes
FILE REPERENCE: 21270US1

CURRENT FILING DATE: 2004-09-28

NUMBER OF SEQ ID NOS: 34

SOFTWARE: PatentIn version 3.2

LENGTH: 766
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                                                                                81.5%; Score 53; DB 100.0%; Pred. No. 22; tive 0; Mismatches
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Best Local Similarity 100.
Matches 8; Conservative
                                                                               Query Match
Best Local Similarity 100.
Matches 8; Conservative
               TYPE: PRT
ORGANISM: Homo sapiens
US-10-295-027-922
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-10-794-899-41
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 LENGTH: 766
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RESULT 20 US-10-476-264-147 ; Sequence 147, Application US/10476264

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US-10-631-467-565

Sequence 565, Application US/10631467

Sequence 565, Application No. Publication No. Sequence 565, Application No. Sequence 565, Tribulation No. September 1 INFORMATION:

APPLICANT: Genox Research Inc. APPLICANT: Genox Research Inc. September 1 ITILE OF INVENTION: Machod for testing for broncheal asthma, or chronic obstructive F. TITLE OF INVENTION: disease TITLE OF INVENTION: disease September 1 ITILE OF INVENTION: Disease September 1 ITILE OF INVENTION: Disease September 1 ITILE NEFERENCE: 3462.1005-000
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US-10-770-712-1
US-10-770-712-1
Sequence 1, Application US/10770712
; Publication No. US20050170333A1
; Publication No. US2005017033A1
; GENREAL INFORMATION:
; APPLICANT: Voidani, Aristo
; TITLE OF INVENTION: IDENTIFICATION OF ETIOLOGY OF AUTISM
; FILE REFRENCE: IMSC12.008A
; CURRENT APPLICATION NUMBER: US/10/770,712
; CURRENT FILING DATE: 2004-02-03
; NUMBER OF SEQ ID NOS: 133
; SOOTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 766;
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GENERAL INFORMATION:
APPLICANT: COOKSON, William OSMOND Charles Michael
APPLICANT: Moffex, Miriam Fleur
APPLICANT: Moffex, Miriam Fleur
APPLICANT: Lench, Nick
TITLE OF INVENTION: Enzyme and SNP marker for disease
FILE REFERENCE: 16721-002US1
CURRENT APPLICATION NUMBER: US/10/476,264
CURRENT FILING DATE: 2003-10-24
FRIOR APPLICATION NUMBER: 2003-10-44
FRIOR APPLICATION NUMBER: GB0110044.5
FRIOR PILING DATE: 2001-04-24
FRIOR APPLICATION NUMBER: GB0110046.0
FRIOR APPLICATION NUMBER: GB0124594.3
FRIOR APPLICATION NUMBER: GB0124594.3
FRIOR APPLICATION NUMBER: GB0124555.2
FRIOR APPLICATION NUMBER: GB0124555.2
FRIOR APPLICATION NUMBER: GB0124555.2
FRIOR FILING DATE: 2001-10-12
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100.0%; Pred. No. 22;
trive 0; Mismatches
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81.5%; Score 53; DB
Best Local Similarity 100.0%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches
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Best Local Similarity
Matches 8; Conserv
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Sequence 38, Application US/10794899
Sequence 38, Application US/10794899
Publication No. US20040146516A1
GENERAL INFORMATION:
TITLE OF INVENTION: Lumen-Exposed Molecules and Methods Targeted Delivery
TITLE OF INVENTION: Lumen-Exposed Molecules and Methods Targeted Delivery
TITLE OF INVENTION: Lumen-Exposed Molecules and Methods Targeted Delivery
CURRENT APPLICATION NUMBER: US/10/794,899
CURRENT FILING DATE: 2004-03-05
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PatentIn version 3.1
SEQ ID NO 38
LENGTH: 767
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Sequence 2, Application WS/10770712;
Publication No. US20050170333A1;
GENERAL INFORMATION:
APPLICANT: Vojdani, Aristo
TITLE OF INVENTION: IDENTIFICATION OF ETIOLOGY OF AUTISM
FILE REFRENCE: IMSCI2.008A
CURRENT PILING DATE: 2004-02-03;
NUMBER OF SEQ ID NOS: 133
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 767
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22;
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Pred. No. 22;
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0, Mismatches
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81.5%; Score 53; DB
Best Local Similarity 100.0%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches
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PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
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; ORGANISM: Rattus norvegicus
US-10-770-712-2
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                                                                                                                               ) ORGANISM: Rattus norvegicus
US-10-165-603-4
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Matches 8; Conservative
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Matches 8; Conservative
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                                                                                        LENGTH: 767
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                                                                  SEQ ID NO 4
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Publication No. US20050181468A1

GENERAL INFORMATION:

APPLICANT: USCOMPATION:

TITLE OF INVENTION: BIOLOGICAL WARKERS AND DIAGNOSTIC TESTS FOR ANGIOTENSIN CONVERTIN

TITLE OF INVENTION: INHIBITOR AND VASOPERTIDASE INHIBITOR ASSOCIATED ANGIOEDEMA

FILE REFERENCE: Atty Docket No. 1242/48/2/2/2

CURRENT APPLICATION NUMBER: US/11/041,674

PRIOR APPLICATION NUMBER: 60/244,524

PRIOR FILING DATE: 2000-10-31

PRIOR FILING DATE: 2001-10-31

PRIOR FILING DATE: 2001-10-31

PRIOR PRIOR FILING DATE: 2001-10-31

PRIOR FILING DATE: 2001-10-31

PRIOR PLING DATE: 2001-10-31

PRIOR FILING DATE: 2001-10-31

SOFTWARE: PARENTIN VERSION 3.1
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APPLICANT: Stevens, Anthony C.
TITLE OF INVENTION: TISSUE-SPECIFIC ENDOTHELIAL MEMBRANE
TITLE OF INVENTION: PROTEINS
FILE REFERENCE: TPTECH.001A
CURRENT APPLICATION NUMBER: US/10/165,603
CURRENT FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: 60/297,021
PRIOR FILING DATE: 2001-06-08
PRIOR PLING DATE: 2001-06-08
PRIOR PLING DATE: 2001-06-08
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Pred. No. 22;
                                                                                                                                                                                                                                                                                                               Score 53; DB : ; Pred. No. 22; 0; Mismatches
                                         PRIOR APPLICATION NUMBER: JP 2003-077212
PRIOR FILING DATE: 2003-03-20
PRIOR APPLICATION NUMBER: JP 2002-229312
PRIOR APPLICATION NUMBER: JP 2002-229312
NUMBER OF SEQ ID NOS: 2086
SOFTWARE: Patentin version 3.1
SEQ ID NO 565
LENGTH: 766
  CURRENT APPLICATION NUMBER: US/10/631,467 CURRENT FILING DATE: 2003-07-31
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Publication No. US20030021792A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                          TYPE: PRT
CORGANISM: Homo sapiens
US-10-631-467-565
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sequence 7006, Application US/10369493
; Sequence 7006, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Chart. States. Steven C.
; APPLICANT: Gldman, Barry S.
; APPLICANT: Gldman, Barry S.
; APPLICANT: Gldman, Barry S.
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; TITLE OF INVENTION: UNMBER: US/10/369,493
; CURRENT APPLICATION NUMBER: US 60/360,039
; PRIOR PEDLICATION NUMBER: US 60/360,039
; PRIOR PELLING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
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Sequence 2, Application US/10723807

Publication No. US20040171104A1

GENERAL INFORMATION:

APPLICANT: Alexander Blinkovsky

APPLICANT: Alexander Blinkovsky

APPLICANT: Michael W. Rey

APPLICANT: Michael W. Rey

APPLICANT: Alan Kitoz

APPLICANT: Alan Kitoz

APPLICANT: Alan Michael

TITLE OF INVENTION: Aminopeptidase Activity And Nucleic Acids Encoding Same

FILE REFERENCE: 5254.200-US

CURRENT APPLICATION NUMBER: US/10/723,807

CURRENT FILING DATE: 1908-05-15

PRIOR FILING DATE: 1998-05-15

PRIOR FILING DATE: 1997-05-16
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                                                                                                                                                                                                                                                                           72.3%; Score 47; DB 5; Length 760
100.0%; Pred. No. 1.6e+02;
iive 0; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: JP 2003-077212
PRIOR FILING DATE: 2003-03-20
PRIOR APPLICATION NUMBER: JP 2002-229312
PRIOR FILING DATE: 2002-08-06
NUMBER OF SEQ ID NOS: 2086
SSEQ ID NO 1390
LENGTH: 760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-7006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 66.7
Matches 6; Conservative
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Matches 7; Conservative
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                                                                                                                                                                                      TYPE: PRT
CORGANISM: Mus musculus
US-10-631-467-1390
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US-10-369-493-7006
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                                                                                                                                                                                                                                                                               Query Match
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Publication No. US20050208496A1
GENERAL INFORMATION:
TITLE OF INVENTION: Method for testing for broncheal asthma, or chronic obstructive J
TITLE OF INVENTION: disease
FILE REFERENCE: 3462.1005-0000
CURRENT APPLICATION NUMBER: US/10/631,467
CURRENT FILING DATE: 2003-07-31
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| Publication No. US20050170333A1
| GENERAL INFORMATION:
| APPLICANT: VOJGANTION:
| TITLE OF INVENTION: IDENTIFICATION OF ETIOLOGY OF AUTISM:
| FILE REFERENCE: IMSCI2.008A
| CURRENT APPLICATION NUMBER: US/10/770,712
| CURRENT APPLICATION NUMBER: US/10/770,712
| NUMBER OF SEQ ID NOS: 133
| SEQ ID NOS: 133
| SEQ ID NOS: 133
| LENGTH: 760
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                     JOS-10-130 / 40-1100.00

JOS-10-130 / 40-1100.00

PUBLICARTION NO. US20030119018A1

GENERAL INFORMATION

APPLICANT: SHIRAM, JUN

APPLICANT: ISHIKAWA, JUN

APPLICANT: SHIRAM, JUN

APPLICANT: SHIRAM, JUN

APPLICANT: SHIRAM, JUN

APPLICANT: HATTOR! MASAHIRA

TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

FILE REFERENCE: 249-262

CURRENT APPLICATION NUMBER: US/10/156,761

CURRENT PLING DATE: 2002-05-29

PRIOR FILING DATE: 2001-05-30

PRIOR FILING DATE: 2001-06-02

PRIOR FILING DATE: 2001-06-02

PRIOR FILING DATE: 2001-06-02

NUMBER OF SEQ ID NOS: 15109

SEROITH: 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-13020
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Best Local Similarity 100.
Matches 7; Conservative
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Matches 7; Conservative
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CORGANISM: Mus musculus
US-10-770-712-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-631-467-1390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 28
US-10-770-712-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.50 INCH DISKETTE
MEDIUM TYPE: 3.50 INCH DISKETTE
COMPUTER: 11EM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD FOR WINDOWS 95
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/336,597
FILING DATE: 03-3an-2003
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67.7%; Score 44; DB 4; Length 323; 60.0%; Pred. No. 2e+02; ive 1; Mismatches 3; Indels
                                                                                                                                                Length 758;
                                                                                                                                                Score 45; DB 4; Length 758
Pred. No. 3.1e+02;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            BROGLIE, KAREN E.
PEARLSTEIN, RICHARD W.
TITLE OF INVENTION: PLANT 4-(-GLUCANOTRANSFERASE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: 1. DUPONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
                                                                 CCATION: (1)..(758)
CTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-2301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB-1101-A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/403,332
FILING DATE: 19-Oct-1999
ATTORNEY/AGENT INFORMATION:
NAME: MAJARIAN, WILLIAM R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-336-597-4
ORGANISM: Schizosaccharomyces pombe FEATURE:
                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/10336597
Publication No. US20030150021A1
GENERAL INFORMATION:
APPLICANT: KREBBERS, ENNO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 323 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 302-992-4926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELEFAX: 302-773-0164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
                                                                                                                                                    69.2%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: WILMINGTON
STATE: DELAWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 YALWWSPNGK 10
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                                                                                                                                                                                                                                                                             178 AVWWSPDG 185
                                                                                                                                   Query Match
Best Local Similarity
Local 6; Conserva
                                                                                                                                                                                                                                       2 ALWWSPNG 9
                                                     NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 35
US-10-156-761-9740
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US-10-336-597-4
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; Sequence 2201, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
    APPLICANT: Gao, Yongwei
; APPLICANT: Slater, Steven C.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
; TITLE OF INVENTION: UNMBER: US/10/369,493
; CURRENT APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROFERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT FPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 19475
LENGTH: 661
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                                                                                                                                                                                                                    DB 4; Length 771;
                                                                                                                                                                                                           Score 46; DB 4; Lens.
Pred. No. 2.2e+02;
O; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 45; DB Pred. No. 2.7e
                                                                                                                                                                                                                                                              3; Mismatches
          PRIOR APPLICATION NUMBER: 60/062,892
PRIOR FILING DATE: 1997-10-20
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 2
LENGTH: 771
                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 32
US-10-369-493-19475
; Sequence 19475, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69.2%;
                                                                                                                                                                                                                    Query Match
Best Local Similarity 70.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Myxococcus xanthus
US-10-369-493-19475
                                                                                                                                                           ; ORGANISM: Aspergillus oryzae
US-10-723-807-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                             205 YALWFSPDGE 214
                                                                                                                                                                                                                                                                                                       1 YALWWSPNGK 10
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171 WWSPDGK 177
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LENGTH: 758
TYPE: PRT
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Gaps

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Sequence 4, Application US/10432198

Publication No. US20040096899A1

GENERAL INFORMATION:
APPLICANT: TAKANOTI
APPLICANT: YONEZAWA, Kayoko
APPLICANT: FUJIMOTO, Noboru
APPLICANT: IWATA, Kazushi
TITLE OF INVENTION: Immunoassay for Membrane-type Matrix Metalloproteinases
FILE REFERENCE: 2003-0679A/WMC/01332
CURRENT FILING DATE: 2003-10-27
CURRENT FILING DATE: 2003-10-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: AOKI, Takanori
APPLICANT: YONEZAWA, Kayoko
APPLICANT: YONEZAWA, Kayoko
APPLICANT: PUJIMOTO, Noboru
APPLICANT: OGAWA, Miva
APPLICANT: IWATA, Kazushi
TITLE OF INVENTION: Immunoassay for Membrane-type Matrix Metalloproteinases
FILE REPERENCE: 2003-0679A/WMC/01332
CURRENT APPLICATION NUMBER: US/10/432,198
CURRENT FILING DATE: 2003-10-27
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66.2%; Score 43; DB 4; Length 189
Best Local Similarity 77.8%; Pred. No. 1.7e+02;
Matches 7; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              66.2%; Score 43; DB 5; 171.4%; Pred. No. 1.18+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
FRIOR APPLICATION NUMBER: PCT/US01/08631
FRIOR FILING DATE: 2001-03-30
FRIOR FILING DATE: 2000-03-31
FRIOR FILING DATE: 2000-08-23
FRIOR FILING DATE: 2000-08-23
FRIOR FILING DATE: 2000-08-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: JP 2000-352491
PRIOR FILING DATE: 2000-11-20
NUMBER OF SEQ ID NOS: 7
SEG ID NO 4
LENGTH: 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/10432198; Publication No. US20040096899A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100 ALFWMPNGK 108
                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 ALWWSPNGK 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 WWSPNGK 10
                                                                                                                                                                                                                                                                                                                                                                                  US-10-450-763-40309
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Sequence 305249, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: APPLICANT: Abou, Yihua
APPLICANT: APPLICANT: Application Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)8
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 305249
LENGTH: 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.7%; Score 44; DB 4; Length 1256;
85.7%; Pred. No. 6.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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Publication No. US20050196754A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Clone ID: MRT4577_41458C.1.pep
US-10-425-115-305249
                       PUBLICANT NO. USZOOJOLIO DE LEGENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIBA, TADAYCSHI
APPLICANT: SHIBA, TADAYCSHI
APPLICANT: SHIBA, TADAYCSHI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT PILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
RIOR PILING DATE: 2001-05-30
SEQ ID NO 9740
LENGTH: 1256
LENGTH: 1256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
     Sequence 9740, Application US/10156761
Publication No. US20030119018A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 66.9
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 85.7
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 36
US-10-425-115-305249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-450-763-40309
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Gaps

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Length 189;

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Sequence 228890, Application US/10424599
| Sequence 228890, Application No. US20040031072A1
| Sequence 228890, Application No. US20040031072A1
| GENERAL INFORMATION:
| APPLICANT: La Rosa Thomas J
| APPLICANT: Cao Vongwei I
| TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
| TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
| TITLE OF INVENTION: 2003-04-28
| CURRENT FILING DATE: 2003-04-28
| SEQ ID NO 225890
| LENGTH: 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Description of Artificial Sequence: MT1PEX US-10-276-272A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 66.2%; Score 43; DB 4; Length 218; Best Local Similarity 77.8%; Pred. No. 2e+02; Matches 7; Conservative 1; Mismarches
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Pred. No. 2.5e+02;
2; Mismatches 1; Indels
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US-10-424-599-225890
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/10276272A

| Sequence 7, Application US/10276272A
| Publication No. US20040120954A1
| GENERAL INFORMATION:
| APPLICANT: SEIKI, Motoharu
| APPLICANT: OBATA, Ken-ichi
| TILE GF INVENTION: REGULATION OF WT1-MMP ACTIVITY
| FILE REFERENCE: 2002-1357A/WMC/01332
| CURRENT APPLICATION NUMBER: US/10/276,272A
| CURRENT FILING DATE: 2001-05-18
| PRIOR FILING DATE: 2001-05-18
| PRIOR FILING DATE: 2000-05-19
| NUMBER OF SEQ ID NOS: 20
| SEQ ID NO 7
                                                                                      Score 43; DB 4; 1; Pred. No. 1.7e+02; 1; Mismatches 1;
; ORGANISM: Oryctolagus cuniculus US-10-432-198-7
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ORGANISM: Artificial Sequence
                                                                                             Query Match
Best Local Similarity 77.8%;
Matches 7; Conservative
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Best Local Similarity 70.v
Best Local 7; Conservative
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ORGANISM: Glycine max
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Sequence 7, Application Wo. US2004009689A1
Sequence 7, Application No. US2004009689A1
GENERAL INFORMATION:
APPLICANT: VONEZAMA, KAZANOTI
APPLICANT: YONEZAMA, KAZUSHI
APPLICANT: TWATA, KAZUSHI
TITLE OF INVENTION: Immunoassay for Membrane-type Matrix Metalloproteinases
FILE REFERENCE: 2003-0679A/WMC/01332
CURRENT APPLICATION NUMBER: US/10/432,198
CURRENT ELLING DATE: 2003-10-27
PRIOR APPLICATION NUMBER: 2003-10-27
PRIOR PELING DATE: 2003-11-20
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Pred. No. 1.7e+02;
1; Mismatches 1; Indels
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Pred. No. 1.7e+02;
1; Mismatches 1; Indels
             PRIOR APPLICATION NUMBER: JP 2000-352491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66.2%;
77.8%;
                                           PRIOR FILING DATE: 2000-11-20
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
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SOFTWARE: PatentIn Ver. 2.0
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Best Local Similarity 77.8
Matches 7; Conservative
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100 ALFWMPNGK 108
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; ORGANISM: Rattue sp.
US-10-432-198-6
                                                                                                                                                                                                                                  ; ORGANISM: Mus sp.
US-10-432-198-5
                                                                                                                                     SEQ ID NO 5
LENGTH: 189
TYPE: PRT
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Publication No. US20040120954A1
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US-11-021-951-185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Description of Artificial Sequence: MT1PEX
US-10-276-272A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 43; DB 4; Length 381;
Pred. No. 3.2e+02;
1; Mismatches 1; Indels
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                                                                                                                        Sequence 10, Application US/10276272A; Sequence 10, Application US/10276272A; Publication No. US20040120954A1
GENERAL INFORMATION:
APPLICANT: SEIMI, Motoharu; APPLICANT: OBATA, Ken-ichi
TITLE OF INVENTION: REGULATION OF MTI-MMP ACTIVITY; FILE REFREENCE: 2002-1357A/MMC/0132A; CURRENT APPLICATION NUMBER: US/10/276,272A; CURRENT FILING DATE: 2003-12-02; PRIOR APPLICATION NUMBER: PCT/JP01/04166; PRIOR FILING DATE: 2001-05-18
PRIOR FILING DATE: 2001-05-18
NUMBER OF SEQ ID NOS: 20
SEQ ID NO 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/10276272A
; Sequence 4, Application US/10276272A
; Publication No. US20040120954A1
; GENERAL INFORMATION:
    APPLICANT: SEIKI, Motcharu
; APPLICANT: OBATA, Ken-ichi
    TITLE OF INVENTION: REGULATION OF MT1-MMP ACTIVITY
; FILE REFERENCE: 2002-1357A/MMC/01332
; CURRENT APPLICATION NUMBER: US/10/276,272A
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: PCT/JP01/04166
; PRIOR APPLICATION NUMBER: DF2000/147739
; PRIOR FILING DATE: 2000-05-19
; PRIOR PILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 20
; SEQ ID NO 4 SEQ ID NOS: 20
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Best Local Similarity 77.8%;
Matches 7; Conservative
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238 YAVSWSPDGK 247
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225 ALFWMPNGK 233
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US-10-276-272A-10
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US-10-276-272A-4
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APPLICANT: ACTERNANN, Andre
APPLICANT: SCHEIDIG, Andreas
APPLICANT: SCHEIDIG, Andreas
APPLICANT: SCHEIDIG, Andreas
APPLICANT: OCTOMEREN: Christian
APPLICANT: COCO, Wayne Michael
TITLE OF INVENTION: New Biological Entities And The Pharmaceutical
TITLE OF INVENTION: New Biological Entities And The Pharmaceutical
TITLE OF INVENTION: New Biological Entities And The Pharmaceutical
TITLE OF INVENTION: NOWBER: US/11/021,951
CURRENT APPLICATION NUMBER: US/11/021,951
CURRENT FILING DATE: 2004-12-22
PRIOR APPLICATION NUMBER: 60/543,518
PRIOR PILING DATE: 2004-02-11
PRIOR PELING DATE: 2004-02-11
PRIOR PELING DATE: 2003-11-25
PRIOR PELING DATE: 2003-11-12
PRIOR PELING DATE: 2003-11-12
PRIOR PELING DATE: 2003-11-10
PRIOR PELING DATE: 2003-11-10
PRIOR PELING DATE: 2003-11-10
PRIOR PELING DATE: 2003-11-10
PRIOR APPLICATION NUMBER: EP 03025851
PRIOR APPLICATION NUMBER: EP 03025851
PRIOR APPLICATION NUMBER: EP 03013819
PRIOR PILING DATE: 2003-11-10
PRIOR APPLICATION NUMBER: EP 03013819
PRIOR PILING DATE: 2003-11-10
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77.8%; Pred. No. 3.9e+02;
tive 1; Mismatches 1; Indels
GENERAL INFORMATION:
APPLICANT: SEIKI, Motcharu
APPLICANT: SEIKI, Motcharu
APPLICANT: OBATA, Ken-ichi
ITTLE OF INVENTION: REGULATION OF WII-MMP ACTIVITY
ITLE OF INVENTION: REGULATION OF WII-MMP ACTIVITY
CURRENT APPLICATION NUMBER: US/10/276,272A
CURRENT APPLICATION NUMBER: US/10/276,272A
CURRENT PILING DATE: 2001-05-18
PRIOR PILING DATE: 2001-05-18
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 20
SEQ ID NO 6
SEQ ID N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 66.2%; Score 43; DB 4; I
Best Local Similarity 77.8%; Pred. No. 3.5e+02;
Matches 7; Conservative 1; Mismatches 1;
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Publication No. US20050175581A1
GENERAL INFORMATION:
APPLICANT: HAUPTS, Ulrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
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SEQ ID NO 185
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Best Local Similarity
Matches 7; Conserva
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RESULT 46 US-10-276-272A-6 ; Sequence 6, Application US/10276272A

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Sequence 2.7 Application US/09916849A

Publication No. US20030086934A1

GENERAL INFORMATION:
APPLICANT: Bostein, et al.
TITLE OF INVENTION: Uses Thereof
FILE REPERENCE: 2002850-0024

CURRENT APPLICANTION NUMBER: US/09/916,849A

CURRENT PILIO DATE: 201-07-26

NUMBER OF SEQ ID NOS: 15

SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 84, Application US/09919497
; Sequence 84, Application US/09919497
; Patent No. US20020106662A1
; GENERAL INFORMATION:
; APPLICANT: Mutter, George L.
; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER;
; FILE REPERENCE: B0801/7225
; CURRENT PILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/221,735
; PRIOR PILING DATE: 2000-07-31
; RIOR APPLICATION NUMBER: US 60/221,735
; RIOR APPLICATION NUMBER: US 60/221,735
; ROWBER OF SEQ ID NOS: 100
; SEQ ID NO 84
; LENGTH: 582
                                 APPLICANT: Milly, Mark
APPLICANT: Raily, Mark
APPLICANT: Rajardo, Mark
APPLICANT: Moss, Patrick
TITLE OF INVENTION: A NOVEL MATRIX METALLOPROTEINASE (MMP-25)
TITLE OF INVENTION: EXPRESSED IN SKIN CELLS
FILE REFERENCE: 240083.509
CURRENT APPLICATION NUMBER: US/09/801,196
CURRENT FILING DATE: 2001-03-06
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 582;
                                                                                                                                                                                                                                                                                                                                                                                                    DB 3; Length 582;
                                                                                                                                                                                                                                                                                                                                                                                                         Score 43; DB 3; I Pred. No. 4.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
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LENGTH: 582
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 77.8
Matches 7; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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US-09-919-497-84
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                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
US-09-801-196-27
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US-09-916-849A-2
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US-09-919-497-84
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                                                                                                                   Sequence 4, Application US/09916658
; Sequence 4, Application US/09916658
; Patent No. US2002002510A1
; GENERAL INFORMATION:
; APPLICANT: Strongin, Alex Y.
; APPLICANT: Deryugina, Elena I.
; TITLE OF INVENTION: Superactivated Alpha v Beta 3 Integrin
; TITLE OF INVENTION: Superactivated Alpha v Beta 3 Integrin
; FILE REFERENCE: P-L4 4811
; CURRENT APPLICATION NUMBER: US/09/916,658
; CURRENT FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: US 60/220,706
; PRIOR APPLICATION NUMBER: US 60/220,706
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FREESEQ for Windows Version 4.0
; SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Abbott Laboratories
APPLICANT: Falduto, Michael T.
APPLICANT: Magnuson, Scott R.
APPLICANT: Magnuson, Scott R.
APPLICANT: Morgan, Douglas W.
TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,
TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
TITLE OF INVENTION: OF USING SAME
FILE REPERENCE: 6073.US.Pl
CURRENT APPLICATION NUMBER: US/09/391,104
CURRENT PILING DATE: 1999-09-07
PRIOR FILING DATE: 1999-03-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 43; DB 3; Length 582;
Pred. No. 4.7e+02;
1; Mismatches 1; Indels
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SOFTWARE: FastSEQ for Windows Version 3.0
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; Patent No. US20020037827A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 28, Application US/09391104
Publication No. US20020031817A1
GENERAL INFORMATION:
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Best Local Similarity 77.8
Matches 7; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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418 ALFWMPNGK 426
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307 ALFWMPNGK 315
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ORGANISM: Homo sapiens
US-09-391-104-28
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ORGANISM: Homo sapiens
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SOFTWARE: Fabr
SEQ ID NO 28
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66.2%;
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Best Local Similarity 77.8
Matches 7; Conservative
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Matches 7; Conservative
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418 ALFWMPNGK 426
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US-10-411-010-26
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Best Local Similarity
US-10-131-985-43
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| Sequence 6, Application US/10133797
| Publication No. US20030109021A1
| GENERAL INFORMATION:
| APPLICANT: Why Shujian
| APPLICANT: Chen, Jian
| APPLICANT: Feder, John
| APPLICANT: Feder, John
| APPLICANT: Ede, Liana
| APPLICANT: Ede, Liana
| APPLICANT: Experex, Stanley
| TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALLOPROTEASE HIGHLY
| TITLE OF INVENTION: EXPRESSED IN THE TESTIS, MMP-29
| TITLE OF INVENTION: EXPRESSED IN THE TESTIS, MMP-29
| FILE REFERENCE: DOIAINP
| CURRENT APPLICATION NUMBER: US/10/133,797
| CURRENT APPLICATION NUMBER: US 60/266,764
| PRIOR FILING DATE: 2001-04-26
| NUMBER OF SEQ ID NOS: 80
| SOFTWARE: Patentin version 3.0
| SEQ ID NO 6
| LENGTH: 582
| TYDE. DATE: CLEAR OF SEQ ID NO 6
| LENGTH: 582
| TYDE OF LENGTH: SA2
| TYDE OF LENGTH: SA2
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                   OTHER INFORMATION: Description of Artificial Sequence:Matrix OTHER INFORMATION: Metalloproteinase US-09-916-849A-2
                                                                                                            Query Match 66.2%; Score 43; DB 3; Length 582; Best Local Similarity 77.8%; Pred. No. 4.7e+02; Matches 7; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 66.2%; Score 43; DB 4; Length 582; Best Local Similarity 77.8%; Pred. No. 4.7e+02; Matches 7; Conservative 1; Mismatches 1; Indels
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US-10-131-985-43

Sequence 43, Application US/10131985

PUBLICALION NO. US20030199440A1

GENERAL INFORMATION:

APPLICANT: Dack, Kevin N

APPLICANT: Fish, Paul V

APPLICANT: Huggins, Jonathan P

APPLICANT: Huggins, Jonathan P

APPLICANT: Morincosh, Fraser S

APPLICANT: Morincosh, Fraser S

APPLICANT: Morincosh, Richolas L

TITLE OF INVENTION: Composition

FILE REFERENCE: PCS 10391A

CURRENT PELING DATE: 2002-04-25

PRIOR PILING DATE: 2002-04-25

PRIOR PILING DATE: 2000-11-30

PRIOR FILING DATE: 1999-12-29

NUMBER OF SEQ ID NOS: 60

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 43

LENTIN CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-133-797-6
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418 ALFWMPNGK 426
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ORGANISM: Homo sapiens
FEATURE:
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Sequence 100, Application US/10773446

Sequence 100, Application US/10773446

Publication No. US20050176662A1

SERENAL INFORMATION:

APPLICANT: MCLAREN, MARGARET

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING AND TREATING RETINAL

TITLE OF INVENTION: WINBER: US/10/773,446

TITLE OF INVENTION: UNBER: US/10/773,446

CURRENT APPLICATION NUMBER: US/10/773,446

CURRENT FILING DATE: 2004-09

NUMBER OF SEQ ID NOS: 131

SOFTWARE PARENTIN version 3.2

SEQ ID NO 100

LENGTH: 582

TYRE: RT

CREATER FOR

CREATER FOR

CURRENT FILING DATE: 2004-09

NUMBER OF SEQ ID NOS: 131

SEQ ID NO 100

LENGTH: 582

TYRE: RT

CREATER FOR

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US-10-773-446-100
                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GRETCHEN FRANTZ
APPLICANT: PAUL POLAKIS
APPLICANT: SUSAN D. SPENCER
APPLICANT: ZEMIN ZHANG
ITILE OF INVENTION: THEATHENT OF TUMOR
TITLE OF INVENTION: TREATHENT OF TUMOR
FILE REFERENCE: P5023H1-US
CURRENT APPLICATION NUMBER: US/10/953,264
CURRENT FILING DATE: 2003-04-10
FRIOR APPLICATION NUMBER: US/10/411,010
FRIOR PELICATION NUMBER: US 60/404,809
FRIOR FILING DATE: 2002-06-19
FRIOR PELING DATE: 2002-06-19
FRIOR PELING DATE: 2002-06-19
FRIOR PELING DATE: 2002-06-16
FRIOR PELING DATE: 2002-06-16
FRIOR FILING DATE: 2002-06-16
FRIOR FILING DATE: 2002-04-16
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                                                                                                                                                                                                                                                         Sequence 26, Application US/10951264
Publication No. US20050042216Al
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Matches 7; Conservative
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418 ALFWMPNGK 426
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418 ALFWMPNGK 426
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2 ALWWSPNGK 10
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ORGANISM: Homo sapien
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Sequence 19, Application US/10276272A
Sequence 19, Sequence 19, Sequence 19, Publication No. US20040120954A1
GENERAL INFORMATION:
APPLICANT: SEIKI, Motcharu
APPLICANT: COBATA, Ken-ichi
TITLE OF INVENTION: REGULATION OF MTI-MMP ACTIVITY
FILE REFRENCE: 2002-1357A/MMC/01332
CURRENT APPLICATION NUMBER: US/10/276,272A
CURRENT APPLICATION NUMBER: PCT/JF01/04166
PRIOR APPLICATION NUMBER: PCT/JF01/04166
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 20
SEQ ID NO 19
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LENGTH: S82
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Publication No. US20050026836A1
GENERAL INFORMATION:
APPLICANT: Davies, Michael J
APPLICANT: Davies, Michael J
APPLICANT: Huggins, Jonathan P
APPLICANT: Huggins, Jonathan P
APPLICANT: McIntosh, Fraser S
APPLICANT: McIntosh, Fraser S
APPLICANT: McIntosh, Fraser S
APPLICANT: McIntosh, Praser S
FILE REFERENCE: PCS 10391A
CURRENT APPLICATION NUMBER: US/10/131, 985
PRIOR FILING DATE: 2002-04-25
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US/99/726, 295
PRIOR FILING DATE: 2000-11-30
PRIOR PILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 60
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68A-7 68A-7 68A-7	68A-3 68A-3	90-29	68A-2	36-35	36-48	*T-*/	44-98	44-10	44-10	44-10	44-11	44-11	44-11	11-44	77-77	***	11-14 1-489	400	688-1	1 488	96-96	24-18	588-1	53-11	684-1	A P P P P P P P P P P P P P P P P P P P	6.48	57-52	39-18	39-22	39-23	39-30	53-16	53-17	53-20	39-16	68A-1	53-21	53-27	68A-2	68A-4	03-10	03-12	86-10	68A-1	68A-2	PRACT	7-50	03-18	16-34	68A-	68A-1	68A-1	68A-3	68A-2	68A-2	68A-2	26A-1	15B-1	68A-1	59-45	68A-1
966-196	96-5-960	339-8	96-5	49-5	149-5	1-40	16-1	16-1	116-1	116-1	16-1	16-1	176-1	7-911	1 9 1	1-011	7-95	0 0	2 3 3 5 6	7 9 6 6	74.0	24-4	706-5	70-0	2000	2000	8-960	467-6	517-9	517-9	517-9	517-9	170-6	170-6	170-6	517-9	960-5	170-6	170-6	0.000	2-960	134-7	134-7	9-860	960	960	2000	0 0 0 0	134-7	140-4	5-960	2-960	960	960	960	960	960	131-8	973-1	960	024-9	96-2
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Sequence 4, Applisequence 6, Applisequence 6, Applisequence 15, Applisequence 15, Applisequence 15, Applisequence 15, Applisequence 15, Applesequence 15, Applesequence 150, Applesequence 150, Applesequence 149, Applesequence 149, Applesequence 149, Applesequence 149, Applesequence 141, Applesequence 134, Applesequence 141, Applesequence 134, Applesequence 141, Applesequence 134, Applesequence 134, Applesequence 141, Applesequence 156, Applesequence 160, Applesequen	Sequence 30610, A Sequence 10291, A Sequence 21722, A Sequence 10401, A Sequence 19846, A Sequence 19846, A Sequence 30004, A Sequence 3134, Ap Sequence 23340, A Sequence 3134, Ap Sequence 172, App Sequence 3153, Ap Sequence 9419, App Sequence 112, App Sequence 112, App Sequence 112, App Sequence 112, App Sequence 1153, Ap Sequence 115, Appl Sequence 12, Appl
US/11/062 US/11/062 US/11/062 US/11/062 US/11/062 US/11/062 US/11/062 US/11-099-76	US-11-096-568A-30610 US-11-087-099-10291 US-11-096-568A-24258 US-11-096-568A-1922 US-11-096-568A-19346 US-11-096-568A-30004 US-11-096-568A-30004 US-11-096-568A-30004 US-11-096-568A-3339 US-11-096-568A-3339 US-11-096-568A-3339 US-11-096-568A-3139 US-11-096-568A-3513 US-11-096-568A-3513 US-11-096-568A-3513 US-11-096-568A-3153 US-11-096-568A-3153 US-11-096-568A-3153 US-11-096-568A-3153 US-11-096-568A-3153 US-11-096-568A-3153 US-11-096-568A-3153 US-11-096-568A-3153 US-11-096-568A-3153 US-11-096-568A-3153 US-11-096-568A-3153 US-11-096-568A-3153
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2 ALWWSPNGK 10
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ORGANISM: Homo sapiens
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TITLE OF INVENTION: Three-dimensional structure of dipeptidyl peptidase IV
FILE REFERENCE: 03-039-FOT.
CURRENT APPLICATION NUMBER: US/10/522,789
CURRENT FILING DATE: 2005-01-28
PRIOR APPLICATION NUMBER: US 60/398,761
PRIOR PILING DATE: 2002-07-29
SOFTWARE: Patentin version 3.1
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                                                                                                     Gaps
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                                                                                                                                                                                                                                                  Sequence 13, Application US/11116939;
Publication No. US20050265995A1;
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Stephen Tomlinson;
APPLICANT: Stephen Tomlinson;
TITLE OF INVENTION: TISSUE TARGETED COMPLEMENT MODULATORS;
FILE REFERENCE: 19113.011/116,939
CURRENT APPLICATION NUMBER: US/11/116,939
CURRENT FILING DATE: 2004-04-28
PRIOR FILING DATE: 2004-04-28
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
                                                                 Score 65; DB 7; Length 760;
Pred. No. 0.005;
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                                                                                                     0; Indels
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                                                                  100.0%;
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 8; Conservative
                                                                 Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
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Matches 8; Conservative
                                                                                                                                                           210 YALWWSPNGK 219
                                                                                                                                       1 YALWWSPNGK 10
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ORGANISM: Homo sapiens
                ; ORGANISM: Homo Sapiens
US-11-186-284-55
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US-11-116-939-13
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TYPE: PRT
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213 ALWWSPNG 220

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Sequence 234, Application US/10501035
Sequence 234. Application US/10501035
Publication No. US20060046249A1
GENERAL INFORMATION:
APPLICANT: Bristol—Myers Squibb Company
TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLECTIDES AND POLYPEPTIDE FOR PREDICTING
TITLE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYROSINE KINASPITILE OF INVENTION: AND/OR PROTEIN TYROSINE KINASPITICATION NUMBER: US/10/501,035
CURRENT APPLICATION NUMBER: US/10/501,035
PRIOR FILING DATE: 2004-07-09
PRIOR FILING DATE: 2002-01-18
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Publication No. US20060019284A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: DOBNIFFCATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF
TITLE OF INVENTION: COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE
TITLE OF INVENTION: KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER
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TITLE OF INVENTION: Immortalized Human Tuberous Sclerosis Null
TITLE OF INVENTION: Immortalized Human Tuberous Sclerosis Null
TITLE OF INVENTION: Angiomyolipoma Cell and Method of Use Thereof
FILE REFERENCE: 24318-502
CURRENT APPLICATION NUMBER: US/11/090,439
CURRENT FILING DATE: 2005-03-25
PRIOR PILING DATE: 2004-03-25
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
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Pred. No. 0.39;
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100.0%; Pred. No. v...
0; Mismatches
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1; Mismatches
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Pred. No.
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US-11-090-439-58
US-11-090-439-58
; Sequence 59, Application US/11090439
; Publication No. US20050266442Al
; GENERAL INFORMATION:
; APPLICANT: Squillace, Rachel
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SEO ID NO 234
LENGTH: 766
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77.8%;
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Best Local Similarity 100..
ماری 8
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Best Local Similarity 77.8
Matches 7; Conservative
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Gaps

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APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT PILING DATE: 2004-07
PRIOR FILING DATE: 2003-04-07
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28;
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Publication No. US20060041961A1
GENERAL INFORMATION:
APPLICANT: ADAG, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21 (53450) B FP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
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Best Local Similarity 71.4%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 1;
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SOFTWARE: pt_SEQ_genes Version 1.0
SEQ ID NO 1610
LENGTH: 2335
                 SOFTWARE: PatentIn version 3.3 SEQ ID NO 477 LENGTH: 964
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Best Local Similarity 50.0
Matches 5; Conservative
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Matches 7; Conservative
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US-11-087-099-7087
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183 HGFWYTPNGK 192
NUMBER OF SEQ ID NOS: 782
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                                                                                ; TYPE: PRT
; ORGANISM: Pinus radiata
US-11-024-959-477
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244 SLAWSPNGK 252
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US-10-821-234-1610
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US-11-087-099-7087
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LENGTH: 475
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                                                                                                                                                                     Query Match
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Publication No. US20060040302A1
GENERAL INFORMATION:
APPLICANT: Bosterin, et al.
TITLE OF INVENTION: Methods of Classifying, Diagnosing, Stratifying and TITLE OF INVENTION: Treating Cancer Patients and Their Tumors FILE REFERENCE: 2002850-0049
CURRENT APPLICANTION NUMBER: US/11/200,822
CURRENT FILING DATE: 2005-08-10
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                 Score 43; DB 7; Length 582; Pred. No. 11; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66.2%; Score 43; DB 7; Length 582; 77.8%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: KODRZYCKÍ, BOB
TITLE OP INVENTION: CELL CYCLE GENES AND RELATED METHODS
FILE REFERENCE: 044463-0360
CURRENT APPLICATION NUMBER: US/11/024,959
CURRENT FILING DATE: 2004-12-30
PRIOR APPLICATION NUMBER: 60/533,036
PRIOR FILING DATE: 2003-12-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 11;
1; Mismatches
        FILE REPERRICE: 10001 NP CURRENT APPLICATION NUMBER: US/11/169,041 CURRENT FILING DATE: 2005-06-28 PRIOR APPLICATION NUMBER: 60/584,405 PRIOR FILING DATE: 2004-06-30 NUMBER OF SEQ ID NOS: 527 SOFTWARE: Patentin version 3.2 LENGTH: 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 477, Application US/11024959;
Publication No. US20060010516A1;
GRNERAL INFORMATION:
APPLICANT: FORSTER, RICHARD L.
APPLICANT: CONNETT, MARIE B.
APPLICANT: EMERSON, SARAH JANE
APPLICANT: RIGGOR, MURRAY ROBERT
APPLICANT: HIGGINS, COLLEEN M.
APPLICANT: MAGUSIN, ANDREAS
APPLICANT: MAGUSIN, ANDREAS
                                                                                                                                                                                                                                                                                                          66.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                     Query Match 66.2
Best Local Similarity 77.8
Matches 7; Conservative
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Matches 7; Conservative
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                                                                                                                                                                                                                  TYPE: PRT
CORGANISM: Homo sapiens
US-11-169-041-130
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    TITLE OF INVENTION:
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US-11-024-959-477
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LENGTH: 582
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US-11-200-822-2
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APPLICANT:
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Sequence 867, Application US/10995561

Publication No. US20050272054A1

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REPERBENCE: CL001559

CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT PILING DATE: 2004111-24

NUMBER OF SEQ ID NOS: 85702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLOOLSS9
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FRAESE for Windows Version 4.0
SEQ ID NO 870
                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                APPLICANT: MAGUSIN, ANDREAS
APPLICANT: KODRZYCKI, BOB
TITLE OF INVENTION: CELL CYCLE GENES AND RELATED METHODS
FILE REPERENCE: 044463-0360
CURRENT APPLICATION NUMBER: 105/11/024,959
CURRENT FILING DATE: 2004-12-30
                                                                                                                                                                                                                                                                                                                                                                                                core 39; DB 7;
Pred. No. 32;
Mismatches 0
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                                                                                                                                                                   PRIOR FILING DATE: 2003-12-30 PRIOR FILING DATE: 2003-12-30 NUMBER OF SEQ ID NOS: 782 SOFTWARE: PatentIn version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 870, Application US/10995561 Publication No. US20050272054A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                60.0%; Scc.
100.0%; Pre
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87.5%;
HIGGINS, COLLEEN M
LUND, STEVEN TROY
MAGUSIN, ANDREAS
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Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 60.0
Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                  , ORGANISM: Pinus radiata US-11-024-959-470
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US-10-995-561-870
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US-10-995-561-870
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US-10-995-561-867
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Publication No. US20060003430A1
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REFRENCE: BB132
CURRENT APPLICATION UNMBER: US/11/009,658
CURRENT FILING DATE: 2004-12-10
PRIOR PREJICATION NUMBER: US/12-10
PRIOR PILING DATE: 2001-08-22
PRIOR PLING DATE: 2001-08-22
PRIOR FILING DATE: 1999-02-22
                                                              APPLICANT: E. I. du -Pont de Nemours and Company TITLE OF INVENTION: Lysophosphatidic Acid Acetyltransferases FILE REFERENCE: BB132 CURRENT APPLICATION NUMBER: US/11/009,658 CURRENT FILING DATE: 2004-12-10 PRIOR APPLICATION NUMBER: US/09/914,098 PRIOR APPLICATION NUMBER: 60/121,119 PRIOR APPLICATION NUMBER: 60/121,119 PRIOR APPLICATION NUMBER: 60/121,119 PRIOR APPLICATION NUMBER: 60/121,119 PRIOR FILING DATE: 1999-02-22 NUMBER OF SEQ ID NOS: 58 SOFTWARE: Microsoft Office 97 SEQ ID NO 16 LENGTH: 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 39; DB 7; Length 255;
Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 39; DB 7; Length 174;
Pred. No. 17;
0; Mismatches 1; Indels
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Publication No. US20060010516A1
GENERAL INFORMATION:
Sequence 16, Application US/11009658
Publication No. US20060003430A1
GENERAL INFORMATION:
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Best Local Similarity 83.3
Matches 5; Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Oryza sativa
US-11-009-658-42
                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Oryza sativa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 WWSPRG 72
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LOCATION: (136)
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Sequence 2562, Application US/11072512
Publication No. US20060029945A1
GENERAL INPORMATION:
APPLICANT: ISOGAI, TAKAO
APPLICANT: OFGURI, TETSUJI
APPLICANT: OFGURI, TETSUJI
APPLICANT: MAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISATO, HIROYUKI
APPLICANT: ISANO, WUNCO
APPLICANT: ISONO, YUUKO
APPLICANT: HOO, YUKI
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Best Local Similarity 62.5
Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens US-11-072-512-2562
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Sequence 869, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michael et al.
APPLICANT: CARGILL, Michael et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFRENCE: CLOOUS59
CURRENT APPLICANTION NUMBER: US/10/995,561
CURRENT PILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 869
LENGTH: 1411
                                                                                                                                                                                                                                                                                                                                           Sequence 868. Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICAMY: CARGILL, Michele et al.
TITLE OF INVENTION: GENERIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE REPERENCE: CLO01559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FaetSEQ for Windows Version 4.0
SEQ ID NO 868
LENGTH: 1366
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Pred. No. 1e+02;
0; Mismatches 1; Indels
                                                                                                                                   Score 39; DB 6; Length 1365;
Pred. No. 1e+02;
0; Mismatches 1; Indels
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Pred. No. 1e+02;
0; Mismatches 1; Indels
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 867
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Best Local Similarity 87.5%;
Matches 7; Conservative
                                                                                                                                       60.0%;
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Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                     Query Match
Best Local Similarity 87.5
Matches 7; Conservative
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CRGANISM: Homo sapiens
US-10-995-561-868
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US-10-995-561-869
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                                                           type: PRT
CORGANISM: Homo sapiens
US-10-995-561-867
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                                           1365
                                         LENGTH:
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APPLICANT: Kapur, Vivek and Gebhart, Connie J.
APPLICANT: Kapur, Vivek and Gebhart, Connie J.
TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
FILE REPERENCE: 0953-128001
CURRENT APPLICATION NUMBER: US/11/098,686
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US03/31318
PRIOR APPLICATION NUMBER: DC 001
PRIOR PILING DATE: 2003-10-04
NUMBER: C SEQ ID NOS: 11433
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10864
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16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                            APPLICANT: NACAHARI, KENNI
APPLICANT: NACAHARI, KENNI
APPLICANT: NASUHO, YASUHIKO
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: 08435-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PALCHIN VET. 2.1
SEQ ID NO 2562
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Pred. No. 16;
1; Mismatches
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; Publication No. US20060024696A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT; ORGANISM: Lawsonia intracellularis US-11-098-686-10864
OTSUKA, KAORU
NAGAI, KEIICHI
IRIE, RYOTARO
TAMECHIKA, ICHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58.5%;
                                                                                           SEKI, NACHIKO
YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
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Sequence 21612, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 21612
LENGTH: 261
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Publication No. US20060048240A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
SUMBER OF SEQ ID NOS: 34471
SEQ ID NO 21611
LENGTH: 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 261;
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| LOCATION: (1) - (1271)
| LOCATION: (1) - (1271)
| US-11-096-568A-21611
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| LOCATION: (1) - (1261)
| TOTER INDORMATION: Ceres Seq. ID no. 12405497
| US-11-096-568A-21612
   Mismatches
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Pred. No.
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ORGANISM: Zea mays subsp. mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 75.0
---- 6; Conservative
5; Conservative
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                                                                4 WWSPNGK 10
                                                                                                                       62 WWCDNGK 68
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      Matches
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APPLICANT: BERTHET, FRANCOIS XAVIER
APPLICANT: CASADEVALL, FRANCESC VAYEDA
APPLICANT: GANZ MARIA, MARIA CRUZ
APPLICANT: GARCIA, TERESA LLOP
APPLICANT: GLE, ANGELS MOR
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING PATHOGEN
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING PATHOGEN
TITLE OF INVENTION: LONDER: US/11/116,144
CURRENT PELING DATE: 2005-04-27
FRIOR APPLICATION NUMBER: PCT/ES04/000581
FRIOR APPLICATION NUMBER: PCT/ES04/000581
FRIOR APPLICATION NUMBER: EP 03380307.3
FRIOR FILING DATE: 2003-12-23
NUMBER OF SEQ ID NOS: 301
SOFTWARE: PATENTIN VOR. 3.3
SEQ ID NO 90
LENGTH: 129
TYPE: PRT

ORGANISM: Anas platyrhynchos
US-11-116-144-90
                                                                                                                                                                                                                                                                                                            Sequence 91, Application US/11116144

PUDI/cation No. US20050277181A1

GENERAL INFORMATION: PRANCOIS XAVIER
APPLICANT: BERTHET, FRANCOIS XAVIER
APPLICANT: SANZ MARIA, MARIA CRUZ
APPLICANT: GARCIA, TERESA LLOP
APPLICANT: OLLE, ANGELS MOR
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING PATHOGEN
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING PATHOGEN
TITLE OF INVENTION: UNBER: US/11/116,144
CURRENT FILING DATE: 2005-04-27
PRIOR APPLICATION NUMBER: PCT/ES04/000581
PRIOR PLING DATE: 2004-12-23
PRIOR PRILING DATE: 2004-12-23
PRIOR APPLICATION NUMBER: EP 03380307.3
PRIOR FILING DATE: 2003-12-23
NUMBER OF SEQ ID NOS: 301
SOFTWARE: PALENTING OFFER PALENTING VARIABLES PALENTES PALENTING VARIABLES PALENTING VARIABLES PALENTING VARIABLES PALENTES VARIABLES VARIABLES PALENTES VARIABLES VARIABLES PALENTES VARIABLES VARIABLES
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27;
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      83.3%; Pred. No. 31;
tive 1; Mismatches
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Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Anas platyrhynchos
US-11-116-144-91
                                      5; Conservative
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Best Local Similarity
Best Local Similarity
Matches 5, Conserv
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54 LWWSPD 59
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APPLICANT: BERTHET,
APPLICANT: CASADEVA
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Sequence 17843, Application US/11096568A
| Sequence 17843, Application US/11096568A
| Publication No. US20060048240A1
| Publication No. US20060048240A1
| General Programment 
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Sequence 10625, Application No. US20060048240A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION: 1952202.
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT APPLICATION NUMBER: 2005-04-01
SEQ ID NOS: 34471
LENGTH: 370
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                                                                                                                                                                                                                                                                                                           Score 37; DB 7; Length 328; Pred. No. 61; 0; Mismatches 2; Indels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 606;
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| LOCATION: (1) - (370)
| PURE INDEMATION: Ceres Seq. ID no. 13596636
US-11-096-568A-10625
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LOCATION: (1)...(606)

OTHER INFORMATION: Ceres Seq. ID no. 12361175

US-11-096-5688-17843
                                 FEATURE:
| NAME/KEY: misc_feature | LOCATION: (1) | LOCATION: 
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Pred. No. 68;
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                                                                                                                                                                                                                                                                                                                Query Match 56.9%;
Best Local Similarity 75.0%;
Matches 6; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56.9%;
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ORGANISM: Triticum aestivum
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Best Local Similarity 75.0
Then 6; Conservative
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TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
FILE REPRESENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
EROGTH: 227
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Publication No. US20060048240A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 10626
LENGTH: 328
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Sequence-Determined Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 10627
LENGTH: 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 56.9%; Score 37; DB 7; Length 272; Best Local Similarity 75.0%; Pred. No. 52; Matches 6; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
i LOCATION: (1)..(327)
cother information: Ceres Seq. ID no. 12405495
US-11-096-5688-21610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | NAME/KEY: misc_feature
| LOCATION: (1).7(272)
| OTHER INDEMATION: Ceres Seq. ID no. 13596638
| US-11-096-568A-10627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-11-096-568A-21610
; Sequence 21610, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Zea mays subsp. mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      148 ALWWSSYG 155
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US-11-096-568A-10626
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APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1522PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 3423
LENGTH: 209
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 209;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: CHIRON SPA
APPLICANT: FONTANA Maria Rita
APPLICANT: PLAZA Mariagrazia
APPLICANT: PLAZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MANUACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REPERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 36; DB 7;
Pred. No. 60;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                           , LOCATION: (1). 7(209)
; OTHER INFORMATION: Ceres Seq. ID no. 12608263
US-11-096-568A-3423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/467,657 CURRENT FILING DATE: 2003-08-11 PRIOR APPLICATION NUMBER: GB-0103424.8 PRIOR FILING DATE: 2001-02-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5656, Application US/10467657 Publication No. US20050260581A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-11-049-536-84
i Sequence 84, Application US/11049536
i Publication No. US20060024297A1
general information:
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APPLICANT: Dransfield, Daniel T.
APPLICANT: Pieters, Henk
APPLICANT: Hoet, Rene
APPLICANT: Hufton, Simon E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 9218
SOFWARE: SegWin99, version 1.04
SEQ ID NO 5656
LENGTH: 929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5656
                                                                                                                                                                                                                                                                                                                                                                                                                                               55.4%;
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               Sequence 3423, Application US/1:
Publication No. US20060048240A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 55.6
Matches 5; Conservative
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                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Glycine max
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17 FWKPNGK 23
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                     TLE OF INVENTION: CELL CYCLE GENES AND RELATED METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 37; DB 7;
Pred. No. 1e+02;
2; Mismatches
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US-11-107-096-51
Sequence 51, Application US/11107096
Publication No. US20060003348A1
GENERAL INFORMATION:
APPLICANT: SIDHU, SACHDEV S.
APPLICANT: SIDHU, SICHNON DIE PEZ COURENT FOR INVENTION: OMI PPZ MODULATORS
FILE REFERENCE: P2100R1
CURRENT APPLICATION NUMBER: US/11/107,096
CURRENT APPLICATION NUMBER: US. 60/563,157
PRIOR FILING DATE: 2004-04-16
SEQ ID NO 51
LENGTH: 9
LENGTH: 9
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                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 044463-0360
CURRENT APPLICATION NUMBER: US/11/024,959
CURRENT FILING DATE: 2004-12-30
PRIOR APPLICATION NUMBER: 60/533,036
PRIOR FILING DATE: 2003-12-30
                                                                                                                                         Sequence 381, Application US/11024959
Publication No. US20060010516A1
                                                                                                                                                                                                                                CONNETT, MARIE B.
ENERSON, SARAH JANE
GRIGOR, MURRAY EOBERT
HIGGINS, COLLEEN M.
LUND, STEVEN TROY
MAGUSIN, ANDREAS
KODRZYCKI, BOB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 782
SOFTWARE: PatentIn version 3.3
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Best Local Similarity 60.0%;
Matches 6; Conservative
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Best Local Similarity 44.4
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Eucalyptus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 YALWWSPNGK 10
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                                        181 LWWFPGG 187
3 LWWSPNG 9
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LENGTH: 607
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 186. Application US/10993543
; Sequence 186. Application US/10993543
; Publication No. US20060036076A1
; GENERAL INPORMATION:
; APPLICANT: Dranefield, Daniel T.
; APPLICANT: Ladner, Robert C.
; TITLE OF INVENTION: Metalloproteinase-Binding Proteins
; FILE REFERENCE: 10280-088001
; CURRENT APPLICATION WHABER: US/10/993,543
; CURRENT FILING DATE: 2004-11-19
; PRIOR FILING DATE: 2003-11-19
; NUMBER OF ESQ ID NOS: 299
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Amino Acid Sequence of Domain Antibody US-10-925-366A-352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53.8%; Score 35; DB 6;
80.0%; Pred. No. 53;
tive 1; Mismatches
              PRIOR APPLICATION NUMBER: DCT/GB2002/03014
PRIOR FILING DATE: 2002-06-8

PRIOR FILING DATE: 2002-12-7

PRIOR FILING DATE: 2002-12-7

PRIOR FILING DATE: 2002-12-7

PRIOR FILING DATE: 2000-06-38

PRIOR FILING DATE: 2004-06-38

PRIOR FILING DATE: 2004-06-30

PRIOR FILING DATE: 2004-01-08

PRIOR FILING DATE: 2004-01-08

PRIOR FILING DATE: 2003-12-24

PRIOR PRILING DATE: 2003-12-24

PRIOR FILING DATE: 2003-12-24

PRIOR FILING DATE: 2003-12-24

PRIOR FILING DATE: 2003-12-28

PRIOR FILING DATE: 2003-11-28

PRIOR FILING DATE: 2003-11-28

PRIOR FILING DATE: 2003-11-28

PRIOR FILING DATE: 2003-11-28

PRIOR FILING DATE: 2003-11-38

PRIOR PILING DATE: 2003-11-38
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; Publication No. US20060024696A1
; GENERAL INFERMATION:
A PEPLICANT: Kapur, Vivek and Gebhart, Connie J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 53.8
Best Local Similarity 80.0
Matches 4; Conservative
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Best Local Similarity
Matches 4; Conserv
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32 YAMWW 36
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US-11-098-686-10681
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APPLICANT: Commonwealth Scientific and Industrial Research Organisation
FILE REPERENCE: 503244
CURRENT APPLICATION NUMBER: US/11/112,882
CURRENT FILING DATE: 2005-04-22
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patentin version 3.1
SEQ ID NO 32
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Publication No. US20050271663A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ignatovich, Olga
APPLICANT: Benjamin, Woolven
APPLICANT: Benjamin, Woolven
APPLICANT: Benjamin, Woolven
APPLICANT: Bensen, Amrik
APPLICANT: Bensen, Amrik
APPLICANT: Brewis, Neil
TITLE OF INVENTION: Compositions and Methods for Treating Inflammatory Disorders
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54.6%; Score 35.5; DB 7; Length 318;

Best Local Similarity 33.3%; Pred. No. 1e+02;

Matches 5; Conservative 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Synthetically generated peptide US-11-049-536-84
TITLE OF INVENTION: TIE COMPLEX BINDING PROTEINS
                    FILE REFERENCE: 10280-128001
CURRENT APPLICATION NUMBER: US/11/049,536
CURRENT FILING DATE: 2005-02-02
PRIOR APPLICATION NUMBER: US 10/916,840
PRIOR FILING DATE: 2004-08-12
PRIOR FILING DATE: 2004-08-12
PRIOR FILING DATE: 2003-08-12
NUMBER OF SEQ ID NOS: 721
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 131
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CURRENT FILING DATE: 2004.08-24
PRIOR APPLICATION NUMBER: US 10/744,774
PRIOR APPLICATION NUMBER: PCT/GB2003/002804
PRIOR PAPLICATION NUMBER: PCT/GB2003/002804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32 YAMWWVRQAPGKGLEWVSSISPSG 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 SNdS---
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; Sequence 32, Application US/11112882
; Publication No. US20050273885A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ::|| :||:
192 FTIWWLVTFVAPNGE 206
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ORGANISM: Mortierella alpina
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US-10-925-366A-352
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DB 7; Length 303;

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Sequence 10683, Application US/11098686
Publication No. US20060024696A1
GENERAL INFORMATION:
APPLICAT: Kapur, Vivek and Gebhart, Connie J.
TITLE OF INVENTION: WICKEIC ACID AND POLYPEPTIDE SEQUENCES
TITLE OF INVENTION: PROM LAWSONIA INTRACELLULARIS AND METHODS OF
PILE REFERENCE: 09531-128001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Anderson, Dirk M.
TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES
FILE REFERENCE: 2923-US
CURRENT APPLICATION NUMBER: US/11/241,056
CURRENT FILING DATE: 2005-09-30
PRIOR APPLICATION NUMBER: US/09/980,464
PRIOR PILING DATE: 2001-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                            CURRENT FILING DATE: 2005-04-08
PRIOR PILING DATE: 2005-04-08
PRIOR FILING DATE: 2005-04-08
PRIOR FILING DATE: 2005-07
PRIOR FILING DATE: 2001-05-07
PRIOR FLING DATE: 2001-05-07
PRIOR FLING DATE: 2001-05-06
PRIOR FLING DATE: 2001-06
PRIOR P
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CURRENT FILING DATE: 2005-04-04
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PRIOR APPLICATION NUMBER: PCT/US03/31318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12, Application US/11241056 Publication No. US20060024807A1
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SOFTWARE; PatentIn version 3.1
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53.8%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Martin, Unja
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Mus musculus
US-11-241-056-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   268 HVLWWKP 274
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Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
Matches 4; Conserv
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US-11-098-686-10683
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3230R1C1
                                         FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prior Application removed - See Palm or File Wrapper NUMBER OF SEQ ID NOS: 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.16+02;
                                                            FILE REFERENCE: 09531-128001
CURRENT APPLICATION NUMBER: US/11/098,686
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US03/31318
PRIOR FILING DATE: 2003-10-01
PRIOR FILING DATE: 2003-10-04
NUMBER OF SEQ ID NOS: 11433
SOFTWARE: FastSEQ for Windows Version 4.0
SEC ID NO 10681
LENGTH: 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/063,703 CURRENT FILING DATE: 2002-05-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 166, Application US/11102240 Publication No. US20050260647A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) ORGANISM: Lawsonia intracellularis US-11-098-686-10681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Godowski, Paul J.
Grimaldi, Christopher J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53.8%;
83.3%;
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Best Local Similarity 55.6%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Watanabe, Colin K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              195 FTLWETPNG 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo Sapien
US-10-063-703-166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 ALWWSP 7
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Length 311;

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APPLICANT: Steer, Walter
APPLICANT: Steer, Walter
APPLICANT: Callen, Walter
APPLICANT: Healey, Shaun
APPLICANT: Hazlewod, Geoff
APPLICANT: Blum, David
APPLICANT: Blum, David
APPLICANT: Blum, David
APPLICANT: Esteghlalian, Alireza
TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
TITLE OF INVENTION: AND WETHODS FOR MAKING AND USING THEM
TITLE REPERENCE: 564462007901
CURRENT APPLICATION NUMBER: US/10/517,939
CURRENT FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: 60/389,299
PRIOR FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: 60/389,299
SEQ ID NOS: 380
SEQ ID NOS: 380
SEQ ID NOS: 380
                                                                                                                                                                                                                                                                                                                                                                                        Length 463;
                  APPLICANT: MAGUIN, ANDREAS
APPLICANT: KODRZYCKI, BOB
TITLE OF INVENTION: CELL CYCLE GENES AND RELATED METHODS
FILE REFERENCE: 044463-0360
CURRENT APPLICATION NUMBER: US/11/024,959
CURRENT FILING DATE: 2004-12-30
PRIOR PILING DATE: 2003-12-30
NUMBER OF SEQ ID NOS: 782
SOFTWARE: Patentin version 3.3
SEQ ID NO 507
LENGTH 463

LENGTH 463
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Pred. No. 1.7e+02;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Obtained from an environmental sample
                                                                                                                                                                                                                                                                                                                                                                                          Score 35; DB 7; I
Pred. No. 1.7e+02;
1; Mismatches 2;
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; Sequence 3591, Application US/11072512
; Publication No. US20060029945A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 250, Application US/10517939; Publication No. US20060003433A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53.8%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                          Query Match 53.8%;
Best Local Similarity 66.7%;
Matches 6; Conservative
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Best Local Similarity 50.0
Matches 5; Conservative
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98 YSDWWADPGK 107
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                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Pinus radiata
US-11-024-959-507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 237 ALSWSPTGR 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 ALWWSPNGK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: SIGNAL
; LOCATION: (1)...(33)
US-10-517-939-250
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ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 44
US-10-517-939-250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Steer, Brian
APPLICANT: Steer, Walter
APPLICANT: Healey, Shulter
APPLICANT: Healey, Shulter
APPLICANT: Healey, Shulter
APPLICANT: Wu, Di
APPLICANT: Wu, Di
APPLICANT: Beteghlalian, Alireza
TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
FILE REFERENCE: 54462007901
CURRENT APPLICATION NUMBER: US/10/517,939
CURRENT FILING DATE: 2003-06-16
PRIOR FILING DATE: 2003-06-16
PRIOR FILING DATE: 2003-06-16
PRIOR FILING DATE: 2003-06-16
NUMBER OF SEQ ID NOSE: 380
SOFTWARE: FREUSED FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                        Query Match 53.8%; Score 35; DB 7; Length 441; Best Local Similarity 55.6%; Pred. No. 1.6e+02; Matches 5; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 35; DB 6; Length 445;
Pred. No. 1.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
OTHER INFORMATION: Obtained from an environmental sample.
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PRIOR FILING DATE: 2003-10-01
PRIOR APPLICATION NUMBER: US 60/416,395
PRIOR FILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 11433
SOFTWARE: F884SEQ for Windows Version 4.0
SEQ ID NO 10893
LENGTH: 441
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Sequence 507, Application US/11024959

PUblication No. US20060010516A1

GENERAL INFORMATION:
APPLICANT: FORSTER, RICHARD L.
APPLICANT: EMERSON, SARAH JANE;
APPLICANT: EMERSON, SARAH JANE;
APPLICANT: HIGGINS, COLLEEN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 368, Application US/10517939
Publication No. US20060003433A1
GENERAL INFORMATION:
                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
US-11-098-686-10683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53.8%;
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Best Local Similarity 55.6
Matches 5; Conservative
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353 FTLWETPNG 361
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; LOCATION: (1)...(23)
US-10-517-939-368
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LENGTH: 445
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Sequence 88, Application US/11080991
| Sequence 88, Application US/2005026437A1
| Sequence 88, Application No. US2005026437A1
| Sequence 88, Application No. US2005026437A1
| GENERAL INFORMATION:
| APPLICANT: Veiby, Petter Ole
| TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
| TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
| TITLE OF INVENTION: AND OVARIAN CANCER
| FILE REFERENCE: MAI-039
| CURRENT APPLICATION NUMBER: US/11/080,991
| CURRENT APPLICATION NUMBER: US/10/176,847
| PRIOR APPLICATION NUMBER: US/10/176,847
| PRIOR FILING DATE: 2002-06-21
| NUMBER OF SEQ ID NOS: 112
| SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: FORETER, RICHARD L.
APPLICANT: CONNETT, MARIE B.
APPLICANT: EMERSON, SARAH JANE
APPLICANT: HIGGINS, COLLEEN M.
APPLICANT: HIGGINS, COLLEEN M.
APPLICANT: HORD, STEVEN TROY
APPLICANT: KODRZYCKI, BOB
TITLE OF INVERTION: CELL CYCLE GENES AND RELATED METHODS
TITLE OF INVERTION: CELL CYCLE GENES AND RELATED METHODS
CURRENT APPLICATION NUMBER: US/11/024,959
                            APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53450) B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
SEQ ID NOS: 12464
LENGTH: 547
                                                                                                                                                                                                                                                                                        Score 35; DB 7; I
Pred. No. 1.9e+02;
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PRIOR APPLICATION NUMBER: 60/533,036
PRIOR FILING DATE: 2003-12-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53.8%;
55.6%;
                                                                                                                                                                                                                                                                                             53.8%;
US20060041961A1
                                                                                                                                                                                                                           ORGANISM: Neurospora crassa
US-11-087-099-10512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 57.1
Matches 4; Conservative
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US-11-080-991-88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 ALWWSPNGK 10
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88 IWWTVNG 94
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LENGTH: 607
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TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(5)450) B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
LENGTH: 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 35; DB 7; I
Pred. No. 1.8e+02;
1; Mismatches 2,
                                                                                                                                                                                                                                                                                                                                                      APPLICANT: NACAHARI, KENJI
APPLICANT: NACAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2001-125
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SEQ ID NO 3591
LENGTH: 484
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US-11-087-099-10512
; Sequence 10512, Application US/11087099
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Publication No. US20060041961A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , ORGANISM: Nicotiana plumbaginifolia
US-11-087-099-9085
                                                                                                                                                                                                                                                                             TAMECHIKA, ICHIRO
SEKI, NAOHIKO
YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
                                                               OTSUKI, TETSUJI
WAKAMATUJ, AI
SATO, HIROYUKI
ISHII, SHIZUKO
YAMAMOTO, JUN-ICHI
ISONO, YUUKO
HIO, YUKI
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                                              SUGIYAMA, TOMOYASU
OTSUKI, TETSUJI
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Best Local Similarity 57.1.
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Best Local Similarity 62.5
Matches 5; Conservative
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NAGAI, KEIICHI
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US-11-072-512-3591
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169 IWRTPNGK 176
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Sequence 23, Application US/10613744

Sequence 23, Application US/10613744

Publication No. US20050272093A1

GENERAL INFORMATION:
APPLICANT: MacKinnon, Roderick
APPLICANT: The Rockefeller University
TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
TITLE OF INVENTION: Cation WUMBER: US/10/613,744

FILE REFERENCE: 018512-002901US
CURRENT APPLICATION NUMBER: US/09/275,252
PRIOR FILING DATE: 1999-03-24

PRIOR FILING DATE: 1999-03-20

PRIOR FILING DATE: 1998-03-20

PRIOR FILING DATE: 1998-03-20

PRIOR FILING DATE: 1998-03-20

PRIOR FILING DATE: 1998-03-20

PRIOR FILING DATE: 1999-03-22

NUMBER OF SEG DI NOS: 42

NUMBER OF SEG DI NOS: 42
TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation; TITLE OF INVENTION: Channel Proteins, and Uses Thereof FILE REFERENCE: 018512-002901US; CURRENT APPLICATION NUMBER: US/10/613,744; CURRENT FILING DATE: 2003-07-03; PRIOR APPLICATION NUMBER: US/09/275,252; PRIOR APPLICATION NUMBER: US/09/275,252; PRIOR FILING DATE: 1999-03-24; PRIOR FILING DATE: 1999-03-24; PRIOR FILING DATE: 1998-03-20; PRIOR APPLICATION NUMBER: US 09/054,347; PRIOR FILING DATE: 1998-04-02; PRIOR FILING DATE: 1999-04-02; PRIOR FILING DATE: 1999-03-22; NUMBER OF SEQ ID NOS: 42; SOFTWARE: Patentin Ver. 2.1; SEQ ID NO 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52.3%; Score 34; DB 6; Length 40; 100.0%; Pred. No. 30; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Streptomyces lividans US-10-613-744-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Streptomyces lividans US-10-613-744-23
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Best Local Similarity 100.،
دامه 5; Conservative
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SEQ ID NO 23
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Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 ALWWS 20
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US-10-613-744-3
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Sequence 41, Application US/10613744
Publication No. US20050272093A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Mackinnon, Roderick
APPLICANT: The Rockefeller University
TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
                                                                                                                                                                                                                                                         Gaps
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Pred. No. 2.7e+02;
                                                                                                                                                                                                          Length 608;
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                                                                                                                                                                                                        Score 35; DB 7;
Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: SEKI, NACHIKO
APPLICANT: SEKI, NACHIKO
APPLICANT: SCENIKAWA, TSUTOMU
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: NACHARI, KENJI
APPLICANT: NACHARI, KENJI
APPLICANT: NACHHORI, NOVEL FULL LEBERENCE: 084335-0191
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PATENTIN VORES: 201-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PATENTIN VORES: 201-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PATENTIN VORES: 201-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PATENTIN VORES: 201-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PATENTIN VORES: 201-11-05
NUMBER OF SEQ ID NOS: 4096
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                                                                                                                                                                                                                                                    1; Mismatches
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Publication No. US20060029945A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: ISOGAL, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISONO, YUUKO
APPLICANT: ISONO, YUUKO
APPLICANT: HOO, YUUKO
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            NUMBER OF SEQ ID NOS: 782
SOFTWARE: Patentin version 3.3
SEQ ID NO 481
LENGTH: 608
                                                                                                                                                                                                          53.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTSUKA, KAORU
NAGAI, KEIICHI
IRIE, RYOTARO
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Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                        Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                   237 YAASWSPDSK 246
                                                                                                                ; TYPE: PRT
; ORGANISM: Pinus radiata
US-11-024-959-481
                                                                                                                                                                                                                                                                                                    1 YALWWSPNGK 10
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US-11-072-512-3453
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476 IWRTPNGK 483
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LENGTH: 91
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AFFLICANI: INE MOCKETELIE UNIVERSITY

TITLE OF INVENTION: Assays for Screening Compounds Which Interact With

TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation

TITLE OF INVENTION: Channel Proteins, and Uses Thereof

TITLE OF INVENTION: Channel Proteins, and Uses Thereof

FILE REFERENCE: 018512-002901US

CURRENT FILING DATE: 2093-07-03

PRIOR PELING DATE: 1999-03-24

PRIOR PELING DATE: 1999-03-24

PRIOR PELING DATE: 1998-03-20

PRIOR PELING DATE: 1998-03-20

PRIOR FILING DATE: 1998-04-02

PRIOR PELING DATE: 1999-03-22

NUMBER OF SEQ ID NOS: 42

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 3

LENGTH: 58
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APPLICANT: MacKinnon, Roderick
APPLICANT: The Rockefeller University
TITLE OF INVENTION: Basays for Screening Compounds Which Interact With
TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
TITLE OF INVENTION: Channel Proteins, and Uses Thereof
FILE REFERENCE: 018512-002901US
CURRENT APPLICATION NUMBER: US/10/613,744
CURRENT FILING DATE: 2003-07-03
PRIOR APPLICATION NUMBER: US/09/275,252
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41;
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PRIOR APPLICATION NUMBER: US 09/045,529
PRIOR PILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: US 09/054,347
PRIOR APPLICATION NUMBER: US 09/054,347
PRIOR APPLICATION NUMBER: WO PCT/US99/06307
PRIOR FILING DATE: 1999-03-22
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.1
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                           , ORGANISM: Clostridium acetobutylicum US-10-613-744-3
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Matches 5; Conservative
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US-10-613-744-25
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LENGTH: 58
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RESULT 55 US-11-096-568A-27334

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Sequence 1578, Application US/11096568A
Sequence 1578b, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
FILE REPREMENCE: 2700-1592 PUS/2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 15558
LENGTH: 156
                                                  APPLICANT: Alexandrov, Nickolai et al.

APPLICANT: Alexandrov, Nickolai et al.

TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 27334
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TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REPERRNCE: 38-21(53450) B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
LENGTH: 134
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Pred. No. 84;
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Pred. No. 60;
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OTHER INFORMATION: unsure at all Xaa locations
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NAME/KEY: misc_feature
NAME/KEY: (1)..(91)
OTHER INFORMATION: Ceres Seq. ID no. 13648513
Sequence 27334, Application US/11096568A Publication No. US20060048240A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Arabidopsis thaliana
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80.0%;
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Matches 5; Conservative
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Matches 4; Conservative
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69 WWSPS 73
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US-11-096-568A-15758
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US-11-087-099-4615
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Search completed: March 11, 2006, 12:32:58
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NAGAI, KEIICHI
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US-11-072-512-2677
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APPLICANT: MacKinnon, Roderick
APPLICANT: The Rockefeller University
TITLE OF INVENTION: Aseays for Screening Compounds Which Interact With
TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
TITLE OF INVENTION: Channel Proteins, and Uses Thereof
TITLE OF INVENTION: Channel Proteins, and Uses Thereof
CURRENT APPLICATION NUMBER: US/10/613,744
CURRENT FILING DATE: 2003-07-03
PRIOR PILING DATE: 1999-03-24
PRIOR FILING DATE: 1999-03-24
PRIOR FILING DATE: 1999-03-20
PRIOR PLING DATE: 1999-03-20
PRIOR PLING DATE: 1999-03-20
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           Query Match 52.3%; Score 34; DB Best Local Similarity 100.0%; Pred. No. 98; Matches 5; Conservative 0; Mismatches
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; Sequence 16, Application US/10613744
; Publication No. US20050272093A1
; GENERAL INFORMATION:
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ORGANISM: Zea mays subsp. mays
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Best Local Similarity
Matches 4; Conserv
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Pred. No. 1.1e+02;
1; Mismatches 1; Indels
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100.0%; Pred. No. 98;
iive 0; Mismatches
PRIOR FILING DATE: 1998-04-02
PRIOR APPLICATION NUMBER: WO PCT/US99/06307
PRIOR FILING DATE: 1999-03-22
PRIOR FILING DATE: 1999-03-22
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 16
LENGTH: 160
TYPE: PRY
ORGANISM: Artificial Sequence
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APPLICANT: YOSHIKWAA, TSUTOMU
APPLICANT: OTSUKA, MOTOVUKI
APPLICANT: MACAHARI, KENLI
APPLICANT: MACAHARI, KENLI
APPLICANT: MACHARI, KENLI
APPLICANT: MACHARI, KENLI
APPLICANT: MACHARI, YASUHIKO
TITLE OF INVENTION: Novel full length cDNA
FILE REFRENCE: 08435-0.91
FILE REFRENCE: 08435-0.91
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR APPLICATION NUMBER: US 2001-379298
PRIOR FILING DATE: 2001-11-05
NUMBER: OF SEQ ID NOS: 4096
SEQ ID NO 2677
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WAKAMATSU, AI
SATO, HIROYUKI
ISHII, SHIZUKO
YAMAMOTO, JUN-ICHI
ISONO, YUUKO
HIO, YUKI
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OTSUKI, TETSUJI
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Matches 5, Conservative
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Aeb94175
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Aar44423 PDGF-act1 Aau30879 Novel hum Aaw80707 S. pneumo Ad822771 Bacterial Aaw38584 Streptoco	Aab28208 Novel hum Adi27148 Mouse LRP	Abo60418 Human gen Abo80770 Pseudomon	Abg29021 Novel hum Aau37458 Staphyloc	Abm89054 Rice abio	Abg77239 Selected	Abjillio Yeast sel Adh87367 Enterococ	Aau50423 Propionib	Abm46942 Propionib Adr10339 Human pro	Aay94436 Streptoco	Abii()34/0 Stapiiyioc Aau38098 Streptoco	Aau37758 Streptoco	Adk48621 Streptoco	Adr94735 Novel S.	Aea58605 Streptoco Ade45246 Bacterial	Adn20853 Bacterial	Abm65766 Propionib	Aawsuzez Canine ne Aau34377 Staphyloc	Aag27964 Arabidops	Aam47938 Human zin	Ada55416 Human pro	Abb09170 Methylomo	Abgaisss nigh grow Abu25027 Protein e	Abu23845 Protein e	Abul6559 Frocein e Abg24277 Novel hum	Ada55496 Human pro	Abg25954 Novel num Abr53180 Protein a	Adk63212 Disease t	Adlo4397 M. catarr	Aag70721 S cerevie	Abo71588 Pseudomon	Adn19019 Bacterial abre2861 Protein B	Adk62332 Disease t	Abb64574 Drosophil Ado07970 Fly polyp	Abb14761 Human ner	Adm25479 Hypertner Aav97729 NS protei	Aae22896 Rhesus ma	Aae28653 Rhesus ma	Aaezbyty Knesus ma Abu64874 NS protei	Abu64769 Parvoviru	Abr43407 Rhesus ma Adi40298 Rhesus ma	Abo68911 Pseudomon	Adw99247 Mouse 12-	Abp31037 Human ORF	Propic	Propic Novel
AAR47423 AAU30879 AAW80707 ADS22771																																													
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6 ABM24928 Ada78158 Human 6 ABM24928 Abm24928 Human 6 ABM0452 Abm24928 Abm24928 Abm24928 Human 6 ABM17366 Abm17366 Human 6 ABM2712 Abm17366 Human 6 ABM21655 Abm17366 Human 6 ABM21655 Abm201655 Human 6 ABM277748 Human 6 ABM77748 Abm77748 Human 6 ABM77748 Human 7 Abm77748 Human 7 Abm77748 Human 8 ABM07758 Abm06259 Human 9 ABM07765 Abm06259 Human	35 46.1 374 6 ABM5515 Abm35216 35 46.1 374 6 ABM5515 Abm35216 35 46.1 374 6 ABM35216 35 46.1 374 6 ABM35217 35 46.1 374 6 ABM2249 Abm20287 35 46.1 374 6 ABM11749 Abm11749 35 46.1 374 6 ABM7249 Abm11749 35 46.1 374 6 ABM7249 Abm20287 35 46.1 374 6 ABM7249 Abm20287 35 46.1 374 6 ABM7249 Abm20287 35 46.1 374 6 ABM29198 Abm20287 35 46.1 374 6 ABM7174 Abm20178 35 46.1 374 6 ABM7174 Abm7174 Abm721268 35 46.1 374 6 ABM7174 Abm71268 35 46.1 374 6 ABM7168 Abm07174 Abm07174 35 46.1 374 6 ABM7168 Abm07174 Abm07176	35 46.1 374 6 ABO41484 Abo41484 Human 35 46.1 374 6 ABO36299 Abo36299 Abo36299 Human 35 46.1 374 6 ABO36299 Abo36299 Abo4388 Human 35 46.1 374 6 ABN76528 Abn76528 Human 35 46.1 374 6 ABN76528 Abn76524 Human 35 46.1 374 6 ABN26148 Abn76524 Human 35 46.1 374 6 ABN26148 Abn26148 Human 35 46.1 374 6 ABO36301 Abo36301 Abo36301 Abo36301 Abo36301 Human 35 46.1 374 6 ABN36895	ALIGNMENTS  F. 1  ADR47257 standard; peptide; 15 AA.  ADR47257;  ADR47257;  Haman alpha2-antiplasmin cleaving enzyme N-terminal sequence.  Antihrlammatory; cytostatic; vulnerary; antiarteriosclerotic; antithrombotic; vascular; cerebroprotective; pulmonary; antithrombotic; vascular; cerebroprotective; pulmonary; attithis; chrin-related disorder; inflammatory condition; arthritis;	KW coronary artery thromboeis; achering; cancer; merastasis; atherothrombotic disease; KW human; N-terminus; alpha2-antiplasmin cleaving enzyme.  XX XX Homo sapiens.  XX PD 26-AUG-2004.  XX PD 26-AUG-2004, 2004WO-US003398.  XX PR 07-FEB-2004; 2004WS-045774P.  PR 06-FEB-2004; 2004US-00774242.  XX PR 07-FEB-2004; 2004US-00774242.  XX PR 07-FEB-2004; 2004US-00774242.  XX PR 06-FEB-2004; 2004US-00774242.  XX PR 06-FEB-2004; 2004US-00774242.  XX PR 06-FEB-2004; 2004US-00774242.
Human Human Human Human Human Human Novel Human Human	Abr9249 Human sec Abu57133 Human PRO Abu86085 Novel hum Abu87372 Novel hum Abu87383 Human PRO Abu8229 Human PRO Abu8129 Human sec Abu68129 Human sec Abu66104 Novel hum Abu66104 Novel hum Abu99974 Novel hum Abu99974 Novel hum Abu99974 Novel hum	Human Human Novel Human Human Human Human Human Human	Abu96026 Human PRO Abu90339 Novel hum Abu90339 Novel hum Abo09754 Human sec Abo11026 Human sec Abu71080 Human sec Abu81556 Human PRO Abu81556 Human PRO Abu81556 Human PRO Abu803770 Human sec Abu80237 Human sec Abu80237 Human sec Abu80237 Human sec Abu1059 Human sec Abu10712 Human sec	Human Human Human Human Human Human Human Human Human Human Human Human
66.1 66.1 66.1 66.1 1374 66.1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	4 4 6 6	4 4 6 6 6 1 1 1 3 3 7 4 4 6 6 6 1 1 1 3 3 7 4 4 6 6 6 1 1 1 3 3 7 4 4 6 6 6 1 1 1 3 3 7 4 4 6 6 6 7 1 1 3 3 7 4 4 6 6 6 7 1 1 3 3 7 4 4 6 6 6 7 1 1 3 7 4 4 6 6 7 1 1 3 7 4 4 6 6 7 1 1 3 7 4 4 6 6 7 1 1 3 7 4 4 6 6 7 1 1 3 7 4 4 6 6 7 1 1 1 3 7 4 4 6 6 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	66.1.3744 66.1.3	46.1 374 6 ABR70775 46.1 374 6 AB005126 46.1 374 6 AB005126 46.1 374 6 AB005741 46.1 374 6 ABR74130 46.1 374 6 ABR81124 46.1 374 6 ABR81124 46.1 374 6 ABR81622 46.1 374 6 AB028927 46.1 374 6 AB028927 46.1 374 6 AB03899 46.1 374 6 AB03899

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a protein having a molecular weight of 180 kD in a dimeric form as determined by SDS-PAGE, where each subunit of the dimeric form as a molecular weight of 97 kD as determined by SDS-PAGE, and where the enzyme cleaves precursor alpha2-antiplesmin at the Pro12-Asn13 bond. The enzyme inhibitors of the enzyme and methods for detecting such inhibitors are useful for treating conditions involving fibrin, e.g. inflammatory conditions such as all forms of arthritis, organ fibrosis, undesirable scarring, cancer or its metastases, or atherothrombotic disease such as cronary artery thromboses, attroke, pulmonary embolism, all other forms of arterial and venous thromboses. This peptide corresponds to the N-terminal sequence of the alpha2-antiplasmin cleaving enzyme.
                                                                                                                                                                                                                                                                                                                                       The invention relates to an alpha2-antiplasmin cleaving enzyme comprising
                                                                                                                                                                  New alpha-2-antiplasmin cleaving enzyme, useful for treating conditions involving fibrin, e.g. inflammatory conditions such all forms of
                                                                                                                                                                                         involving fibrin, e.g. inflammatory conditions such all forn arthritis, organ fibrosis, undesixable scarring, cancer, or
                                                                                                                                                                                                                                                                                        Claim 2; SEQ ID NO 1; 40pp; English.
                                                                      Lee KN, Jackson KW,
(JACK/) JACKSON K W.
(CHRI/) CHRISTIANSEN V J.
                                                                                                                                                                                                                                        atherothrombotic disease.
                                                                                                                     WPI; 2004-625848/60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15 AA;
                                                                      Mckee PA,
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Query Match Best Local Similarity

0; Indels 100.0%; Score 76; DB 8; L 100.0%; Pred. No. 1.1e-06; ive 0; Migmatches 0; 1 IVLRPSRVHNSEENT 15 15; Conservative Matches ò

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Gaps ö

Length 15;

1 IVLRPSRVHNSEENT 15 윱 AEB94176 standard; protein; 50 AA. AEB94176; 

06-OCT-2005 (first entry)

Human soluble FAP alpha dimer N-terminal fragment SEQ ID NO:19.

Ammunouppressively graft Verbus incle disease; transpiant, superturing, ammunouppressively graft Verbus incle disease; altergy; antiallergic; asthma; antiasthmatic; musculoskeletal disease; altergy; antiallergic; asthma; antiasthmatic; inflammation; respiratory disease; atherosclerosis; antiarteriosclerotic; cardiovascular disease; metabolic disorder; hashimotos disease; antithyroid; endocrine disease; inflammatory bowel disease; antithflammatory; gastrointestinal-gen.; gastrointestinal disease; rheumatorid arthritis; antirheumatory; hepatotropic; sutcommune hepatitis; antinheumatory; hepatotropic; systemic lupus erythematosus; dermatological; dermatological disease; uveitis; ophthalmological; autoimmune hemolytic anemia; antianemic; hematological disease; rheumatic; fever; antipyrettic; Crohns disease; respiratory syncytial virus infection; respiratory-gen.; virucide. immune inhibition; fibroblast activation protein alpha dimer; FAP alpha dimer; guillain barre syndrome; antiinflammatory; cns-gen.; immune disorder; neurological disease; autoimmune disease; immunosuppressive; graft versus host disease; transplant rejection;

Homo sapiens

10-JAN-2005; 2005WO-US000709

(POIN-) POINT THERAPEUTICS INC.

Christiansen VJ;

Jesson MI Miller GT, Jones B, Mclean PA,

WPI; 2005-564220/57.

Down-regulating an immune response comprises administering to a subject in need a fibroblast activation protein (FAP) alpha dimer enzyme in an amount effective to down-regulate an immune response.

Example 1.4; SEQ ID NO 19; 177pp; English.

The method further comprises administering to the subject a second agent.

The method further comprises administering to the subject a second agent.

The second agent is an anti-inflammatory agent, immunosuppressant, or

anti-infective agent such as antibacterial, antiviral, antifungal, anti
controlled anti-inflammatory agent, immunosuppressant, or

anti-infective agent such as antibacterial, antiviral, antifungal, anti
controlled agent such as antibacterial, antiviral, antifungal, anti
controlled anti-inflammatory agent. The FAP alpha dimer enzyme is a truncation.

The FAP alpha dimer enzyme. The FAP alpha dimer enzyme is a truncation.

Controlled monomer. The FAP alpha dimer enzyme comprises an anino acid

conbstitution relative to wild type FAP alpha dimer. The amino acid

conbstitution relative to wild type FAP alpha dimer. The amino acid

constitution relative to wild type FAP alpha dimer. The amino acid

constitution relative to wild type FAP alpha dimer. The amino acid

condition, abnormal immune response selected from inflammation,

crejection, toxic shock syndrome, allergy, asthma, atherosclerosis,

cresponse is subsequent to an infection, such as an RSV infection. Immune disease, selected from inflammation and antifection, such as an RSV infection. acceptable carrier, and a non-adjuvant second agent; a composition comprising a FAP alpha diner enzyme comprising an antho acid substitution of A657D; and a composition comprising a FAP alpha diner enzyme lacking amino acids 269-448 and comprising amino acids 269-448 from mouse FAP. The invention relates to a method of down-regulating an immune response, which comprises administering to a subject a fibroblast activation protein (FAP) alpha dimer enzyme in an amount effective to down-regulate an immune response. Also included are the following: a composition comprising a FAP alpha dimer enzyme in a pharmaceutically acceptable carrier, where the composition is sterile and lacks an adjuvant; a composition comprising a FAP alpha dimer enzyme in a pharmaceutically autoimmune disease is selected from c, autoimmune thyroiditis, systemic lupus erythematosus (SLE), uveitis, hemolytic anemias, rheumatic fever, Crohn's disease, Guillain-Barre's syndrome, psoriasis, Graves disease, myssthenia gravis, glomerulonephritis, autoimmune hepatitis and multiple sclerosis. The subject does not have cancer or a predisposition to cancer. The present sequence represents the N-terminal 50 amino acids of human wild type FAP.

Sequence 50 AA;

Gaps ö 100.0%; Score 76; DB 9; Length 50; 100.0%; Pred. No. 4.6e-06; Indels Mismatches ö 15; Conservative Query Match Best Local Similarity Matches

1 IVLRPSRVHNSEENT 15

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AAW31963 standard; protein; 759 AA. RESULT 3 AAW31963

AAW31963;

(first entry) 21-JAN-1998 Human fibroblast activation protein-alpha (FAP-alpha)..

Fibroblast activation protein-alpha; FAP-alpha; human; 

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This sequence represents the dimeric fibroblast activation protein alpha (FAP-alpha). The FAP-alpha molecule is capable of degrading extracellular matrix proteins and exhibite structural features typical of type II integral membrane proteins, including a large COOH-terminal extracellular domain, a hydrophobic transmembrane segment and a short cytoplasmic tail. The putative extracellular domain is described as containing five potential N-glycosylation sites, eleven conserved cysteine residues and three segments corresponding to highly conserved cysteine residues and three segments corresponding to highly conserved catalytic domains characteristic of serine proteases. Most common types of epithelial cancers including breast, ulug, skin, pancreas and colorectal carcinomas contain abundant FAP-alpha reactive stronal fibroblasts which accompany tumour blood vessels. The induction of FAP-alpha fibroblasts which accompany tumour blood vessels. The induction of FAP-alpha fibroblasts at times and carcinogenesis is consistent with its putative role in normal fibroblast physiology. FAP alpha inhibitors, particularly a collagen derivative or (S)-valyl-pyrrolidine-2(R)-boronic acid, may be used to treat various epithelial cancers, e.g. breast, lung, skin, pancreas or colon cancer. Note: This sequence differs from the amino acid sequence of FAP-alpha
                                                                                                                            49. .51
//note= "Asn is N-glycosylated"
191. .209
/label= fap-1
/note= "Putative functional element; not defined further
                                                                                                                                                                                                                                               220. 240
220. 240
/label= fap-2
/note= "Putative functional element; not defined further
in specification"
                                                                                                                                                                                                                                                                                                510. .521 // Nabel= fap-3 // note="Putative functional element; not defined further in specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dimeric fibroblast activation protein alpha - capable of degrading extracellular matrix protein, useful to treat epithelial cancers.
                                                                                                                                                                                                                                                                                                                                                                                                    525. .668
/note= "alternative sequence found in AAW27438"
                                                                                                              'note= "Fibroblast activation protein alpha"
type II integral membrane proteins; epithelial cancer.
                                                                                                                                                                                                                                  214. .216
/note= "Asn is N-glycosylated"
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/note= "Asn is N-glycosylated"
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(BOEH ) BOEHRINGER INGELHEIM INT GMBH.
                                                              Location/Qualifiers
                                                                                 l. .759
/label= FAP-alpha
                                                                                                                                                                                                                in specification"
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                                                                                                                                                                                                                                                                                                                                                                                                                                   637. .639
/note= "As
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-480164/44.
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                                                                                                                             Modified-site
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                                Homo sapiens
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                                                                                 Protein
                                                                                                                                                                Region
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This sequence represents a dimeric fibroblast activation protein alpha (FAP-alpha) which is capable of degrading extracellular matrix proteins. The FAP-alpha molecule exhibite structural features typical of type II integral membrane proteins, including a large COM-terminal extracellular chambrane proteins, including a large COM-terminal extracellular common types of epithelial cancers including breast, lung, skin, pancreas and colorectal carcinomas contain abundant FAP-alpha reactive stromal fibroblasts which accompany tumour blood vessels. The induction of FAP-alpha fibroblasts at times and sites of tissue remodelling during fetal development, tissue repair and carcinogenesis is consistent with the putative role in normal fibroblast physiology. FAP alpha inhibitors, particularly a collagen derivative or (8)-valyl-pyrrolidine-2(R)-boronic scid, may be used to treat various epithelial cancers, e.g. breast, lung, skin, pancreas or colon cancer. Note: This sequence differs from the main acid sequence of FAP-alpha found in AAW31963 between residues 625
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                                  Gарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dimeric fibroblast activation protein alpha - capable of degrading extracellular matrix protein, useful to treat epithelial cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "alternative sequence found in AAW31963"
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                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1. .760
/label= FAP-alpha
/note= "Pibroblast activation protein alpha"
625. .670
100.0%; Score 76; DB 2; Length 759; 100.0%; Pred. No. 0.0001; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                             Fibroblast activation protein-alpha; FAP-alpha; human; type II integral membrane proteins; epithelial cancer.
                                                                                                                                                                                                                                                                                               Human fibroblast activation protein-alpha (FAP-alpha)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (LUDW-) LUDWIG INST CANCER RES.
(BOEH ) BOEHRINGER INGELHEIM INT GMBH.
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                                                                                                                                                                                            AAW27438 standard; protein; 760 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zimmerman R, Park JE, Rettig W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97WO-US004215.
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                                                                      1 IVLRPSRVHNSEENT 15
                                                                                             24 IVLRPSRVHNSEENT 38
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                                                                                                                                                                                                                                                              21-JAN-1998 (first entry)
                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-480164/44.
N-PSDB; AAT90148.
                 Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                              AAW27438;
     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
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                                                                                                    a
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100.0%; Score 76; DB 2; Length 760;

Sequence 760 AA;

Query Match

Human BEC/LEC-related protein sequence SeqID475.

(first entry)

01-JUL-2004

ADN95552;

ADN95552 standard; protein; 760 AA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a method for assessing whether a patient is afflicted with breast cancer. The method comprises comparing the level of expression of a marker (gene/polypeptide see ACCS0076 to ACCS034 and ABR47386 to ABR47632) in a patient sample and the normal level of expression of the marker in a control non-breast cancer sample, where a significant increase in the level of expression of the marker in the patient sample and the normal level is an indication that the patient is a fallicted with breast cancer. The breast cancer associated sequences from the present invention have cytostatic activities and can be used in gene therapy. The method is useful for diagnosing and treating breast cancer. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Breast cancer diagnosis or treatment by comparing the level of expression of a marker in a patient sample with that in the control non-breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glatt K, Hoersh S, Kamatkar S;
Myer V, Wang Y, Xu Y, Zhao X, Meyers RE;
Pusztai L, Meric F, Sahin A, Mills GB;
                                 Gaps
                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 76; DB 6; Length 760; 100.0%; Pred. No. 0.0001; ive 0; Mismatches 0; Indels
                                 Indels
                                                                                                                                                                                                                                                                             Breast cancer associated protein sequence SEQ ID NO:136.
Pred. No. 0.0001;
                                                                                                                                                                                                                                                                                                             Human; breast cancer; cytostatic; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 136; 128pp; English.
                                                                                                                                                                             ABR47452 standard; protein; 760 AA.
   100.0%; Pre
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18-JUL-2001; 2001US-0305501P. 
25-SEP-2001; 2001US-0355002P. 
05-MAR-2002; 2002US-0362585P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-MAY-2002; 2002US-0380391P.
                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUN-2002; 2002WO-US019669
                                                                                  (MILL-) MILLENIUM PHARM INC
                                                                1 IVLRPSRVHNSEENT 15
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Monahan JE, M
Hortobagyi GN,
                                                                                                                                                                                                                                             12-JUN-2003 (first entry)
                              15; Conservative
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                Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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Bast RC, Ho
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ID ABR
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This invention relates to a method of differentially modulating the CC growth or differentiation of blood endothelial cells (BEC) comprising an agent that differential cells with a candothelial cells with a composition comprising an agent that differentially modulates blood or composition comprising an agent that differentially modulates blood or Ivmphatic endothelial cells. Treating hereditary lymphoedema comprises identifying a human subject with lymphoedema and with a mutation in at least one allele of a gene encoding a LEC protein, where the mutation correlates with lymphoedema in human subjects, and with the proviso that the LEC protein is not VEGFR-1; and administering to the subject a composition composition composition allowed and polymuclecides. The invention may be useful for the development of compounds with an antiangiogenic, cytostatic, or visotropic or antimifiammatory activity or for gene therapy. The method is useful in modulating the growth or differentiation of blood endothelial cells or lymphoedema, in screening for an endothelial cells, in treating hereditary lymphoedema, in screening for an endothelial cells, in manufacturing a medicament for the disorder or in monitoring the efficacy or toxicity of a drug on endothelial cells. The agent is useful in manufacturing a cell or lymphatic vessel endothelial cell growth or differential in coll growth or differential cell growth as medicament of hereditary lymphoedema resulting from a mutation in a LEC gene or of other diseases involving the lymphatic vessels, such as the treatment of collect diseases involving the lymphatic vessels, warious inflammatory diseases and cancer metastasis via the lymphatic cyptem. The superior of a human LEC/BEC differentially cells when an experient or the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence does not appear in the specification but was obtained by the indexer using the source data given in table 14 of the specification.
                                                                                                                                                                                             Iymphatic endothelial cell; LEC; hereditary lymphoedema; VEGFR-3;
lymphatic growth agent; VEGF-C; VEGF-D; antiangiogenic; cytostatic;
vasotropic; antiinflammatory; gene therapy; endothelial cell disorder;
inflammatory disease; cancer metastasis; lymphatic system; human.
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                                                                                                                                                                        growth; differentiation; blood endothelial cell; BEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; SEQ ID NO 475; 176pp; English.
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N-PSDB; ADN95553.
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Best Local Similarity 100. Matches 15; Conservative

Query Match

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Tumor-associated antigenic target; TAT430; cancer; neoplasm; cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Prolyl oligopeptidase family homology'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   phosphorylation site"
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/note= "Dipeptidyl peptidase IV"
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nith V, Wolf B, Wu TD, Zhang Z;
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fumor-associated antigenic target TAT430
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                                                                                                                    1. .28
/label= Signal_peptide
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/label= Mature protein
                                                                                                   cocation/Qualifiers
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                                           ovary tumor; uterus tumor
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                                                                                                      Key
Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual dand a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarche indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic act sequences may be useful in diagnostic and screaming applications. The current sequence is that of a human soft tissue sarcoma-upregulated protein of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.
                                                                                                                                                                                                                       soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
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                                                                                                                                                                                           Human soft tissue sarcoma-upregulated protein - SEQ ID 4171.
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Pred. No. 0.0001;
Mismatches 0; Indels
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                                                                                                        ADQ21351 standard; protein; 760 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                  (PROT-) PROTEIN DESIGN LABS INC.
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Best Local Similarity 100.
Matches 15; Conservative
                   24 IVLRPSRVHNSEENT
    1 IVLRPSRVHNSEENT
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Aziz N,

Gonzalez L;

RESULT 8 ADW14775

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polypeptide, or may lack the associated signal peptide, or may comprise an extracellular domain with or without its associated signal peptide, or may be any of these fused to a heterologous polypeptide such as an entrope tag, or the Fc region of an immunoglobulin. TAT polypeptides of the invention, and their encoding nucleic acids, provide targets for the
                                                New Tumor-associated Antigenic Target polypeptides useful for diagnosing, preventing or treating cell proliferative disorders such as cancer or
                                                                                                                                                                                                          The present sequence is that of novel tumor-associated antigenic target polypeptide TAT430. TAT polypeptides have been identified ADM14770-ADM14776 whose expression is upregulated in particular tumor tissues. Tissue expression profiling using GeneExpress indicated that TAT430 is upregulated in breast, pancreatic, colon, adrenal, bladder, kidney, liver, lung, lymphoid, ovarian, prostate and stomach tumor stroma as compared to the corresponding healthy tissues. Upregulation in ovarian tumor tissue was confirmed by quantitative analysis of TAT mRNA expression, and upregulation in breast, pancreatic, colon, adrenal and bladder tumors was confirmed by gene expression profiling in silico (GEPIS) analysis. The TAT polypeptide may comprise the full-length
                                                                                                                                                             Claim 1; SEQ ID NO 13; 141pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnosis and therapy of cancer
N-PSDB; ADW14768
                                                                                                            Lumor.
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Seguence 760 AA;

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Gaps

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Score 76; DB 9; Length 760; Pred. No. 0.0001; Mismatches 0; Indels 100.0%; Sc 100.0%; Pr cive 0; 1 IVLRPSRVHNSEENT 15 24 IVLRPSRVHNSEENT 38 Query Match
Best Local Similarity 100. g δ

AEB94159 standard; protein; 760 AA. 06-OCT-2005 (first entry) AEB94159; RESULT 9 **AEB94159** 

Human wild type fibroblast activation protein (FAP) alpha dimer.

immune inhibition, fibroblast activation protein alpha dimer;

FAP alpha dimer; guillain barre syndrome; antinflammatory; cns-gen.;

fimmune disorder; neurological disease; autoimmune disease;

immunosuppressive; graft versus host disease; transplant rejection;

endotoxic shock; osteoarthritis; antiarthritic; osteopathic;

endotoxic shock; osteoarthritis; antiarthritic; asthma; antiasthmatic;

inflammation; respiratory disease; atherosclerosis; antiarteriosclerotic;

cardiovascular disease; metabolic disorder; hashimotos disease;

antichyroid; endocrine disease; inflammatory bowel disease;

antinflammatory; gastrointestinal-gen.; gastrointestinal disease;

rheumatoid arthritis; antirheumatory; hepatogropoic;

autoimmune hepatitis; antinflammatory; hepatogropoic; systemic lupus erythematosus; dermatological; dermatological disease; uveitis, ophthalmological; autoimmune hemolytic anemia; antianemic; hematological disease; rheumatic fever; antipyretic; Crohns disease; psoriasis; antipsoriatic; graves disease; antithyroid; respiratory syncytial virus infection; respiratory-gen.; virucide; enzyme.

Homo sapiens

WO2005071073-A1.

04-AUG-2005

10-JAN-2005; 2005WO-US000709.

Down-regulating an immune response comprises administering to a subject in need a fibroblast activation protein (FAP) alpha dimer enzyme in an amount effective to down-regulate an immune response. Jesson MI; Disclosure; SEQ ID NO 2; 177pp; English. Miller GT, (POIN-) POINT THERAPEUTICS INC. 09-JAN-2004; 2004US-0535577P. Jones B, WPI; 2005-564220/57. N-PSDB; AEB94158. dclean PA,

The invention relates to a method of down-regulating an immune response, which comprises administering to a subject a fibroblast activation by protein (FAP) alpha dimer enzyme in an amount effective to down-regulate an immune response. Also included are the flective to down-regulate an immune response. Also included are the flecks an adjuvant; a composition comprising a FAP alpha dimer enzyme in a pharmaceutically acceptable carrier, where the composition is sterile and lacks an adjuvant; a composition comprising a FAP alpha dimer enzyme in a pharmaceutically acceptable carrier, and a non-adjuvant second agent; a composition comprising a FAP alpha dimer enzyme in a pharmaceutically acceptable carrier, and a non-adjuvant second agent; a composition comprising a FAP alpha dimer enzyme la subject a second agent. The method further comprises administering to the subject a second agent. The second agent is an anti-inflammatory agent, immunosuppressant, or anti-infective agent such as antibacterial, antiviral, antifungal, anti-infective agent such an anti-infectial, antiviral, antifungal, anti-infective agent such an anti-infectial, antiviral, antifungal, anti-infective agent such antibacterial agent. The FAP alpha dimer enzyme is a truncation anti-infective comparise is a fusion or chimmer protein. The TAP alpha dimer enzyme is a truncation anti-infective to wild type FAP alpha dimer. The FAP alpha dimer enzyme is a substitution relative to wild type FAP alpha dimer. The amino acid substitution is present in the beta-propeller domain, the catalytic domain, or an N-linked glycosylation site and altered disulfide bond formation. The immune response is an especially and remainded formation, and the personner and an especial formation. The formation and an response is subsequent to an infection, such as an RSV infection. The autoimmune disease is selected from c, autoimmune thyroiditis, systemic lupus erythematosus (SLE), uveitis, hemolytic anemias, rheumatic fever, Crohn's disease, Guillain-Barre's syndrome, psortiasis, Graves' disease, myasthenia gravis, glomerulonephritis, autoimmune hepatitis and multiple sclerosis. The subject does not have cancer or a predisposition to acid sequence of human autoimmune disease, sepsis, graft versus host disease, transplant rejection, toxic shock syndrome, allergy, asthma, atherosclerosis, osteoarthritis, and Guillain-Barre's syndrome. The abnormal immune cancer. The present sequence represents the amino acid sec wild type fibroblast activation protein (FAP) alpha dimer

Sequence 760 AA;

Gapa .. 0 100.0%; Score 76; DB 9; Length 760; 100.0%; Pred. No. 0.0001; ive 0; Mismatches 0; Indels Mismatches .; 0 Best Local Similarity 100 Matches 15; Conservative Query Match

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1 IVLRPSRVHNSEENT 15 24 IVLRPSRVHNSEENT

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AEB94218 standard, protein; 734 AA. 06-OCT-2005 (first entry) AEB94218; AEB94218 ID AEBS XXXXXXXX

RESULT 10

Human soluble (FAP) alpha dimer SEQ ID NO:61

The pape alpha dimer; guillain barre syndrome; antiinflammatory; cns-gen; mmune disorder; neurological disease; autoimmune disease; mmune disorder; neurological disease; autoimmune disease; mmunosuppressive; graft versus host disease; transplant rejection; mnosuporessive; graft versus host disease; mniatrinitic; osteopathic; musculoskeletal disease; allergy; antiallergic; asthma; antiasthmatic; minflammatory seathwaterory disease; antiarteriosclerotic; ardiovascular disease; metabolic disorder; hashimotos disease; antithyroid; endocrine disease; inflammatory bowel disease; antithyroid; endocrine disease; inflammatory bowel disease; antithyroid; antitifammatory gastrointestinal-gen; gastrointestinal disease; antitypematory neutoimmune hepatitis; antithenmatic; multiple sclerosis; neuroprotective; systemic lupus erythematosus; dermatological; dermatological disease; well of dermatological disease; multipyretic; Crohns disease; multipyretic; crohns disease; multipyretic; crohns disease; multipyretic; dermatological; multipyretic; crohns disease; multipyretic; dermatological; multipyretic; dermatological; multipyretic; crohns disease; multipyretic; dermatological; multipyretic; crohns disease; multipyretic; dermatological; der respiratory syncytial virus infection; respiratory-gen.; virucide. immune inhibition; fibroblast activation protein alpha dimer; (POIN-) POINT THERAPEUTICS INC 09-JAN-2004; 2004US-0535577P. 10-JAN-2005; 2005WO-US000709. WO2005071073-A1. Homo sapiens. 04-AUG-2005. 

Mclean PA, Jones B, Miller GT,

Jesson MI;

WPI; 2005-564220/57.

Down-regulating an immune response comprises administering to a subject in need a fibroblast activation protein (FAP) alpha dimer enzyme in an amount effective to down-regulate an immune response.

Claim 134; SEQ ID NO 61; 177pp; English.

The invention relates to a method of down-regulating an immune response, which comprises administering to a subject a fibrobiast activation protein (FAP) alpha dimer enzyme in an amount effective to down-regulate an immune response. Also included are the following: a composition comprising a FAP alpha dimer enzyme in a pharmaceutically acceptable carrier, where the composition is sterile and lacks an adjuvant; a composition comprising a FAP alpha dimer enzyme in a pharmaceutically acceptable composition comprising a FAP alpha dimer enzyme in a pharmaceutically acceptable composition comprising a FAP alpha dimer enzyme in an amino acid substitution of A657D; and a composition comprising a FAP alpha dimer enzyme lacking amino acides 269-448 and composition comprising a FAP alpha dimer enzyme lacking an inti-infective agent such as antibacterial, immunosuppressant, anti-infective agent such as antibacterial, antifungal, and parasitic or anti-mycobacterial agent. The FAP alpha dimer enzyme is a heart of a FAP alpha dimer enzyme is a heart of a FAP alpha dimer. The amino acid substitution is present in the becapropaler domain, the catalytic domain, or an N-linked glycosylation site and alters disliked bond condition, abnormal immune response selected from inflammation, autoimmune disease, sepals, graft versus host disease, transplant condition, abnormal immune response is an especially an IL-I mediated condition, abnormal immune response is an especially and alters deceeded condition, autoimmune disease, sepals, graft versus host disease, transplant condition, and substitution substitution substite and multiple, systemic condition, toxic shock syndrome, altery, asthma, atheroaclerosis,

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immune inhibition; fibroblast activation protein alpha dimer;

KW FAP alpha dimer; guillain barre syndrome, antiinflammatory; cns-gen.;

KW FAP alpha dimer; guillain barre syndrome, antiinflammatory; cns-gen.;

KW immune disorder; neurological disease; attanaplant rejection;

KW immune shock; osteoarthritis, antiarthriti; osteopathic;

KW musculoskeletal disease; allergy; antiallergic; asthma; antiasthmatic;

KW musculoskeletal disease; allergy; antiallergic; asthma; antiarteriosclerotic;

KW cardiovascular disease; metabolic disorder; hachimotos disease;

KW antithyroid; endocrine disease; inflammatory bowel disease;

KW antichlammatory; gastrointestinal-gen.; gastrointestinal disease;

KW antioimmune hepatitis; antirheumatic; multiple sclerosis; neuroprotective;

KW autoimmune hepatitis; antinflammatory; hepatotropic;

KW systemic lupus erythematosus; dermatological disease;

KW hematological disease; rheumatic fever; antipyretic; Crohns disease;

KW hematological disease; rheumatic fever; antipyretic; Crohns disease;

KW respiratory syncytial virus infection; respiratory-gen.; virucide.
                                                                                                                                                                            ö
cancer. The present sequence represents the amino acid sequence of human soluble fibroblast activation protein (FAP) alpha dimer (corresponding to AEB94159 minus N-terminal amino acids 1-26).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a method of down-regulating an immune response, which comprises administering to a subject a fibroblast activation protein (FAP) alpha dimer enzyme in an amount effective to down-regulate an immune response. Also included are the following: a composition comprising a FAP alpha dimer enzyme in a pharmaceutically acceptable carrier, where the composition is sterile and lacks an adjuvant; a composition comprising a FAP alpha dimer enzyme in a pharmaceutically acceptable carrier, and a non-adjuvant second agent; a composition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Down-regulating an immune response comprises administering to a subject in need a fibroblast activation protein (FAP) alpha dimer enzyme in an amount effective to down-regulate an immune response.
                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse soluble FAP alpha dimer N-terminal fragment SEQ ID NO:21.
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                                                                                                                             84.2%; Score 64; DB 9; Length 734;
100.0%; Pred. No. 0.015;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                             AEB94178 standard; protein; 50 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POIN-) POINT THERAPEUTICS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-OCT-2005 (first entry)
                                                                                                                                                          Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                         4 RPSRVHNSEENT 15
                                                                                                                                                                                                                                                          1 RPSRVHNSEENT 12
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                                                                                              Sequence 734 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                       AEB94178;
                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                    RESULT 11
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comprising a raw alpna anner enzyme comprising an amino acida substitution cof A657D, and a composition comprising a rape alpha dimer enzyme lacking amino acida 269-448 and comprising amino acida 269-448 from mouse FAP.

The method further comprises administering to the subject a second agent.

The second agent is an anti-inflammatory agent, immunosuppressant, or anti-infective agent such as antibacterial, antiviral, antifungal, anti-parasitic or anti-mycobacterial agent. The FAP alpha dimer enzyme is a truncation type FAP alpha dimer enzyme is a truncation cutton. The FAP alpha dimer enzyme is a truncation cutton relative to wild type FAP alpha dimer. The antimo acid substitution relative to wild type FAP alpha dimer. The amino acid substitution relative to wild type FAP alpha dimer. The amino acid substitution is present in the beta-propeller domain, the catalytic domain, or an N-linked glycosylation site and alters disulfide bond formation. The immune response is an especially an IL-I mediated condition, abnormal immune response is elected from inflammation.

Condition, abnormal immune response selected from inflammation, crancion. The immune disease, sepsis, graft versue host disease, transplant craft formation is osteoarthritis, and Guillain-Barre's syndrome. The abnormal immune creponse is subsequent to an infection, such as an RSV infection. Crohn's disease, Guillain-Barre's syndrome. The abnormal immune creponse (Grohn's disease, Guillain-Barre's syndrome, pasoriasis, Theumatic fever, Crohn's disease, Guillain-Barre's syndrome, pasoriasis, Graves' disease, guillain-Barre's syndrome, pasoriasis, Graves' disease, guillain-Barre's syndrome, pasoriasis, Graves' disease, guillain-Barre's syndrome, pasoriasis, The subject does not have cancer or a predisposition to cancer. The present sequence represents the N-terminal 50 amino acids of comprising a FAP alpha dimer enzyme comprising an amino acid substitution mouse wild type FAP 

Sequence 50 AA;

68.4%; Score 52; DB 9; Length 50; 73.3%; Pred. No. 0.11; 3; Indels 1; Mismatches 1 IVLRPSRVHNSEENT 15 24 IVLRPSRVYKPEGNT 38 Best Local Similarity 73.3 Matches 11; Conservative Query Match g ò

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Gaps

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AEB94163 standard; protein; 761 AA. AEB94163; RESULT 12 AEB94163

(first entry) 06-OCT-2005

Mouse wild type fibroblast activation protein (FAP) alpha dimer.

immune inhibition; fibroblast activation protein alpha dimer;

KW FAP alpha dimer; guillain barre syndrome; antiinflammatory; cns-gen.;

KW FAP alpha dimer; guillain barre syndrome; antiinflammatory; cns-gen.;

KW immune disorder; neurological disease; autoimmune disease;

KW immune suppressive; graft versus host disease; transplant rejection;

KW endotoxic shock; osteoarthritis; antiarthritic; osteopathic;

KW musculoskeletal disease; allergy; antiallergic; asthma; antiasthmatic;

KW antiammaton; respiratory disease; inflammatory bowel disease;

KW antithyroid; endocrine disease; inflammatory bowel disease;

KW antiinflammatory; gastrointestinal disease;

KW antiinflammatory; antiinflammatory bowel disease;

KW autoimmune hepatitis; antiinflammatory; hepatotropic;

KW systemic lupus erythematosus; dermatological; dermatological disease;

KW westis; ophthalmological; autoimmune hemolytic anemia; antianemic;

KW hematological disease; rheumatic fever; antipyretic; Crohns disease;

KW respiratory syncytial virus infection; respiratory-gen.; virucide; 

Mus musculus.

WO2005071073-A1

04-AUG-2005

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The invention relates to a method of down-regulating an immune response, which comprises administering to a subject a fibroblast activation which comprises administering to a subject a fibroblast activation protein (FAP) alpha dimer enzyme in a mount effective to down-regulate an immune response. Also included are the following: a composition comprising a FAP alpha dimer enzyme in a pharmaceutically acceptable carrier, where the composition is sterile and lacks an adjuvant; a composition comprising a FAP alpha dimer enzyme in a pharmaceutically acceptable carrier, and a non-adjuvant second agent; a composition of A657D; and a composition comprising a FAP alpha dimer enzyme lacking amino acids 269-448 and comprising amino acids 269-448 from mouse FAP.

CC A657D; and a composition comprising an amino acids adjustive accord agent is a mati-inflammatory agent, immunosuppressant, or anti-infective agent such as anti-inflammatory agent, immunosuppressant, or anti-infective agent such as antibacterial, antiviral, antifungal, anti-infective agent such as a pagent is a truncation current of parasitic or anti-invocation at the FAP alpha dimer enzyme is a fusion or chimeric procein. The FAP alpha dimer enzyme is a fusion or chimeric procein, and parasitic or substitution is present in the beta-propeller domain, the catalytic condition, abnormal immune response is an especially an IL-I mediated condition, abnormal immune response selected from inflammation. The response is subscited from inflammation is antered agent of subscited from inflamme disease, seaples, graft versue as an RSV infection. The response is allowed as an RSV 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              autoimmune disease is selected from c, autoimmune thyroiditis, systemic lupus erythematosus (SLE), uveitis, hemolytic anemias, rheumatic fever, Crohn's disease, Guillain-Barre's syndrome, psoriasis, Graves' disease, myasthenia gravis, glomerulonephritis, autoimmune hepatitis and multiple sclerosis. The subject does not have cancer or a predisposition to cancer. The present sequence represents the amino acid sequence of mouse wild type fibroblast activation protein (FAP) alpha dimer.
                                                                                                                                                                                                                                                                                                                            Down-regulating an immune response comprises administering to a subject in need a fibroblast activation protein (FAP) alpha dimer enzyme in an amount effective to down-regulate an immune response.
                                                                                                                                                                                        Jesson MI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 6; 177pp; English.
                                                                                                                                                                                           Miller GT,
                                                                                                                                   (POIN-) POINT THERAPEUTICS INC.
                    10-JAN-2005; 2005WO-US000709.
                                                                               09-JAN-2004; 2004US-0535577P
                                                                                                                                                                                           Jones B,
                                                                                                                                                                                                                                                  WPI; 2005-564220/57.
                                                                                                                                                                                                                                                                             N-PSDB; AEB94162.
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                                                                                                                                                                                           Mclean PA,
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ö 68.4%; Score 52; DB 9; Length 761; 73.3%; Pred. No. 2.4; ive 1; Mismatches 3; Indels 11; Conservative Query Match Best Local Similarity Matches

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AAB97649 standard; protein; 407 AA. 25-SEP-2001 (first entry) AAB97649; RESULT 13 AAB97649 C X X X X E X Kallabis H;

Munnes M,

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Predicting, diagnosing or prognosing malignant neoplasia by detecting at least two markers, where the markers are genes from one or more chromosomal regions altered in malignant neoplasia,.
                                                                                                                                                                                                                                                                 Claim 11; SEQ ID NO 95; 267pp; English.
                                                            09-MAY-2003; 2003EP-00010447
                                                                                    21-MAY-2002; 2002EP-00010291.
13-FEB-2003; 2003EP-00003112.
                                                                                                                                                                           WPI; 2004-073279/08
                                                                                                                         (FARB ) BAYER AG.
                                                                                                                                                                                        N-PSDB; ADH13223
           EP1365034-A2
                                   26-NOV-2003
                                                                                                                                                  Wirtz R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                             This sequence represents human sperm protein 45. The protein has a molecular weight of 45 kD, and has 27% identity and 45% homology over a 268 amino acid stretch with an Ensis minor male gonad nuclear protein (GenBank accession number L181814). The invention relates to human sperm protein 45 (AAB97649), nucleic acids encoding it (AAH46211), and a method for the recombinant production of the protein. The present invention additionally discloses an antagonist of sperm protein 45 for therapeutic use, and an antibody which specifically binds to operm protein 45. Sperm protein 45, and nucleotides which encode it may be used for treating a variety of diseases, such as malignant tumours, blood diseases, HIV inflammatory conditions. The protein may also be used to screen for modulators of its activity or for peptide fingerprinting identification.
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                      Human sperm protein 45; recombinant production; malignant tumour; cancer; blood disease; HIV infection; human immunodeficiency virus; immune disorder; inflammatory condition; cytostatic; anti-HIV; antiinflammatory; immunomodulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lons or as a probe for hybridisation reactions, or in producing gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      malignant neoplasia; cytostatic; breast cancer; ovarian cancer; gastric cancer; colon cancer; oesophageal cancer; mesenchymal cancer; bladder cancer; non-small cell lung cancer; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                      Human sperm protein 45 and encoded polynucleotide, applicable in diagnosis and treatment of cancer, hemopathy, HIV infection, immunological diseases and various inflammation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human malignant neoplasia-related protein SeqID95
                                                                                                                                                                                                                   (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 32-33; 41pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADH13246 standard; protein; 425 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55.3%;
63.6%;
                                                                                                                                                                   18-DEC-2000; 2000WO-CN000583.
                                                                                                                                                                                           99CN-00125689.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 55.3
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               279 RPSKLHNSKVN 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 RPSRVHNSEEN 14
  Human sperm protein 45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chips or microarrays
                                                                                                                                                                                                                                                                     WPI; 2001-441666/47.
                                                                                                                                                                                                                                                                                  N-PSDB; AAH46231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 407 AA;
                                                                                                                 WO200146236-A1
                                                                                                                                                                                                                                            Mao Y, Xie Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                            22-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-MAR-2004
                                                                                         Homo sapiens
                                                                                                                                          28-JUN-2001
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This invention relates to a novel method for the prediction, diagnosis, or prognosis of malignant neoplasia by the detection of at least two markers. The invention may also be useful for the development of cytostatic compounds through the regulation of the expression of a gene or activity of a protein associated with malignant neoplasia. The method is useful for prediction, diagnosis or prognosis of malignant neoplasia cauch as breast cancer, ossophageal cancer, wesenchymal cancer, bladder cancer or non-small cell ung cancer. The polymucleotides and polymethides cancer or non-small cell specification, antisense polymucleotides targeting either one of the polymucleotides or polypeptides, antibodies targeting either one of the polymucleotides or polypeptides, and compounds identified by the screening methods are useful for preferably breast cancer. The present sequence is that of a human preferably breast cancer. The present sequence is that of a human malignant neoplasia-related protein which may be used in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Diagnosis; prognosis; cancer; breast tumor; ovary tumor; stomach tumor; colon tumor; esophagus tumor; bladder tumor; non-small-cell lung cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Pred. No. 81;
3; Mismatches 1; Indels
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Matches 7; Conservative
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297 RPSKLHNSKVN 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytostatic; neoplasm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 425 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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Matches
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8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method of predicting response to cancer treatment comprising detection of at least 2 markers, where the markers are genes and fragments or genomic nucleic acid sequences that are located on one chromosomal region, which is altered in malignant neoplasia. The invention also relates to a method for the prediction, diagnosis or prognosis of malignant neoplasia, methods for detecting deregulations in malignant neoplasia and breast cancer, a method of determining the phenotype of a cell or tissue, a method for identifying genomic regions which are altered on the chromosomal level and encode genomic neoplasia and breast cancer, methods of screening for agents which regulate the activity of a polypeptide or a polymucleotide and malignant neoplasia and breast cancer, methods of screening for agents which regulate the activity of a polypeptide or a polymucleotide and polypeptide. The method is useful for predicting response to cancer treatment. The methods and compositions are useful for predicting diagnosing, preventing or treating malignant neoplasia, and preventing or treating malignant encorated and cancer, mesenchymal cancer, pastric cancer or non-small-cell concerned the inventional polypeptide used in the cancer of the inventional polypeptide used in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         abiotic stress tolerance; transgenic plant; plant; cereal; agriculture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                       Predicting a response to cancer treatment by detecting at least 2 markers, which are genes or genomic nucleic acid sequences that are located on one chromosomal region, which is altered in malignant
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0
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Pred. No. 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rice abiotic stress responsive polypeptide SEQ ID NO:4397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                    Claim 8; SEQ ID NO 95; 464pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABM86151 standard; protein; 837 AA.
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2001US-0314662P.
2001US-0325277P.
2001US-0332132P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUN-2002; 2002WO-US019668
 28-OCT-2003; 2003EP-00024565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55.3%;
                       (FARB ) BAYER HEALTHCARE AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 63.00
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |||::|||: |
297 RPSKLHNSKVN 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 RPSRVHNSEEN 14
                                                                                                                                                                                                                                                                                                                                                                                                                            scope of the invention
                                                                       2005-372393/38.
                                               Wirtz R, Munnes M;
                                                                                  N-PSDB; AEA15110
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 425 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2003008540-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-JUN-2001; 24-AUG-2001; 26-SEP-2001; 21-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryza Bativa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-JUN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JAN-2003
                                                                                                                                               neoplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABM86151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABM86151
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The invention relates to novel abiotic stress responsive polynucleotides and polypeptides. Also disclosed are vectors, expression cassettes, host calls, and plants containing such polynucleotides. Also disclosed are methods for using the polynucleotides and polypeptides to alter the responsiveness of a plant to abiotic stress. The invention is useful in agriculture. The nucleic acid is useful for determining whether a test plant has been exposed to an abiotic stress condition. It is also useful for plant has been expession in a plant cell, and to identify a homolog or polynucleotide expression in a plant cell, and to identify a homolog or or tholog to an abiotic stress responsive polynucleotide. The nucleic acid or holog to an abiotic stress responsive polynucleotide. The nucleic acid cresponsiveness of a plant to an abiotic stress, such as cold stress, sait stress, osmotic stress or any of their combinations. The present sequence is used in the exemplification of the invention
                                                                                                                                                                                                              New stress-responsive nucleic acid, useful for altering the responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold stress, salt stress or osmotic stress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                           Katagiri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 42; DB 7; Length 837;
Pred. No. 1.8e+02;
1; Mismatches 1; Indels
                                                           Goff SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Propionibacterium acnes immunogenic protein #6464.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mitcham JL, Wang SS,
, Jen S, Carter D;
                                                               Glazebrook J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dermatological; osteopathic; neuroprotectant
                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 4397; 89pp; English
(SYGN ) SYNGENTA PARTICIPATIONS AG.
                                                               Cooper B, Gl
N, Ricke D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU45568 standard; protein; 119 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-APR-2000; 2000US-0199047P.
02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55.3%;
58.3%;
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L'maisonneuve J, Zhang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 VLRPSRVHNSEE 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Propionibacterium acnes
                                                               Kreps J, Briggs SP,
Moughamer T, Provart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
les 7; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-616774/71.
N-PSDB; AASS9526.
                                                                                                                                                            WPI; 2003-248011/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 837 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU45568;
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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by each acrea and sorders include SAPHO syndrome (synovitis, acne, pustubosis, hypercosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne valgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention olypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by chis patent did not form part of the printed specification, but was this patent did not form the printed specification, but was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                    Propionibacterium acnes polypeptides and nucleic acide useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maisonneuve JL;
Jones R, Carter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Propionibacterium acnes predicted ORF-encoded polypeptide #6763.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 41; DB 4; Length 119;
Pred. No. 29;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mitcham JL, . Skeiky YAW, Persing DH, Bhatia A,
Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR,
Barth B, Vallieve-Douglass J;
                                                                                                                                                         Example 1; SEQ ID NO 6763; 1069pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunostimulant; immune response; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABM42087 standard; protein; 119 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-OCT-2002; 2002WO-US032727.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 RPSRVHNSEENT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |||||||| : |
82 RPSRVHNIDAAT 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Propionibacterium acnes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CORI-) CORIXA CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 119 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2003033515-A1.
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The invention relates to an isolated polymucleotide (ACF64435-ACF64733)

concoding a Propionibacterium acnes protein. The invention also relates to polymeptides encoded by the polymucleotides (ABMS5624-ABM64536) and to immunogenic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a colymucleotide of the invention; antibodies against polypeptides of the invention; polymeptide of the invention; and an isolated T cell population comprising T cells prepared to invention; and an isolated T cell population comprising T cells prepared to polymeptide and an isolated T cell population comprising T cells prepared via this method; a vaccine composition (comprising P. acnes polypeptides, polymucleotides, antibodies, fusion proteins, T cell populations, or antigen-presenting cells that express the polymeptide); a method and kit cfor detecting or determining the presence or absence of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a conference or patient. The P. acnes polypeptides, polymeptides, polyme
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotific condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield;
or for stimulating an immune response specific for a P. acnes protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plant full length insert polypeptide segid 64668.
                                                      Example 1; SEQ ID NO 6763; 1481pp; English
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05-NOV-2001; 2001US-00985678.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Conservative
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82 RPSRVHNIDAAT 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 119 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US2004034888-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADY08853
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Wang
Wall
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAM50586
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, heabicides, extreme camporing plant tolerance to cold, heat, drought, heabicides, extreme camporing plant tolerance to cold, heat, drought, herbicides, extreme camporing pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing gladactomannan, increased resistance to plant disease, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one arress condition or for modifying seed oil or protein yield and/or content. This is the amino acid sequence of a plant full length insert properties that can be used in the recombinant DNA construct of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
                                                                                                                        New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                              Cao Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 41; DB 8; Length 458; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                              Zhou Y, Kovalic DK, Screen SE, Tabaska JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein encoded by Prokaryotic essential gene #6108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                   Claim 1; SEQ ID NO 64668; 15pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABU20581 standard; protein; 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001US-00948993.
2001US-0342923P.
2002US-00072851.
2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    53.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 53.5
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 IVLRPSRVHN 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteroides fragilis.
          ZHOU Y.
KOVALIC D K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               332 IVLLPSRMHN
                                                                                                   WPI; 2004-180133/17.
                                              TABASKA J E
                                SCREEN S E.
                                                                                                                                                  pests, for confeimproving yield.
                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence 458 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200277183-A2.
                                                         CAO Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-SEP-2001;
25-OCT-2001;
08-FEB-2002;
06-MAR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABU20581;
                       (KOVA/)
(SCRE/)
                                                       CAOY/)
                                              TABA/)
                                                                               Liu J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 20
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The invention relates to an isolated nucleic acid comprising any one of
the 6213 antisense sequences given in the specification where expression
of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a prointeration of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid
cenceding a polypeptide whose expression is inhibited by the antisense
comucleic acid; (4) an antibody capable of specifically binding
the polypeptide of its fragment whose expression is inhibited by the
antisense nucleic acid; (4) an antibody capable of specifically binding
the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
cc proliferation or the activity of a gene in an operon required for
proliferation; (7) identifying a compound that influences the activity of
the gene product or that has an activity against a biological pathway
cc proliferation, or that inhibits proliferation of an
capanism acts; (9) manufacturing an antibiotic; (10) profiling a
compound's activity; (11) a culture comprising strains in which the gene
cc product is overexpressed or underexpressed; (12) determining the extent
ct o which each of the strains is present in a culture or collection of
ct o which each of the strains is present in a culture or collection of
cstrains; or (13) identifying the tearget of a compound that inhibits the
cc proliferation of an organism. The antisense nucleic acids are useful for
identifying proteins or screening for homologous nucleic acids required
for proliferation to isolate candidate molecules for rational
drug discovery programs, or for screening homologous nucleic acids
cellular proliferation to isolate candidate molecules for rational
drug discovery programs, or for screening sequence is encoded by one of
the target prokaryotic essential genes. Note: The sequence data for this
content of format directly from MIPO at
                                                                                                                                                                                                                                                                                New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       directly from WIPO at
                                                               Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JT156897; benign prostatic hyperplasia; BPH; human; prostate; differential expression; diagnosis; marker; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 41; DB 6; Length 499;
Pred. No. 1.5e+02;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Benign prostatic hyperplasia associated protein JT156897.
                                                                   Ohlsen KL,
Forsyth RA,
                                                                   α̈́
                                                                   Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 25; SEQ ID NO 48505; 1766pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ftp.wipo.int/pub/published_pct_sequences
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                                                                   Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53.9%;
                                                                       Malone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LILRPSEISNSPE 340
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ELITRA PHARM INC.
                                                                   Zamudio C,
Trawick JD,
                                                                                                                                                                               WPI; 2003-029926/02
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Best Local Similarity
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                                                                                                                                                                                                                     N-PSDB; ACA24451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 n electronic
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(ELIT-)
                                                                          ο'n
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Ren F, Wang D; Zhang J, Zhao QA;

Qian XB, Yang Y,

Ma Y, ( Xue AJ,

Chen R,

(GENE-)

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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypoptides (AAM38642-AAM42213) with nootropic, concoded polypoptides (AAM38642-AAM42213) with nootropic, concoded polypoptides are useful immunosuppressant and cytostatic activity. The polymuclectides are useful confidence in gene therapy. A composition containing a polypoptide or polymuclectide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous as system diseases, such as localised neuropathy and contral nervous system diseases, such as lateral sclerosis, and central nervous system diseases, such as a lateral sclerosis, and Shy-Drager Syndrome. Other uses include the cutilisation of the activity, cancer simmune system suppression, call thrombolytic activity, cancer diagnosis and therapy, drug screening, cassays for receptor activity, arthritis and inflammation. leukaemias and control states. Note: The sequence data for this patent did not form control to the printed specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein identification, signal transduction pathway, metabolic pathway; hybridisation assay, genetic mapping, gene expression control; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acids and polypeptides, useful for treating disorders such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53.9%; Score 41; DB 4; Length 666; 35.7%; Pred. No. 2.1e+02; ive 7; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana protein fragment SEQ ID NO: 37717.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; SEQ ID NO 6429; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Liu C, Asundi V, Chen R, Wang Z, Wehrman T, Xu C, Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               as central nervous system injuries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAG31412 standard; protein; 835 AA.
                                                                                                                                                                       21-JAN-2000; 2000US-00488725.
25-APR-2000; 2000US-00552317.
20-JUN-2000; 2000US-00598042.
                                                                                                                                                                                                                                                                             03-AUG-2000; 2000US-00653450.
14-SEP-2000; 2000US-00662191.
19-OCT-2000; 2000US-00693036.
29-NOV-2000; 2000US-00727344.
                                                                                                   26-DEC-2000; 2000WO-US034263
                                                                                                                                                                                                                                                        19-JUL-2000; 2000US-00620312
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Query Match
Best Local Similarity 35./*,
Best Si Conservative
5; Conservative
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76 VVMKPAKIEHKEEN 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 IVLRPSRVHNSEEN 14
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                                                                                                                                                                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC.
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WO200153312-A1
                                                                                                                                                       23-DEC-1999;
                                                   26-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang J,
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is that of UT156897 protein, which is encoded by an mRNA species that is differentially expressed in human benign prostatic hyperplasia (BPH) tissue compared to normal human tissue. J156897 cDNA (see AA171055) was obtained from a placental CDNA library following identification of differentially expressed BPH mRNA. Up-regulation of JT156897 is diagnostic of BPH in symptomatic patients. Since BPH with symptomatic patients. Since BPH with gymptoms is associated with hypertrophic growth of the prostate and/or a low grade chronic inflammatory response, up-regulation of JT156897 bNA. Or of protein products derived from it, is likely to be of diagnostic cyalue in disease states involving inflammatory responses or hypertrophic growth in tissues in which JT156897 is found (e.g. breast and cervix). A claimed method of diagnosing a disease involves determining the level of expression of a JT156897 is found (e.g. breast and cervix). A claimed method of diagnosing a disease involves determining the level of expression of a JT156897 is found (e.g. breast and cervix). A claimed method of diagnosing a disease involves determining partners. Dominant negative proteins, DNAs encoding these proteins, antibodies to these proteins, peptide fragments or mimics may be introduced into cells to affect function. The protein also provides novel targets for the screening of synthetic small molecules and combinatorial or naturally-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                 Novel JT460914 and JT156897 polypeptides associated with Benign Prostatic Hyperplasia, useful as a diagnostic agent or marker of Benign Prostatic Hyperplasia and other hyperplastic diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral scleroals; SNy-brager Syndrome; chemotactic; chrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                           Getzenberg RH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 16; Page 54-55; 57pp; English.
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                                                                                                           15-JUN-2001; 2001WO-US019157.
                                                                                                                                                            20-JUN-2000; 2000US-0212726P.
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52 VVMKPAKIEHKEEN 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                        (NISB ) JAPAN TOBACCO INC
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                                                                                                                                                                                                                                                                                           Munger WE, Kulkarni P,
                                                                                                                                                                                                             LOGIC INC
                                                                                                                                                                                                                                                                                                                                              WPI; 2002-114572/15.
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        WO200198456-A2
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prostate

Ouery Match

Matches

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Gaps

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termination sequence Arabidopsis thaliana

Homo sapiens

AAM41498;

AAM41498 RESULT

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990S-0152363P.
990S-0153070P.
990S-0153758P.
990S-0154018P.
99US-0142154P.
99US-0142205P.
99US-0142205P.
99US-0142200P.
99US-0142874P.
99US-014342P.
99US-0144005P.
99US-0144085P.
99US-0144085P.
99US-0144085P.
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990S-0144834P
990S-0144884P
990S-0144884P
990S-0145086P
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990S-0145088P
990S-0145088P
990S-0145192P
990S-0145192P
990S-0145192P
990S-0145193P
990S-0145318P
990S-0145318P
990S-0146388P
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990S-0147418P
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99US-01497
99US-01497
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99US-01,
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990S-01
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15-SEP-1999;
16-SEP-1999;
                                                                9908-0121825P.
9908-012180P.
9908-01257848P.
9908-01257848P.
9908-01257848P.
9908-0126749P.
9908-0128744P.
9908-0130449P.
9908-0130449P.
9908-0131449P.
9908-0131449P.
9908-0132407P.
9908-0132407P.
9908-0132407P.
9908-0134219P.
9908-0134219P.
9908-0134218P.
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990S-0139763P
990S-013989P
990S-0140353P
990S-0140353P
990S-0140853P
990S-0140823P
990S-0140823P
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99US-0139459P.
99US-0139460P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0139457P
                                              2000EP-00301439
    EP1033405-A2
                                             25-FEB-2000;
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9905-0123548P

9905-0125788P

9905-0125788P

9905-01217462P

9905-01217462P

9905-0121744P

9905-0128714P

9905-0128714P

9905-0130449P

9905-01310491P

9905-01310491P

9905-01314218P

9905-01314518P

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9905-014051P
99US-0123180P
       09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
01-APR-1999;
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16-APR-1999;
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01-JUL-1999;
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14-MAY-1999
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Pred. No. 2.7e+02;
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9908-0154779P.
9908-0155438P.
9908-015548P.
9908-015548P.
9908-015548P.
9908-015753P.
9908-0158232P.
9908-0158232P.
9908-0159294P.
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9908-0159330P.
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9908-016091P.
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20-SEP-1999
23-SEP-1999
24-SEP-1999
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Matches
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PR 15-7UL-1999; 99105-014(105.P)
PR 16-7UL-1999; 99105-014(105.P)
PR 16-7UL-1999; 99105-014(105.P)
PR 16-7UL-1999; 99105-014(105.P)
PR 19-7UL-1999; 99105-014(131.P)
PR 19-7UL-1999; 99105-014(131.P)
PR 20-7UL-1999; 99105-014(131.P)
PR 21-7UL-1999; 99105-014(131.P)
PR 22-7UL-1999; 99105-014(131.P)
PR 22-7UC-1999; 99105-014(131.P)
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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Pred. No. 3e+02;
2; Mismatches 2; Indels
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99US-0123180P.
99US-012558P.
99US-0126264P.
99US-0126785P.
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99US-0157751P.
99US-015865P.
99US-0158232P.
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99US-0159344P.
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99US-0161992P.
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99US-0162142P
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Best Local Similarity 60.0
Matches 6; Conservative
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658 PSKIHNGSEN 667
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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
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01-APR-1999;
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07-0CT-1999;
12-0CT-1999;
13-0CT-1999;
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AAG31410
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19-JUL-1999; 19-JUL-1999; 20-JUL-1999; 20-JUL-1999; 21-JUL-1999; 21-JUL-1999; 22-JUL-1999; 22-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999;	27-JUL-1999; 27-JUL-1999; 27-JUL-1999; 28-JUL-1999; 02-AUG-1999; 02-AUG-1999; 04-AUG-1999; 04-AUG-1999; 05-AUG-1999; 06-AUG-1999; 06-AUG-1999; 06-AUG-1999; 11-AUG-1999; 11-AUG-1999; 11-AUG-1999; 11-AUG-1999; 11-AUG-1999; 11-AUG-1999; 11-AUG-1999; 11-AUG-1999;	16-MUG-1999; 17-AUG-1999; 20-AUG-1999; 20-AUG-1999; 23-AUG-1999; 25-AUG-1999; 27-AUG-1999; 27-AUG-1999; 30-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999;	13-SEP-1999; 16-SEP-1999; 20-SEP-1999; 22-SEP-1999; 23-SEP-1999; 24-SEP-1999; 24-SEP-1999; 04-OCT-1999; 06-OCT-1999; 06-OCT-1999; 07-OCT-1999; 13-OCT-1999; 13-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated mechanical stress induced polynucleotide, useful for diagnosis, treatment, prevention or control of osteoporosis, osteopenia, osteopetrosis, osteosethritis, periodontitis, bone
The present sequence is the protein sequence for AT4G10590, a ubiquitin-
specific C-terminal hydrolyzing protease. AT4G10590 can be used for
regulating pseudo-arabis protein degradation. The function of the
AT4G10590 gene is closely related to the development, differentiation am
programmed cell death (apoptosis) of plant cells, signal transduction and
cell period regulation
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; mechanical stress; protein 608; OCP; CMF608; osteoporosis; bone fracture; bone elongation; osteopenia; osteoarthritis; osteopetrosis; osteosclerosis; periodontitis; low bone density; osteopathic; antiinflammatory; antiarthritic; adlican-2.
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Pred. No. 1.1e+03;
7; Mismatches 2; Indels
                                                                                                                                            Length 937;
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Pred. No. 3.1e+02;
2; Mismatches 2; Indels
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08-MAR-2001; 2001US-00802318.
13-JUL-2001; 2001US-00905129.
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35.7%;
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|666 PSKIHNGSEN
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Best Local Similarity
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                                                                                                                 Sequence 937 AA;
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Pred. No. 3.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
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99US-0161360P.
99US-0161361P.
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99US-0159637P.
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60.0%;
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99US-0162142P
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Best Local Similarity 60.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-230553/23.
N-PSDB; ABZ81430.
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                                                                     14-0CT-1999;
14-0CT-1999;
18-0CT-1999;
21-0CT-1999;
21-0CT-1999;
                                                                                                                                                   1-OCT-1999;
1-OCT-1999;
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                                                                                                                                                                                   21-OCT-1
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RESULT 26 ABP59344 ID ABP

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RESULT ABG3131

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Homo

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The invention relates to a composition comprising an isolated mechanical stress induced polypeptide identified as adlican or its functional portion or a polypeptide which is at least homologous or identical to it, and a physiologically acceptable excipient. Also included are an anticadican antibody or composition containing it, a composition comprising an isolated nucleic acid molecule encoding adlican and a physiologically acceptable excipient and a composition comprising a vector that comprising a ceptable excipient and a physiologically acceptable excipient and a physiologically acceptable excipient. The compositions and antibody are useful for preventing, treating or controlling osceoporosis, or for fracture healing, bone elongation, osteopenia, periodontosis, low bone density, osteopetrosis, osteoperisis, low bone density, osteopetrosis, cateoscierosis, osteopetrosis, cateoscierosis, osteopetrosis, low bone density, osteopetrosis, cateoscierosis, cateosci
                                                                                                                         Human, OCP, osteoclast protein, osteoporosis; osteopenia; osteopetrosis; osteoscierosis; osteoarthritis; periodontosis; bone fracture;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated mechanical stress induced polypeptide useful for preventing, treating or controlling osteoporosis, bone elongation, osteopenia, periodontitis, low bone density or for fracture healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53.9%; Score 41; DB 5; Length 2828; 35.7%; Pred. No. 1.1e+03; Live 7; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Faerman A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Skaliter R, Feinstein E,
                                                                                                                                                                                mechanical stress; adlican; gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           11-WAY-1998; 98US-0084944P.
15-WAY-1998; 98US-0085673P.
30-WAY-2000; 2000US-0207821P.
04-DEC-2000; 2000US-00729485.
                                                                                                                                                                                                                                                                                                                                                                                            08-MAR-2001; 2001US-00802318
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                      27-NOV-2002 (first entry)
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Best Local Similarity 35.7
Matches 5; Conservative
                                                                          Human Adlican protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-681611/73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Segev O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FAERMAN A.
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SEGEV O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ABSS4195
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(FEIN/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to the isolation of genes associated with mechanical stress, and the proteins encoded by them. The genes of the provention are designated protein 608, oCP or CMF608. The OCP polymucleotide and polypeptide sequences are useful for preventing, treating or controlling osteoporosis, bone fractures, bone elongation osteopomia, osteopomia, osteopomis, osteopomis, osteopomis, osteopomis, periodomitis, only bone and ansity or other conditions involving mechanical stress in a subject. The present sequence represents human adlican protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated mechanical stress induced polynucleotide, useful for diagnosis, treatment, prevention or control of osteoporosis, osteopenia, osteopetrosis, osteosclerosis, osteosarthritis, periodontitis, bone
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                                                                                                                                                                                                                                                                                                                                                                                                                           Human; mechanical stress; protein 608; OCP; CMF608; osteoporosis; bone fracture; bone elongation; osteopenia; osteoarthritis; osteoaclerosis; periodontitis; low bone density; osteopathic; antiinflammatory; antiarthritic; adlican.
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Pred. No. 1.16+03;
7; Mismatches 2; Indels
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                                                                                                                                                                                                                    ABG31319 standard; protein; 2828 AA.
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35.7%;
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08-MAR-2001; 2001US-00802318.
13-JUL-2001; 2001US-00905129.
06-NOV-2001; 2001US-00991630.
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2238 VVMKPAKIEHKEEN 2251
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                                 1 IVLRPSRVHNSEEN 14
                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Conservative
                                                                                                                                                                                                                                                                                                                                                                               Human adlican protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-590536/63.
N-PSDB; ABK90044.
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Best Local Similarity
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ADI17071;

ABG32897 standard; protein; 2828 AA.

RESULT 29 ABG32897

Matches

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ABG32897;

(CURA-) CURAGEN CORP

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human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes; inflammation; autoimmune disorder; allergy; blood disorder; acquired immunodeficiency syndrome; AIDS; obesity; asthma; immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis; Alzheimer's disease; infection; str.
           Human NOVX protein homologue SeqID 607.
                                                                                                                                                                                                                                                                                                                                                                                                                    001US-0318115P
                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001US-0332701P
                                                                                                   31-JAN-2002; 2002WO-US002785
(first entry)
                                                                                                                                                                                                                                                   001US-027
                                                                          WO200268649-A2
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14-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                 21-AUG-2001;
28-AUG-2001;
                                                              Homo sapiens.
15-APR-2004
                                                                                                                                                            07-FEB-2001;
                                                                                                                                                                  08-FEB-2001;
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                                                                                                                                                                                     26-FEB-2001;
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                                                                                      06-SEP-2002
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This invention relates to a novel nucleic acids, and encoded polypeptides thereof, which have properties related to the stimulation of biochemical corporated responses in a cell, tissue, organ or organism.

Cor physicological responses in a cell, tissue, organ or organism.

Cor diagnostic and prognostic assays and furthermore in the treatment of diagnostic and prognostic assays and furthermore in the treatment of diagnostic and prognostic seaves and furthermore in the treatment of human and murine NOVX proteins, as well as methods to modulate their expression using antisense oligos, ribozymes and peptide nucleic acids.

The NOVX polypeptides, polynucleotides and antibodies are useful in treating or preventing NOVX-associated disorders, e.g. cardiomyopathy, atherosclerosis, cancer and diabetes. Furthermore, they may be used in treating or preventing diseases such as inflammation, autoimmune disorders, alterating or preventing diseases such as inflammation, autoimmune disorders, alterating or preventing diseases such as inflammation, autoimmune disorders, alterating or preventing diseases such as inflammation, autoimmune companience, anthritis, Alzheimer's disease, infections, stroke, muscular dystrophy arthritis, nephrotropic, antiarthitic, happitorpolic, antialing muchanience, antiarthitic, happitorpolic, antiarthitic, happitorp
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                                                                                                                                                                                                                     New NOVX polypeptides and nucleic acids, useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
                                                                                                                      Burgess CE;
                                          Tchernev VT, Spytek KA, Zerhusen BD, Patturajan M, Shimkets RA;
Li L, Gangolli EA, Padigaru M, Anderson DW, Rastelli L, Miller CE;
Gerlach VL, Taupler RJ, Gueev VY, Colman SD, Wolenc AR, Pena CEA;
Purtak K, Grosse WM, Alsobrook JP, Lepley DM, Rieger DK, Burgess Ci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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35.7%; Pred. No. 1.1e+03;
ive 7; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 607; 1498pp; English.
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2238 VVMKPAKIEHKEEN 2251
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Best Local Similarity 35.7
Matches 5; Conservative
                                                                                                                                                                           WPI; 2002-706998/76.
                                                                                                                                                                                                                                                                                                          pharmacogenomics.
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This invention relates to a novel nucleic acids, and encoded polypeptides thereof, which have properties related to the stimulation of biochemical thereof, which have properties related to the stimulation of biochemical or physiological responses in a cell, tissue, organ or organism.

CC or physiological responses in a cell, tissue, organ or organism.

CC diverse pathological conditions. The present invention describes novel human and murine NOVX proteins, as well as methods to modulate their expression using antisense oligos, ribozymes and peptide nucleic acids.

The NOVX polypeptides, polynuclectides and antibodies are useful in treating or preventing NOVX-associated disorders, e.g. cardiomyopathy, atherosals, cancer and diabetes. Purthermore, they may be used in treating or preventing diseases such as inflammation, autoimmune of sisorders, allergies, blood disorders, equired immunodeficiency syndrome of sorders, allergies, blood disorders, acquired immunodeficiency syndrome of sorders, allergies, blood disorders, stroke, muscular dystrophy arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy and epilepsy. Accordingly, these molecules have many activities including cytostatic, cardiant, antidiabetic, antiarteriosclerotic, antiallergic, antiarteriosclerotic, antiallergic, antiarteriosclerotic, antiallergic, antiarteriosclerotic, antiarteriosclerotic, antiarteriosclerotic, antiarteriosclerotic, antiarteriosclerotic, antiarterior crelaxant and anticonvulsant. In addition, they are useful in screening assays to identify small molecules that modulate or inhibit, for example, crelating and angiogenesis. The nucleic acids are also neurogenesis. Wound healing and angiogenesis. The nucleic acids are also the angent and anticonnyments and anticonnyments. This polypeptide is a homologue of a human NOVX protein of the constants.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 41; DB 5; Length 2828;
Pred. No. 1.1e+03;
7; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human breast cancer / ovarian cancer related protein #27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; cytostatic; breast cancer; ovarian cancer
                 Disclosure; SEQ ID NO 608; 1498pp; English.
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27-JUN-2001; 2001US-0301351P.
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35.7%;
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N-PSDB; ABT31920.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2828 AA
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Burgess CE,
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garu M, Anderson DW, Rastelli L, Miller CE;
Gusev VY, Colman SD, Wolenc AR, Pena CEA;
Dobrook JP, Lepley DM, Rieger DK, Burgess CR
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                                                                                                     2001US-0265395P.
2001US-0265412P.
2001US-0265514P.
2001US-0265517P.
2001US-0266406P.
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05-FEB-2001; 2
07-FEB-2001; 2
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Bast
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                                                                                                                                                                                                                                                                                                                                                             Lung cancer-associated polypeptide, cytostatic; emphysema; antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis; small cell lung cancer; benign lesion; precancerous lesion; bronchitis; chronic obstructive pulmonary disease; hypersensitivity pneumonitis; interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polymucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits increased or decreased expression in lung cancer samples. Lung cancer associated polymucleotides and polypeptides are used for identifying a compound that modulates a lung cancer-associated polypeptide, for
                               The invention comprises a method for assessing whether a patient is afflicted with breast cancer or ovarian cancer. The method involves the use of specific DNA markers. The method of the invention is useful in the detection and treatment of ovarian and breast cancer. Amino acid sequences ABJ37025 - ABJ37080 represent human breast/ovarian cancer-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased expression in lung cancer.
                                                                                                                                                              Gaps
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                                                                                                                                     53.9%; Score 41; DB 6; Length 2828; 35.7%; Pred. No. 1.1e+03; ive 7; Mismatches 2; Indels
            Disclosure; Page 149-155; 233pp; English.
                                                                                                                                                                                                                                                                                                                                         Lung cancer-associated polypeptide #202.
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                                                                                                                                                                                                                                                                      ABUS6609 standard; protein; 2828 AA.
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29-NOV-2001; 2001US-0334370P.
12-APR-2002; 2002US-0372246P.
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2001US-0290492P.
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                                                                                                                             Query Match
Best Local Similarity 35...
Local Similarity 55...
Conservative
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N-PSDB; ABX76338.
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                                                                                                                  Sequence 2828 AA;
                                                                                            related proteins
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ID ABUS
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inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by administerating a modulatory compound identified. The methods are useful for treating lung cancer, such as small cell lung cancer, non-small cell lung cancer or other benign or precancerous lesions, e.g. atelectasis, hypersensitivity pneumonitis, interstitial pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma bronchiectasis. The genes, polynucleotides and polypeptides are useful compounds that modulate lung cancer, such as antibodies. Sequences ABUS6408-ABUS6745 represent lung cancer-associated polypeptides of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Breast cancer diagnosis or treatment by comparing the level of expression of a marker in a patient sample with that in the control non-breast
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yer V, Wang Y, Xu Y, Zhao X, Meyers RE;
Pusztai L, Meric F, Sahin A, Mills GB;
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Pred. No. 1.1e+03;
7; Mismatches 2; Indels
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Pusztai L,
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2001US-0306501P.
2001US-0325002P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUN-2001; 2001US-0299887P
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35.7%;
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2238 VVMKPAKIEHKEEN 2251
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I, Monahan JE, My
Hortobagyi GN, P
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Best Local Similarity 35...
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  cancer associated sequences from
afflicted with breast cancer. The breast cancer associated sequences from the present invention have cytostatic activities and can be used in gene therapy. The method is useful for diagnosing and treating breast cancer. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOVX; cytostatic; antiarteriosclerotic; antidiabetic; antiasthmatic; antiallergic; antiinflammatory; respiratory; antiarthritic; dermatological; antibacterial; cerebroprotective; vasotropic; cardiant;
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                                                                                                                                                                                       53.9%; Score 41; DB 6; Length 2828; 35.7%; Pred. No. 1.1e+03; Live 7; Mismatches 2; Indels
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22-DEC-2000; 2000US-0258171P.
20-FEB-2001; 2001US-0269940P.
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29-MAR-2001; 2001US-0279840P.
11-APR-2001; 2001US-028291P.
13-APR-2001; 2001US-0283556P.
31-JUL-2001; 2001US-0309247P.
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17-AUG-2001; 2001US-0313331P
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ZERHUSEN B D.
PATTURAJAN M.
LEPLEY D M.
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hes 5; Conserv
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The invention relates to a novel isolated NOVX polypeptide. The colypeptide demonstrates cytostatic, antiarteriosclerotic, antidiabetic, antiasthmatic, antiallergic, antianflammatory, respiratory, antiasthmatic, dermatological, antiabacterial, cerebroprotective, cardiant, haemostatic, hypotensive, hepatotropic, cardiant, haemostatic, indoctropic, neuroprotective, anorectic, nootropic, antialoer, muscular, endocrine, cophthalmological, osteopathic, antipporiatic, endocrine, ophthalmological, osteopathic, antipporiatic, endocrine, cophthalmological, osteopathic, antipporiatic, endocrine, cophthalmological, osteopathic, antipporiatic, or anticonvulsant, cophthalmological, osteopathic, antiporiatic, antiporatic, antiporatic, antiporatic, cophthalmological, osteopathic, antiporation anticonvulsant, continued and osteopathic, antiporatic, antiporation anticonvulsant, continued as crivities, nucleic antibody of the cinvention may be useful for treating or preventing a NOVX-associated disorder, such as cardiomyopathy, atherosclerosis, diabetes or a disorder related to cell signal processing and metabolic pathway modulation. Furthernore, the NOVX polypeptides may be useful for diagnosing, treating cor preventing diseases such as asthmia, allergies, emphysema, autoimmune disease, graft-versus-host disease, arthritis, cancer, stroke, consenting as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine or pharmacogenomics. The current sequence is that of a protein of the invention which is related to human NOVX protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New NOVX polypeptides and nucleic acid molecules, useful for diagnosing, preventing or treating NOVX-associated polypeptide disorder, e.g. cardiomyopathy, atherosclerosis, diabetes, cancer, Parkinson's disease or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Grosse WM;
FL, Gorman L;
                                                                                                                                                                                                                                                                                                                                                                                                                                              JP, Tchernev VT, Liu X, Spytek KA, Zerhusen BD; M, Lepley DM, Burgess CE, Shimkets RA, Grosse WM; S, Vernet CAM, Li L. Casman SJ, Boldog FL, Gorman A, Fernandes ER, Rieger DK, Edinger SR, Gunther E; Sciore P, Ellerman K, Macdougall JR, Smithson G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C227.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 41; DB 7; Length 2828;
Pred. No. 1.18+03;
7; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, SEQ ID NO 126; 263pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alsobrook JP, Tchernev VT, Liu X, Sp
Patturajan M, Lepley DM, Burgess CE,
Szekeres ES, Vernet CAM, Li L, Caema
Gangolli EA, Pernandes ER, Rleger DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADN39857 standard; protein; 2828 AA.
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35.7%;
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                                                                                                                                                                                                                                                                                                                                                              MACDOUGALL J R.
                                                                                            GANGOLLI E A.
FERNANDES E R.
RIEGER D K.
EDINGER S R.
GUNTHER E.
CASMAN S J.
BOLDOG F L.
GORMAN L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-898249/82.
                                                                                                                                                                                                                                                                                                                             ELLERMAN K.
                                                                                                                                                                                                                                                                                                                                                                                            SMITHSON G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                  MILLET I.
SCIORE P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2828 AA;
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                                                                                                                                                              (RIEG/)
(EDIN/)
(GUNT/)
                                                                                                                                                                                                                                                                                                (SCIO/)
(ELLE/)
                                    (BOLD/)
(GORM/)
                                                                                                   (GANG/)
(FERN/)
                                                                                                                                                                                                                                                                                                                                                                                            SMIT/)
                                                                                                                                                                                                                                                                                                                                                              MACD/)
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Matches
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:|::|::: ||| 2238 VVMKPAKIEHKEEN 2251

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whose expression is upregulated or downregulated in specific cancers or other diseases such as angiogenic or fibrotic disorders, and to methods of elecamining the presence or absence of a pathological call in a patient by detecting a nucleic acid at least 80% identical to those of the invention or by detecting a polypeptide of the invention. The invention also relates to expression vectors and host calls comprising a nucleic acid of the invention; antibodies which specifically bind a polypeptide of the invention; use of such antibodies for drug targeting; and methods of screening for modulators of activity or expression of the polypeptides and mucleic acids. The nucleic acids, polypeptides, antibodies and methods are useful for disgnosing, prognosing and treating cancer and other conditions such as psoriasis, ischaemia, heart disease, a theoretic acids in inflammatory diseases, autoimmune diseases, retinal neovascularistaion syndromes, scarring and uterine fibroids. They may also be useful in wound healing and in contraception. The present sequence represents a polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.
fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
         inflammatory disease; autoimmune disease; retinal neovascularistaton syndrome; scarring; uterine fibroid; detection; diagnoslis; prognosls; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; vulnerary; gene therapy; vaccine.
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Wilson KE, Zlotnik A;
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                                                                                                                                                                                                                                                                                  2001US-0332464P.
2001US-0334393P.
2001US-0335394P.
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                                                                                                                                                                                                                                 13-NOV-2002; 2002WO-US036810
                                                                                                                                                                                                                                                                                                                                       2001US-0340376P.
2002US-0347211P.
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N-PSDB; ADN39639.
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                                                                                                                                                         WO2003042661-A2.
                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                       14-DEC-2001;
08-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                                            10-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                           13-FEB-2002;
20-FEB-2002;
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                                                                                                                                                                                                                                                                   13-NOV-2001;
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Mack DH,
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Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.
                                                                                                       Human, differential expression, cancer, angiogenic disorder,
fibrotic disorder, psoriasis, ischaemia, heart disease, atherosclerosis,
inflammatory disease, autoimmune disease,
                                                                                                                                    retinal neovascularistation syndrome; scarring; uterine fibroid; detection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; vulnerary; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PA;
                                                                                   Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:58.
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A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glynne R,
E, Zlotnik
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Wilson KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 12; SEQ ID NO 58; 1385pp; English.
                     ADN38740 standard; protein; 2828 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ginsburg WM,
R, Watson SR,
                                                                                                                                                                                                                                                                                           2001US-0332464P.
2001US-033339P.
2001US-0343374P.
2002US-0347211P.
2002US-0347349P.
2002US-0355714P.
2002US-0356714P.
2002US-0356714P.
2002US-036809P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (EOSB-) EOS BIOTECHNOLOGY INC
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                                                               17-JUN-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-468649/44.
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10-JAN-2002;
08-FEB-2002;
13-FEB-2002;
20-FEB-2002;
                                                                                                                                                                                               Homo sapiens.
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                                         ADN38740;
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RESULT 37
ADN38740
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Gaps

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Score 41; DB 7; Length 2828; Pred. No. 1.1e+03; 7; Mismatches 2; Indels

53.9%; 35.7%;

7; Mismatches

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1 IVLRPSRVHNSEEN 14
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                                                              RESULT 39
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                     셤
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polypeptides and nucleic acids. The nucleic acids, polypeptides, and machods are useful for diagnosing, prognosing and treating cancer and other conditions euch as psoriasis, ischaemia, heart disease, atherosclerosis, inflammatory diseases, autoimmune diseases, retinal neovascularistation syndromes, scarring and uterine fibroids. They may also be useful in wound healing and in contraception. The present sequence represents a polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated human mechanical stress-induced 608 nucleic acid molecule. The polypeptide encoded by the nucleic acid molecule is identified as human protein 608 (or OCP), or a functional portion of protein 608 or Adlican-2, or a polypeptide which is at least substantially homologous to it. The 608 polynucleotides and polypeptides are useful for disgnosing, treating, preventing and controlling osteoperosis, osteosacoma, osteoperial osteoperosis, osteosclerosis, osteosclerosis, represents a human OCP protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New human mechanical stress-induced 608 nucleic acid and polypeptide, useful for diagnosing, treating, preventing and controlling osteoporosis, osteosarcoma, osteosarthritis, periodontitis, or bone fractures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                  Human; OCP; mechanical stress-induced 608 nucleic acid; protein 608; Adilcan-2; osteoporosis; osteosaxcoma; osteoponia; osteopetrosis; osteoastronitis; osteosclerosis; osteoarthritis; periodonitis; bone fracture; osteopathic; antiarthritic; antiaflammatory; cytostatic.
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                                                                                                                                Length 2828;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Faerman A,
                                                                                                                                                        2; Indels
                                                                                                                                53.9%; Score 41; DB 7; I 35.7%; Pred. No. 1.1e+03; ive 7; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Feinstein E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 19; SEQ ID NO 21; 255pp; English.
                                                                                                                                                                                                                                                                              ADL02241 standard; protein; 2828 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-MAY-1999; 99US-00312216.
04-DEC-2001; 2001WO-US046400.
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                                                                                                                                                                                                              2238 VVMKPAKIEHKEEN 2251
                                                                                                                                                                                     1 IVLRPSRVHNSEEN 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (QUAR-) QUARK BIOTECH INC.
                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                            Human OCP protein #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-238583/22.
                                                                                                                                           Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Segev O,
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                                                                                                         Sequence 2828 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                  03-JUN-2004
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                                                                                                                                                                                                                                                                                                        ADL02241;
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                                                                                                                                 Query Match
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The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual determinal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of a gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue samples, where a higher level of protein expression. The mit is soft tissue samples, where a higher level presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue ascoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma upregulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                          soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          specification per se but was submitted in CD format by the inventor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                           Human soft tissue sarcoma-upregulated protein - SEQ ID 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; SEQ ID NO 554; 210pp; English.
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                                                                                                                                                                                        ADQ17737 standard; protein; 2828 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zlotník A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PROT-) PROTEIN DESIGN LABS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-NOV-2003; 2003WO-US038193.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-NOV-2002; 2002US-0429739P.
Query Match
Query Match
Best Local Similarity 35./*,
-hos 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 IVLRPSRVHNSEEN 14
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                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-441208/41.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2004048938-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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Characterizing the state of a neoplastic disease in a subject by comparing the pattern of determined expression levels of marker genes in a biological sample with reference patterns of expression levels.
                                                                                                                                                                                                                                                                                                                                        The invention relates to a novel method for characterizing the state of neoplastic disease in a subject comprising determining the pattern of expression levels of at least 6, 8,10,15, 20, 30, 47 or 67 marker genes in a biological sample, comparing the pattern of expression levels with reference patterns of expression levels and characterizing the state of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           subject, preferably breast cancer, in gene therapy and for screening for compounds having a curative effect on a neoplastic disease. The current sequence is that of the human breast cancer marker RAD52 protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                  the neoplastic disease in the subject from the outcome of the comparison The method of the invention demonstrates cytostatic applications and may be useful in characterizing the state of a neoplastic disease in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumor marker; colon tumor; cancer; cytostatic; neoplasm; diagnostic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention which is differentially expressed in neoplastic tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human protein from gene overexpressed in cancer, DKFZp56411922.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53.9%; Score 41; DB 9;
35.7%; Pred. No. 1.1e+03
iive 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (FARB ) BAYER HEALTHCARE LLC. (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 328; 542pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thiagalingam A, A, Thibodeau S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AEA04479 standard; protein; 2828 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-2004; 2004WO-US036404.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-NOV-2003; 2003US-00700439.
30-JUN-2004; 2004EP-00015374
                                        06-OCT-2003; 2003EP-00022587.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (FARB ) BAYER HEALTHCARE AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            microarray; drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 IVLRPSRVHNSEEN 14
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Boardman LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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N-PSDB; AEA04386.
REFSEQ; NP_056234.
                                                                                                                                                              WPI; 2005-265481/28.
                                                                                                                        Munnes M, Bojar H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2828 AA;
                                                                                                                                                                               N-PSDB; ADZ09719
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Burgart L,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bladder cancer (BC), or monitoring its progression, that uses (I), (II) or agents (Z) that inhibit, or bind to, (I) or (II), labelled with a reporter; and (3) a method for treating BC that uses (I), (II) or (Z). (I) and (II) have cytostatic activity. (I) and (II) can be used to detect (and monitor progression of) bladder cancer (BC), or the risk of developing it; to screen for specific binding agents (Z), and to treat BC. (Z) are also useful as diagnostic and therapeutic agents. The present sequence represents a human amino acid sequence associated with bladder cancer, which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes nucleic acids (I) associated with bladder cancer tissue. Also described: (1) peptides and proteins (II) containing an amino acid sequence encoded by (I); (2) a method for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acids, and encoded proteins, from bladder cancer tissue, useful for diagnosis, treatment and in screening for specific binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neoplasm; tumor marker; cytostatic; breast tumor; gene therapy; RAD52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Specht T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 41; DB 8; Length 2828; Pred. No. 1.1e+03; 7; Mismatches 2; Indels ...
                                                                                                                                                                                                                                                                                                                                                                                                                                     Pilarsky C,
    Human bladder cancer associated amino acid sequence.
                                            bladder cancer tissue; bladder cancer; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human breast cancer marker RAD52 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Staub E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADZ09884 standard; protein; 2828 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Dahl E,
                                                                                                                                                                                                         24-FEB-2004; 2004WO-DE000364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 35.7%;
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Hinzmann B,
                                                                                                                                                                                                                                                                                                                             DAHL E.
STAUB E.
PILARSKY C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-653385/63
                                                                                                                                                                                                                                                                                                            HINZMANN B.
                                                                                                                                                                                                                                                                                                                                                                                                 SPECHT T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2828 AA;
                                                                                                                          WO2004076613-A2
                                                                                                                                                                                                                                                                                       HERR A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                    Homo sapiens
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                                                                                                                                                                   10-SEP-2004.
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RESULT 41 ADZ09884

XBXBXBXBXGX

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(PILA/) (SPEC/) Herr A,

STAU/)

agents.

(HERR/) (HINZ/) (DAHL/) ő

Gaps

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1.1e+03;

Length 2828;

Molino G;

Maimonis P, Lewis M;

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The invention relates to detecting differential expression of one or more nucleic acid sequences (appearing as AEA04356-AEA0448 in a biological sample comprising obtaining the sample from a subject, and detecting a canaple comparising obtaining the sample from a subject, and detecting a relative to a control expression level of one or more nucleic acid sequences, is now also included are detecting comparising the expression level of one or more nucleic acid sequences in a biological sample from the subject (comprising comparising the expression level of one or more nucleic acid sequences in a biological sample from the subject (comprising comparing the expression level of the nucleic acid sequences is indicative of cancer or pre-malignant condition), moritoring the onset (or progression, or regression) level of the nucleic acid sequences is indicative of cancer or pre-malignant condition), in a subject (by detecting in a biological sample of the aubject (by detecting in a biological sample of the subject (comprisaing detecting in the expression level is indicative of progression of cancer or its pre-malignant condition in the subject (comprisaing detecting in a biological sample of the subject, determining precedences, comparing the expression level where a concer or its pre-malignant condition in a subject (comprisaing detecting in a biological sample of the subject, the expression level with a reference or call sequences, comparing the expression level with a subject (comprisaing detecting in a subject (comparing the expression level with a subject, determining the efficacy of a test compound for inhibiting cancer in a subject, inhibiting cancer in a subject, a left comparing the efficacy of a test comparing the expression level with a subject (comparisor) of a test comparing the end of a polypeptide end or the end of a polypeptide sequence, and detecting in a biologi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer), monitoring the onset, progression, or regression of cancer or a pre-malignant condition, or determining prognosis for cancer or its pre-malignant condition in a subject, or for determining the efficacy of a test compound for inhibiting cancer in a subject. The compound is useful for inhibiting cancer in a subject. The antibodies may also be used to treat cancer. The present sequence is a protein from a human gene overexpressed in cancer samples.
                  Detecting expression of one or more nucleic acid sequences in biological sample, useful for detecting cancer, comprises detecting a change in the expression level of one or more nucleic acid sequences relative to a
                                                                                                                                                                           Claim 20; SEQ ID NO 124; 256pp; English.
                                                                                                                    control expression level.
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ö Length 2828; 53.9%; Score 41; DB 9; Length 282 35.7%; Pred. No. 1.1e+03; ive 7; Mismatches 2; Indels :|::|::: ||| 2238 VVMKPAKIEHKEEN 2251 1 IVLRPSRVHNSEEN 14 Query Match
Best Local Similarity 35.7
Matches 5, Conservative ઠે

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Gaps

Human; anti-HIV; antiallergic; cerebroprotective; antiparkinsonian; anticonvulsant; nootropic; neuroprotective; immunosuppressive; dermatological; anti-inflammatory; cytostatic; antiarteriosclerotic; gene therapy; cell adhesion; extracellular matrix; CADECM; Human cell adhesion and extracellular matrix protein, CADECM-7. ABR40110 standard; protein; 2853 AA. (first entry) 04-JUL-2003 ABR40110; RESULT 43 ABR40110 

immune system disorder; AIDS; allergy; neurological disorder; stroke; Parkinson's disease; epilepsy; developmental disorder; Down's syndrome; cerebral palsy; connective tissue disorder; systemic lupus erythematosus; genetic disorder; Alport's syndrome; cell proliferative disorder; cancer; 03-MG-2001; 20010S-0310119P. 17-AUG-2001; 2001US-0310119P. 31-AUG-2001; 2001US-0311671P. 07-SEP-2001; 2001US-0317896P. 21-SEP-2001; 2001US-0324781P. 05-OCT-2001; 2001US-0328960P. 12-OCT-2001; 2001US-0328960P. 09-NOV-2001; 2001US-0344471P. 17-MAY-2002; 2002US-0381291P. 02-AUG-2002; 2002WO-US024649 atherosclerosis WO2003027230-A2 Homo sapiens. 03-APR-2003 

Burford N, Warren BA, Duggan BM, Mason PM, Richardson TW, Yue Forsythe IJ, Elliott VS, Griffin JA, Gorvad AE, Azimzal Y; Kallick DA, Xu X, Honchell CD, Baughn MR, Gletzen KJ, Lee S; Walla NK, Tang YT, Mguyen DB, Becha SD, Lee SY, Ramkumar J;

(INCY-) INCYTE GENOMICS INC.

Yue H;

2003-354645/33. N-PSDB; ACC00398 New human cell adhesion and extracellular matrix proteins (CADECM), useful for diagnosing, treating or preventing disorders associated with aberrant CADECM expression, e.g. cancer, AIDS, atherosclerosis, allergies or stroke.

Claim 1; Page 178-185; 234pp; English.

The present invention relates to novel human cell adhesion and extracellular matrix proteins, CADECM-1 to CADECM-22, and their coding sequences sequences (ACC00392-ACC00413 and ABR40104-ABR40125). The coding sequences and proteins are useful in diagnosing, treating and preventing disorders associated with aberrant expression of CADECM, such as immune system disorders (e.g. AIDS or allergies), neurological disorders (e.g. stroke, Parkinson's disease or epilepsy), developmental disorders (e.g. bown's syndrome or cerebral palsy), connective tissue disorders (e.g. systemic lupus erythematosus), genetic disorders (e.g. Alport's syndrome) or cell proliferative disorders or atherosclerosis)

53.9%; Score 41; DB 6; Length 2853; Pred. No. 1.1e+03; 7; Mismatches 2; Conservative Local Similarity Sequence 2853 AA; . 2 Query Match Best Loc Matches

:|::|::: ||| 2263 VVMKPAKIEHKEEN 2276

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1 IVLRPSRVHNSEEN 14

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Gaps

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Indels

ABG23884 standard; protein; 2993 AA. ABG23884; RESULT 44 BXXXXXX

Novel human diagnostic protein #23875. 18-FEB-2002 (first entry)

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food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                        biodiversity.
                              Homo sapiens.
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                                                                                  11-OCT-2001
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Matches
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ID ABP1
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AC ABP1
XX
DY 24-J
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KW Huma
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KW Aege
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                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cutivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and mapping, identification of mutations in dispnostice for generic disorders or other traits to assess blodiversity represent cond to produce other types of data and products dependent on DNA and and to produce other types of data and products dependent on DNA and and to produce other types of data and products dependent on DNA and and cond sequences. Agonomological expensions of mino acid sequences of the invention. Note: The sequence data for this parent did not appear in the printed specification, but was obtained in celetronic format directly from WIPO at (IP) will be printed sequences.
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                                                                                                                                                                                                                                                                                                           New isolated polynuclectide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                 Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; chromosome mapping; gene mapping; gene therapy; forensic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 41; DB 4; Length 2993;
Pred. No. 1.2e+03;
7; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                 Claim 20; SEQ ID NO 54243; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human diagnostic protein #8552.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG08561 standard; protein; 5266 AA
                                                                                                                                          30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                           Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53.9%;
                                                                                                                                                                    31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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2413 VVMKPAKIEHKEEN 2426
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Best Local Similarity
                                                                                                                                                                                                                                        Liu C,
                                                                                                                                                                                                                                                                     WPI; 2001-639362/73
                                                                                                                                                                                                               (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2993 AA;
                                                                                                                                                                                                                                                                                  N-PSDB; AAS88071
                                                                                     WO200175067-A2
                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-FEB-2002
                                                                                                                                                                                                                                           Drmanac RT,
                                                                                                               11-OCT-2001
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    EXEXEXEX
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain recaction (PCR) primers, oligomers, and for chromosome and spen mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging polypeptide and polymucleotide sequences have applications in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30317 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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35.7%; Pred. No. 2.2e+03;
tive 7; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 20; SEQ ID NO 38920; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABP11166 standard; protein; 55 AA.
                                                                                                                                                                                                                                        31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Tang YT;
                                                                                                                                                            30-MAR-2001; 2001WO-US008631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-639362/73
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                                                                                                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC
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WO200175067-A2.
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The invention comprises a modified cell containing a heterologous nucleic acid encoding an artificial transcription factor that confers stress resistance to the modified cell. The modified cell of the invention is useful for altering a phenotypic trait of a cell or organism. The present amino acid sequence represents a transcriptional activation domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New modified cell comprising a heterologous nucleic acid encoding an artificial transcription factor that confers stress resistance, useful for altering a phenotypic trait of a cell or organism.
                                                           modified cell; artificial transcription factor; stress resistance; phenotypic trait alteration; transcriptional activation domain; UME6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 zinc finger protein; gene evaluation; transcription factor; finger domain; UME6.
                   Transcriptional activation domain from UME6 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seol W, Lee H, Lee S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 40; DB 7
Pred. No. 31;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 133; 169pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UME6 protein repression domain fragment.
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                                                                                                                                                                                                                                                                                                                                        26-APR-2002; 2002US-0376053P.
02-AUG-2002; 2002US-0400904P.
05-AUG-2002; 2002US-0401089P.
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                                                                                                                                                                                                                                                                        07-DEC-2002; 2002WO-KR002309.
                                                                                                                                                                                                                                                                                                                     07-DEC-2001; 2001US-0338441P
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64 VLRPILLRIHNSEQ 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-JUN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Park K, Lee D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-513760/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                     (TOOL-) TOOLGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                WO2003048345-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 90 AA;
                                                                                                                                     Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-MAR-2004
                                                                                                                                                                                                                           12-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADM72635;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kim J,
Jang Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          zinc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes substantiarly purinter from the present invention describes substantiarly purinted from the proteins given in ABP00010 to ABP11500. ORFX proteins are useful for proteins given in ABP00010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a syndrome associated with ORFX-associated disorder. ORFX polynucleotide syndrome associated in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhoats of liver, psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage, osteoarthritis, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases, diabetes mellitus, systemic lupus erythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, various immune deficiencias and disorders, infectious disease, autoimmune thyroiditis, mysthenia gravis, graft-versus-host disease and autoimmune thyroiditis, mysthenia gravis, graft-versus-host disease and autoimmune thyroiditis, mysthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also cusful for treating burns, inclaions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodottis, corperiodottis, mysthenia gravis, graft-versus-host protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from systemic cytokine damage. NB. The sequence date for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/published_pot_sequences
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cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present invention describes substantially purified human proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human polypeptides and polynuclectides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, SEQ ID NO 22314; 1037pp; English.
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Pred. No. 18;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                            30-MAY-2000; 2000US-0206132P.
29-AUG-2000; 2000US-0228716P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52.6%;
                                                                                                                                                                                                                                                                               29-MAY-2001; 2001WO-US010836
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Leach MD;
                                                                                                                                                                                                                                                                                                                                                                                                 (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-106308/14.
                                                                                                 myasthenia gravis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ABN26918.
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                                                                                                                                                                                         WO200192523-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                               Shimkets RA,
                                                                                                                                              Ното варіепв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-MAY-2004
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RESULT 47 ADL33594

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Gaps

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7; Length 90; 1; Indels

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Yang H,

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                                                                                                                                     The invention relates to evaluating several cellular genes. The method involves providing several cells containing nucleic acid encoding confidence tartificial, chimeric transcription factor, expression nucleic acids in cells, evaluating expression of several genes in cells to provide expression information and identifying from expression confidence information, a set of two or more genes whose expression altered by first and second transcription factors. The nucleic acids encoding the different artificial, chimeric transcription factors comprise a comprise an extificial, chimeric transcription factor confidence and extificial, chimeric transcription factor comprises a first zinc finger domain, and further comprises a second and third zinc finger domain. The first zinc finger domain is a naturally occurring zinc finger domain. The first zinc finger domain is a mammalian zinc finger domain. Bach cell of several cells is an animal or human cell. The method is useful for evaluating several callular genes. The present sequence represents the amino acid sequence collular genes. The present sequence represents the amino acid sequence collular genes.
                                                                                                                                                                                                                                                                                                                                                                                                                        ä
                                                                  Evaluating cellular genes by expressing nucleic acid encoding different artificial, chimeric transcription factor in cells and identifying set of genes altered by transcription factors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA binding domain; zinc finger domain; VEGF, VEGF-A; transcription activation domain; transcription repression domain; protein transduction domain; p65; VP16 activation domain; Kid; KOX repression domain; TAT protein; VP22 protein; Antennapedia homeodomain; cytostatic; antiinflammatory; angiogenesis; neoplastic disorder; inflammatory disorder; angiogenesis-based disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel zinc finger protein-related yeast UME6 repression domain SeqID119
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                              Score 40; DB 8; Length 90; Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                   Disclosure; SEQ ID NO 7; 124pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADP71011 standard; protein; 90 AA.
                        Kim Y;
                                                                                                                                                                                                                                                                                                                                                                                                52.6%;
64.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               2 VLRP--SRVHNSEE 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 VLRPILLRIHNSEQ 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kwon H;
                         'n
                         Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TOOL-) TOOLGEN INC.
                                              WPI; 2004-248440/23.
  (TOOL-) TOOLGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shin H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2004053130-A1.
                                                                                                                                                                                                                                                                                                                                                                          Sequence 90 AA;
                        Lee D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-SEP-2004
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                         Kim J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kim J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 49
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This invention relates to a novel polypeptide comprising a DNA binding domain that includes a plurality of zinc finger domains, where the DNA commain that includes a plurality of zinc finger domains, where the DNA compined to a site in a VECF gene, and at least two of the zinc finger domains each include respective zinc finger domain motifs comprises in the VECF gene expression. The polypeptide further comprises a transcription activation domain, a transcription repression compines p65 or VP16 activation domain. The transcription activation compains protein transduction domain activation domain. The transcription activation compains post of the invention may be useful for the production compounds with a cytostatic or antiinflammatory activity acting as of compounds with a cytostatic or antiinflammatory activity acting as angiogenesis modulators. The polypeptides and nucleic acids are useful for for modulating angiogenesis whilst the compounds may be useful for preventing or treating a neoplastic disorder, an inflammatory disorder, or an anglogenesis-based disorder. The present sequence is that of a cytostation domain which is related to the invention.
                                                    New polypeptide comprising a DNA binding domain that includes a plurality of zinc finger domains, and at least two of the zinc finger domains each include respective zinc finger domain motifs, useful for modulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cellular transport; neoplasm; inflammation; angiogenesis disorder; UME6; cytostatic; antiinflammatory; antiangiogenic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
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Pred. No. 31;
2; Mismatches
                                                                                                                                                                                                                             Disclosure; SEQ ID NO 119; 176pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADV39071 standard; protein; 90 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-JUN-2003; 2003US-0477459P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |||| | |:||||:
64 VLRPILLRIHNSEQ 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kim J, Shin H, Kwon H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2005-031673/03.
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Best Local Similarity
9; Conserve
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WPI; 2004-468871/44.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 90 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-MAR-2005
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                                                                                                                                                                     angiogenesis
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20-MAY-2004
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                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                     RESULT
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                   The invention relates to a chimeric protein comprising zinc finger

domains and a heterologous protein transduction domain for translocating

the protein across a cellular membrane. The invention also relates to a

pharmaceutical composition comprising the chimeric protein and a carrier,

a nucleic acid comprising a coding sequence that encodes a polypeptide

that comprises a zinc finger domain and a heterologous protein

transduction domain, located N-terminal to the zinc finger domain, a

c transduction domain, located N-terminal to the zinc finger domain, a

that contains an exogenous polypeptide, but not a nucleic acid that

c altering gene expression in a cell of a subject, a method of

that contains an exogenous polypeptide, but not a nucleic acid that

c encodes the exogenous polypeptide, but not a nucleic acid that

c encodes the exogenous polypeptide, but not a nucleic acid that

c encodes the exogenous polypeptide. The chimeric protein that is

c heterologous to the DNA binding domain and a method for preparing a

c transducible DNA binding polypeptide. The chimeric protein is useful in

preparing a composition for treating a subject having or being suspected

of having a neoplastic, inflammatory or angiogenesis-based disorder. This

sequence represents the yeast UME6 repression domain used in the scope of

the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene.
                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ochiai K, Yokoi H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
                                                                                                                                                                                                                                                                                                                                                ..
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                                                                                                                                                                                                                                                                                                                  Score 40; DB 9; Length 90;
Pred. No. 31;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Науавһі М,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C glutamicum protein fragment SEQ ID NO: 5581.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H, Ando S, Hayash
Ikeda M, Ozaki A;
  Disclosure; SEQ ID NO 9; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAG91827 standard; protein; 115 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-DEC-1999; 99JP-00377484.
07-APR-2000; 2000JP-00159162.
03-AUG-2000; 2000JP-00280988.
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                                                                                                                                                                                                                                                                                                                     52.6%;
                                                                                                                                                                                                                                                                                                       Query Match
Query Match
Best Local Similarity 64.33,
Best Local Similarity 64.33,
Conservative
                                                                                                                                                                                                                                                                                                                                                                                               64 VLRPILLRIHNSEQ 77
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Senoh A, Ike
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organic acid synthesis.
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N-PSDB; AAH67046.
                                                                                                                                                                                                                                                                                           Sequence 90 AA;
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Tateishi N,
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are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Offlice
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention comprises a modified cell containing a heterologous nucleic acid encoding an artificial transcription factor that confers stress resistance to the modified cell. The modified cell of the invention is useful for altering a phenotypic trait of a cell or organism. The present amino acid sequence represents a protein which contains zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New modified cell comprising a heterologous nucleic acid encoding an artificial transcription factor that confers stress resistance, useful for altering a phenotypic trait of a cell or organism.
                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modified cell; artificial transcription factor; stress resistance; phenotypic trait alteration; zinc finger domain.
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                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 115;
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                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 42;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zinc finger domain-containing protein #1
                                                                                                                                                                                                                                                                                                                                                                           Score 40;
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26-APR-2002; 2002US-0376053P.
02-AUG-2002; 2002US-0400904P.
65-AUG-2002; 2002US-0401089P.
                                                                                                                                                                                                                                                                                                                                                                           52.6%;
72.7%;
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Best Local Similarity
Matches 9; Conserval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43 PLRVHASSENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 210 AA;
                                                                                                                                                                                                                                                                                                                    Sequence 115 AA;
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New modified cell comprising a heterologous nucleic acid encoding an artificial transcription factor that confers stress resistance, useful for altering a phenotypic trait of a cell or organism.
                                                                                                                                                                                                                                                      modified cell; artificial transcription factor; stress resistance; phenotypic trait alteration; zinc finger domain.
                                                                                                                                                                                             Zinc finger domain-containing protein #2.
ADL33682 standard; protein; 238 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-APR-2002; 2002US-0376053P.
02-AUG-2002; 2002US-0400904P.
05-AUG-2002; 2002US-0401089P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-DEC-2001; 2001US-0338441P.
26-APR-2002; 2002US-0376053P.
02-AUG-2002; 2002US-0400904P.
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                                                                                                                              20-MAY-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-513760/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TOOL-) TOOLGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                         WO2003048345-A1.
                                                                                                                                                                                                                                                                                                                                                          Unidentified
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                                                                  ADL33682;
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Jang Y;
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ID ADL3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to evaluating several cellular genes. The method involves providing several cells containing nucleic acid encoding different artificial, chimeric transcription factor, expressing nucleic acids in cells, evaluating expression of several genes in cells to provide expression information and identifying from expression is altered by information, a set of two or more genes whose expression is altered by circumation, a set of two or more genes whose expression is altered by information, a set of two or more genes whose expression is altered by circumation, and encoding the different artificial, chimeric transcription factors comprise a condition acids, where each member of the preselected set of nucleic acids encodes an artificial, chimeric transcription factor comprises an artificial, chimeric transcription factor comprises a first zinc finger domain, and further comprises a second and third zinc finger domains. The first zinc finger domain is a manumalian zinc finger domain. Each cell of several cells is an animal or human cell. The method is useful for evaluating several cellular genes. Sequences ADMANS637-ADMAS647 removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Evaluating cellular genes by expressing nucleic acid encoding different artificial, chimeric transcription factor in cells and identifying set of genes altered by transcription factors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZFP; zinc finger protein; gene evaluation; transcription factor;
zinc finger domain; zinc finger domain; ZFD.
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Pred. No. 83;
2; Mismatches 1; Indels
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sequences of zinc finger domains (ZFD) of K1 to K11.
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                                                                                                                                                                                                                                  ADM72637 standard; protein; 210 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                Amino acid sequence of ZFD of Kl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kim Y;
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07-MAR-2003; 2003US-0453111P.
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Best Local Similarity 64.3%;
Matches 9; Conservative
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184 VLRPILLRIHNSEQ 197
         VLRP--SRVHNSEE 13
                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-248440/23.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2004022575-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lee D,
                                                                                                                                                                                                                                                                                                                                                                03-JUN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
         N
                                                                                                                                                                                                                                                                                                 ADM72637;
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                                                                                                                                                                      RESULT 53
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Lee Y;

Yang H,

Lee S,

Lee H,

Seol W,

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The invention comprises a modified cell containing a heterologous nucleic acid encoding an artificial transcription factor that confers stress resistance to the modified cell. The modified cell of the invention is useful for altering a phenotypic trait of a cell or organism. The present amino acid sequence represents a protein which contains zinc finger
                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified cell; artificial transcription factor; stress resistance; phenotypic trait alteration; zinc finger domain.
                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                  Length 238;
                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                    Score 40; DB 7
Pred. No. 96;
2; Mismatches
                                                                                                                                                                                                  DB
96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zinc finger domain-containing protein #4.
                                                                                                                                                                                                                                                                                                                                                                                                              ADL33684 standard; protein; 238 AA.
Example 3; Page 99; 169pp; English.
                                                                                                                                                                                                    52.6%;
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212 VLRPILLRIHNSEQ 225
                                                                                                                                                                                                                                                                             2 VLRP--SRVHNSEE 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-MAY-2004 (first entry)
                                                                                                                                                                                                    Query Match 52.6
Best Local Similarity 64.3
Matches 9; Conservative
                                                                                                                                                                   Sequence 238 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2003048345-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified
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1;

Gaps

5;

54

2 VLRP--SRVHNSEE 13

ઠે 셤 encoding

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Gaps

5

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involves providing several cells containing nucleic acid encoding different artificial, chimeric transcription factor, expressing nucleic acids in cells, evaluating expression of several genes in cells to provide expression information and identifying from expression information and identifying from expression is altered by first and second transcription factors. The nucleic acids encoding the different artificial, chimeric transcription factors comprise a preselected set of nucleic acids, where each member of the preselected set of nucleic acids encodes an artificial, chimeric transcription factor that can alter a cellular phenotype. Each artificial, chimeric transcription factor comprises a second and third zinc finger domains. The first zinc finger comprises
                                                                                                            The invention comprises a modified cell containing a heterologous nucleic acid encoding an artificial transcription factor that confers stress resistance to the modified cell. The modified cell of the invention is useful for altering a phenotypic trait of a cell or organism. The present amino acid sequence represents a protein which contains zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Evaluating cellular genes by expressing nucleic acid encoding different artificial, chimeric transcription factor in cells and identifying set of genes altered by transcription factors.
New modified cell comprising a heterologous nucleic acid encoding an artificial transcription factor that confers stress resistance, useful for altering a phenotypic trait of a cell or organism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention relates to evaluating several cellular genes. The method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZFP; zinc finger protein; gene evaluation; transcription factor;
zinc finger domain; zinc finger domain; ZFD.
                                                                                                                                                                                                                                                                                  Length 238
                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                    7;
                                                                                                                                                                                                                                                                            DB 7
                                                                                                                                                                                                                                                                                  Score 40; DB 7
Pred. No. 96;
2; Mismatches
                                                                             Example 3; SEQ ID NO 223; 169pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADM72638 standard; protein; 238 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amino acid sequence of ZFD of K2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kim Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-SEP-2002; 2002US-0408862P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-SEP-2003; 2003WO-KR001827
                                                                                                                                                                                                                                                                                  52.6%;
                                                                                                                                                                                                                                                                                                                                                                                                 212 VLRPILLRIHNSEQ 225
                                                                                                                                                                                                                                                                                                                                                               2 VLRP--SRVHNSEE 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                         9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-248440/23
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                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                 Sequence 238 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-JUN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADM72638;
                                                                                                                                                                                                              domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kim J,
                                                                                                                                                                                                                                                                                                         Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 57
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                                                                                                                                                                                                                                                                                                     New modified cell comprising a heterologous nucleic acid encoding an artificial transcription factor that confers stress resistance, useful for altering a phenotypic trait of a cell or organism.
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                                                                                                                                                                                                            Lee Y;
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96;
                                                                                                                                                                                                              Yang H,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                            H, Lee S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lee S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                 Example 3; SEQ ID NO 224; 169pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 40;
Pred. No. 9
                                                                                                                                                                                                                Lee
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                                                                                                                                                                                                              Seol
                                                                         07-DEC-2001; 2001US-0338441P.
26-APR-2002; 2002US-0376053P.
02-AUG-2002; 2002US-0400904P.
05-AUG-2002; 2002US-0401089P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-DEC-2001; 2001US-033841P.
26-APR-2002; 2002US-0376053P.
02-AUG-2002; 2002US-0400904P.
                                        07-DEC-2002; 2002WO-KR002309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64.3%;
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212 VLRPILLRIHNSEQ 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Conservative
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                                                                                                                                                                                                              Park K, Lee
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                                                                                                                                                                                                                                                                  WPI; 2003-513760/48.
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                                                                                                                                                                         (TOOL-) TOOLGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TOOL-) TOOLGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 238 AA;
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     12-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                            Kim J,
Jang Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     domains.
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Jang Y;
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ADL33683

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Gaps

.. 7

Length 238; 1; Indels

8

DB 6

Score 40; Pred. No.

52.6%;

Query Match
Best Local Similarity 64.3
Matches 9; Conservative

2; Mismatches

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8

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RESULT 59
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ID ADM7
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                                                                                                                                                                                                                                                                                                                    1;
domain is a naturally occurring zinc finger domain. The first zinc finger domain is a mammalian zinc finger domain. Each cell of several cells is an animal or human cell. The method is useful for evaluating several cellular genes. Sequences ADM72637-ADM72647 represents the amino acid sequences of zinc finger domains (ZFD) of K1 to K11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Evaluating cellular genes by expressing nucleic acid encoding different artificial, chimeric transcription factor in cells and identifying set of
                                                                                                                                                                                                                                                                                                                 Gaps
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7
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                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                        Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genes altered by transcription factors.
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                                                                                                                                                                                                                                                        52.6%;
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212 VLRPILLRIHNSEQ 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                     Query Match
Best Local Similarity
9; Conserve
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                                                                                                                                                                                           Sequence 238 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 58
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ZFP; zinc finger protein; gene evaluation; transcription factor; zinc finger domain; zinc finger domain; ZFD.

X 4

Amino acid sequence of ZFD of

(first entry

03-JUN-2004

ADM72640;

ADM72640 standard; protein; 238 AA

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involves providing several calls containing nucleic acid encoding different artificial, chimeric transcription factor, expressing nucleic acides in cells to acides in cells to acides in cells evaluating expression of several genes in cells to provide expression information and identifying from expression cells to information, a set of two or more genes whose expression is altered by first and second transcription factors. The nucleic acids encoding the different artificial, chimeric transcription factors comprise a preselected set of nucleic acids, where each member of the preselected in the can alter a cellular phenotype. Each artificial, chimeric transcription factor comprises a first zinc finger domain, and further comprises a second and third zinc finger domains. The first zinc finger domain is a naturally occurring zinc finger domain. The first zinc finger domain is a mammalian zinc finger domain. Bach cell of several cells is an animal or human cell. The method is useful for evaluating several.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention relates to evaluating several cellular genes. The method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cellular genes. Sequences ADM72637-ADM72647 represents the amino acid sequences of zinc finger domains (ZFD) of K1 to K11.
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7
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Pred. No. 96;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; SEQ ID NO 12; 124pp; English
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Best Local Similarity
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Matches
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comprises a second and third zinc finger domains. The first zinc finger domain is a naturally occurring zinc finger domain. The first zinc finger domain is a mammalian zinc finger domain. Each cell of several cells is

an animal or human cell. The method is useful for evaluating several cellular genes. Sequences ADM72637-ADM72647 represents the amino acid sequences of zinc finger domains (ZFD) of K1 to K11.

Sequence 238 AA;

Evaluating cellular genes by expressing nucleic acid encoding different artificial, chimeric transcription factor in cells and identifying set of genes altered by transcription factors.

Kim Y;

Park J,

Lee D,

Kim J,

WPI; 2004-248440/23.

05-SEP-2002; 2002US-0408862P.

(TOOL-) TOOLGEN INC.

05-SEP-2003; 2003WO-KR001827.

WO2004022575-A2.

18-MAR-2004.

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212 VLRPILLRIHNSEQ 225

ADR10155; RESULT 60 ADR10155 ID ADR: 

ADR10155 standard; protein; 310 AA.

(first entry)

04-NOV-2004

Human protein useful for treating neurological disease Seq 3661.

human; oligo-capping method; diagnostic marker; gene therapy; osteoporosis; neurological disease; Alzheimer's disease; Parkinson's disease; dementia; short memory; cancer; sense or motor function; emotional reaction; fear response; panic; osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic; tranquiliser.

Homo sapiens.

EP1447413-A2.

18-AUG-2004.

12-FEB-2004; 2004EP-00003145.

14-FEB-2003; 2003JP-00102207. 09-MAY-2003; 2003JP-00131452.

(REAS-) RES ASSOC BIOTECHNOLOGY.

Sugiyama T, Nishikawa T, Isono Y, Nagai K, Irie R;

Otsuki T;

Isogai T, Yamamoto J, Wakamatsu A, Ishii S,

WPI; 2004-583265/57.

N-PSDB; ADR08199

New 1995 cDNA, useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.

Claim 1; SEQ ID NO 3661; 2686pp; English.

This invention relates to novel, isolated full length human cDNA molecules and the encoded proteins thereof. Specifically, it refers to conditions obtained by an oligo-capping method, where none of these clones are identical to any known human mankas. The present invention describes an immunoassay to identify agonists and antagonists, as well as antibodies, antisense molecules and siRNAs that can all be used to bind to and modulate expression of the ODNA molecules. As such, these concludes are useful for diagnostic markers or therapeutic targets for molecules are useful for diagnostic markers or therapeutic targets for the various diseases or morbid states. In particular, they are useful in gene therapy for treating ostcoporosis, neurological disease, Alzheimer's disease, Parkinson's disease, dementia, short memory and various cancers, as well as for maintening equilibrium of sense or morbid cancers, for treating emotional reaction, fear response and panic. Accordingly, they exhibit ostcopathic, neuroprotective, nootropic, antiparkinsonian, excepted by a full length human cDNA sequence of the invention. NOTE: This sequence is not given in the sequence listing of the specification but to the obtained on CD-ROM from the European Patent Office, Vienna Sub-

Sequence 310 AA;

Gaps ö 52.6%; Score 40; DB 8; Length 310; 46.7%; Pred. No. 1.3e+02; tive 3; Mismatches 5; Indels Query Match
Best Local Similarity 46.7<sup>3</sup>
Matches 7; Conservative

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Search completed: March 11, 2006, 12:18:16 Job time : 161.132 secs

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GenCore version Copyright (c) 1993 - 2006 protein search, using sw model March 11, 2006, 12:19:28; Se	US-10-774-242A-1 76 I IVLRPSRVHNSEENT 15 BLOSUM62 Gapop 10.0 , Gapext 0.2 283416 seqs, 96216763 ; hits satisfying chosen length: 0 length: 0 length: 2000000000	num match in match in the second in the seco	Macch Length DB ID  100.0  55.9  56.9  57.9  57.9  57.0  57.
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glutamate synthase hypothetical prote TyB protein - yeas DNA-directed RNA p ploxin A - fruit f DNA-directed RNA p	RNA polymerase II hypothetical prote transcription fact SEC16 protein - ye hypothetical prote calcium channel pr hypothetical prote hypothetical prote	gp330 protein prec cyclosporin synthe regulatory protein hypothetical prote hypothetical prote hypothetical prote nitrogen permease hypothetical prote F4489.6 protein - ring-infected eryt	enamelin precureor DNA-directed RNA p protein kinase AKI hypothetical prote B cell surface ant ribosomal protein hypothetical prote ribosomal protein probable \$14 ribos
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## ALIGNMENTS

Isbaba Libroblast activation protein-alpha - human N;Alternate names: PAP-alpha C;Species: Homo sapiens (man) C;Date: 090-Mar-1996 #sequence\_revision 09-Mar-1996 #text\_change 29-Aug-1997 C;Accession: 138593 R;Scanlan, M.J.; Raj, B.; Calvo, B.; Garin-Chesa, P.; Sanz-Moncasi, M.P.; Healey, J.; Ol. Proc. Natl. Acad. Sci. US.A. 91, 5657-5661, 1994 A;Title: Molecular cloning of fibroblast activation protein alpha, a member of the serin. A;Reference number: 138593; MUID:94261645; PMID:7911242 A;Retus: preliminary A;Residues: 1-759 <RES> A;Cross-references: UNIPARC:UPI000017587D; EMBL:U09278; NID:9507749; PID:9507750 C;Genetics: A;Gene: GDB:RAP A;Cross-references: GDB:374184; OMIM:600403 A;Map position: 2423-2423 C;Superfamily: dipoptidy1-peptidase IV C;Keywords: transmembrane protein Query Match
100.0%; Score 76; DB 2; Length 759;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels RESULT 1 RESULT 2 g ò

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Gaps

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AD2031 hypothetical protein all1802 [imported] - Nostoc sp. (strain PCC 7120)

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Gaps

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A;Map position: 4
A;Introns: 51/2; 122/2; 170/3; 190/3; 250/3; 375/3; 422/3; 479/3; 565/3; 617/2; 795/2; 8
A;Note: T4F9.50
C;Superfamily: ubiquitin C-terminal hydrolase Ubp12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kin
C;Reymords: calcium binding; EF hand; phosphotransferase
F;487-519/Domain: calmodulin repeat homology <EFH>
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NyAlternate names: CAR80 protein; protein YD8142A.04c; protein YDR207c; transcription fa
C;Species: Saccharomyces cerevisiae
C;Date: 09-Mar-1996 #sequence revision 12-Apr-1996 #text_change 05-Oct-2004
S;Accession: S61570; S45175; F53420; S51874
R;Murphy, L; Harris, D.
Submitted to the EMBL Data Library, December 1995
A;Reference number: S61117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cross-references: UNIPROT:P39001; UNIPARC:UPI000005313A; EMBL:Z68194; NID:g1204148; PI
Experimental source: strain AB972
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A;Residues: 1-100,'G',102-836 <KUM>
A;Cross-references: UNIPARC:UP10000168D23; EMBL:D23663; NID:g432373; PIDN:BAA04890.1; P<sup>1</sup>
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R; Strich, R.; Surosky, R.T.; Steber, C.; Dubois, E.; Messenguy, F.; Esposito, R. Genes Dev. 8, 796-810, 1994
A; Title: UME6 is a key regulator of nitrogen repression and meiotic development. A; Reference number: A53420; MUID:95011581; PMID:7926768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Daucus carota (carrot)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cross-references: UNIPROT: P28582; UNIPARC: UPI0000127447; EMBL: X56599
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38;
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submitted to the EMBL Data Library, November 1993
A;Reference number: 845175
A;Accession: 845175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, January 1997
A, Reference number: 217988
A, Accession: T14335
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2; Mismatches
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Pred. No.
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Best Local Similarity 53.8
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666 PSKIHNGSEN 675
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C;Species: Nostoc sp. PCC 7120

A;Note: Nostoc sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C;Accession: AD2031

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001

A;Reference number: AB1807; MUD:21595285; PMID:11759840

A;Reference number: AB1807; MUD:21595285; PMID:11759840

A;Status: preliminary

A;Status: preliminary

A;Status: DN: NAPROT: O8YW14; UNIPARC: UPI00000CE1F8; GB:BA000019; PIDN:BAB73501.1;

A;Experimental source: strain PCC 7120

C;Genetics:

A;Gene: all1802

C;Superfamily: Na+-ATP synthase chain J
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26140
R;Kershaw, J
submitted to the EMBL Data Library, September 1999
A;Reference number: 220159
A;Reference number: 220159
A;Accession: T26140
A;Accession: T26140
A;Accession: T26140
A;Accession: U26140
A;Cession: T26140
A;Cession:
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A;Residues: 1-937 <BEV>
A;Cross-references: UNIPROT:O9TOB8; UNIPARC:UPI00000A40D1; EMBL:AL049523
A;Experimental source: cultivar Columbia; BAC clone T4F9
C;Genetics:
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Pred. No. 29;
5; Mismatches 2; Indels
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Pred. No.
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Best Local Similarity 46.2%;
Matches 6; Conservative
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Best Local Similarity 63.6%;
Matches 7; Conservative
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204 MFKPSKKHNNKEN 216
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430 RPTRIHYPEEN 440
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A,Residues: 522-917 «CHE»
A,Cross-references: UNIPARC:UPI000016DB96; EMBL:X13435; NID:g16403; PIDN:CAA31787.1; PID
A,Cross-references: UNIPARC:UPI000016DB96; EMBL:X13435; NID:g16403; PIDN:CAA31787.1; PID
A,Orde: the translation of the nucleotide sequence is not complete
C,Comment: This enzyme catalyzes the reduction of nitrate to nitrite in cytoplasm; each of comment: This enzyme catalyzes the reduction of nitrate of nitrate assimilation in plants, fungi, and bacteria.
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C; Complex: homodimer
C; Complex: homogimer
C; Complex: homodimer
C; City, Complex: homodimer
C; City, Complex: homodimer
C; City, City, Cys)
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Cispecies: Archaeoglobus
Richaei, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, F. Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, B.F.
Alchaei, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
Alchaeoglobus G.R.; Venter, J.C.
Smith, H.O.; Wosse, C.R.; Venter, J.C.
Smith, H.O.; Wosse, C.R.; Venter, J.C.
Alther The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeor
Alther number: A69250; WUID:98049343; PMID:9389475
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| IPLRPNAVHPITRENSGDNT 119
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Matches 5; Conservative
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A,Molecule type: DNA
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D133-11ke protein [imported] - Arabidopsis thaliana
D133-11ke protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Peb-2001 #sequence_revision 16-Peb-2001 #text_change 09-Jul-2004
C;Accession: D85068
R;anonymous, The Buropean Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin Nature 402, 769-777, 1999
A;Title: Sequence and analysis of Chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A65001; MUID:20083488; PMID:10617198
A;Accession: D8506B
A;Accession: D8506B
A;Accession: D8506B
A;Accession: J8506B
A;Accession: 
A;Cross-references: UNIPARC:UPI000005313A; EMBL:L24539; NID:g435117; PIDN:AAC14472.1; PIR:Smart, W.C.; Park, H.D.; Cooper, T.G.
Bibmitted to the EMBL Data Library, May 1994
A;Description: Sequence of the UME6/CAR80 gene from Saccharomyces cerevisiae.
A;Reference number: S51874
A;Reference number: S51874
A;Molecule type: DNA
A;Residues: 1-362, VV, 364-442, T', 444-464, D', 466-836 <SMA>
A;Cross-reference: UNIPARC:UPI000168841; EMBL:L32186; NID:g479018; PIDN:AAA34471.1; PIC:Genetics:
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A;Map position: 4
C;Superfamily: Saccharomyces cerevisiae hypothetical protein YLR215c
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Pred. No. 29;
1; Mismatches 1; Indels
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F;766-803/Domain: GAL4 zinc binuclear cluster homology <GAL4>
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77.8%;
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Best Local Similarity 77.8
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PNRVHNFEE 66
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A; Molecule type: mRNA
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F,93-98/Region: GTP binding #status predicted F,116-119/Region: GTP binding #status predicted F,250-253/Region: GTP binding #status predicted P,341-345/Region: GTP binding #status predicted
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207 MILRDYRIHNAE 218
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PSKIHNGSDN 654
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181 LVIRPSKVH 189
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Matches 6, Conserv
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Matches 6; Conserv
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A, Residues: 1-948 <DEV>
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C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 19-Mar.1997 Heaquence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S74287; S19337
R;Voct, M.; Volckaert, G.
submitted to the Protein Sequence Database, September 1996
A;Reference number: S74277
A;Recession: S74287
A;Molecule type: DNA
A;Redidues: 1-259 <VOR
A;Reference number: S74277
A;Recession: S19337
A;Reference number: S19337
A;Recession: S19
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                                        A;Cross-references: UNIPROT:084329; UNIPARC:UPI0000C0B30; GB:AE001305; GB:AE001273; NID A;Experimental source: serotype D, strain UM-3/Cx C;Genetics: A;Genetics: 
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A;Molecule type: DNA
A;Residues: 1-368 <HEB>
A;Cessidues: 1-368 <HEB>
A;Cessidues: U-368 <HEB>
A;Experimental source: UNIPROT:P53295; UNIPARC:UPI000013AF8C; EMBL:Z72958; NID:g1323305;
A;Experimental source: strain S288C
C;Genetics:
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N;Alternate names: hypothetical protein G7112; hypothetical protein YGR173w
C;Species: Saccharomyces cerevisiae
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C;Accession: S64487
R;Hebling, U: Hofmann, B.; Delius, H.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S64003
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Pred. No. 34;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                            50.0%; Score 38; DB 2; Length 62; 66.7%; Pred. No. 7.4;
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                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
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A, Map position: 3L
A, Note: YCL010c
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Best Local Similarity 66.7
Matches 6; Conservative
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16 RIHSDEENT 24
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Best Local Similarity
Matches 8; Conserv
                    <ARN>
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               A;Residues: 1-62
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C;Accession: T04192
R;Bevan, M.; Wedler, H.; Wedler, B.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.F submitted to the Protein Sequence Database, March 1999
A;Reference number: Z15260
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A,Experimental source: strain 972h-; cosmid c17A5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Introns: 51/2; 122/2; 161/3; 181/3; 214/3; 328/1; 401/3; 458/3; 544/3; 596/2; 774/2;
A;Noce: T4F9.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable peroxin-6, AAA family atpase - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
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A;Residues: 1-928 «ABL».
A;Cross-references: UNIPROT:Q9TOB6; UNIPARC:UPI00000A4AD0; EMBL:AL049523
A;Experimental source: cultivar Columbia; BAC clone T4F9
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R;Devlin, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, submitted to the EMBL Data Library, August 1997
A;Reference number: 221737
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Length 368;
                                                  Indels
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Pred. No. 1.3e+02;
3; Mismatches 2;
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DB 1;
49;
                                                                                                                                                                                                                                                                                   hypothetical protein T4F9.30 - Arabidopsis thaliana
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Score 38; DB
Pred. No. 49;
4; Mismatches
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50.0%;
50.0%;
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Gaps

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Cispecies: Trabidopsis thaliana (mouse-ear cress)
Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cipate: Preb-1999 #sequence_revision 19-Feb-1999 #text_change 09-Jul-2004
Cipate: Tolsio
RiJohnson, A.F.; de la Bastide, M.; Lodhi, M.; Hoffman, J.; Hasegawa, A.; Gnoj, L.; Gotte Martienssen, R.; McCombie, W.
Antienssen, R.; McCombie, W.
A.; Description: The sequence of the Arabidopsis thaliana T10M13 BAC.
A; Reference number: Z14346
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A;Molecule type: DNA
A;Residues: 1-202 <JOH>
A;Residues: 1-202 <JOH>
A;Residues: UNIPROT:004712; UNIPARC:UPI00000C58F; EMBL:AF001308; NID:g2104523; EA;Experimental source: cultivar Columbia
C;Genetics:
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A;Residues: 1-272 <MUR>
A;Cross-references: UNIPROT:Q12331; UNIPARC:UPI00006B0A5; EMBL:Z68290; NID:g1134887; PI)
A;Experimental source: strain AB972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable membrane protein YDR265w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YD9320B.01
C;Species: Saccharomyces cerevisiae
C;Date: 23-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: Saccharomyces cerevisiae probable membrane protein YDR262w C;Keywords: transmembrane protein F;1-17/Domain: transmembrane #status predicted <TMM>
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                                                                                Length 128;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
C;Superfamily: streptokinase
C;Keywords: hydrolase; plasminogen activator; virulence
                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein T10M13.10 - Arabidopsis thaliana
                                                                                   DB 2;
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R; Murphy, L.; Harris, D.
submitted to the EMBL Data Library, December 1995
A; Reference number: S61117
A; Accession: S61117
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Pred. No. 40;
1; Mismatches
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submitted to the EMBL Data Library, March 1996
A;Reference number: S67454
                                                                                Score 37;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 53.3%;
Matches 8; Conservative
                                                                                   48.7%;
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                                                                                      Query Match
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                         7 RPKAVHNSAE 16
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Best Local Similarity
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A;Residues: 1-272 <MUW>
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                                      probable secreted protein PFB0675w - malaria parasite (Plasmodium falciparum)
C.Species: Plasmodium falciparum
C.Species: 13-Nov-1998 #text_change 09-Jul-2004
C.Accession: A71609
C.Accession: A71609
R.Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O. Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum. A;Reference number: A71609
A;Reference number: A71609
A;Reference number: A71609
A;Residues: 1-1278 <GAR>
A;Residues: 1-1278 <GAR>
A;Cesssrereferences: UNIPROT:096228; UNIPARC:UPI0000178630; GB:AE001410; GB:AE001362; NIC C;Genetics: PFB0675%
A;Genetics: PFB0675w
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Cispecies: Streptococcus pyogenes
Cispecies: Streptococcus pyogenes
Cispecies: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
Cispecies at 77673
Rikapur, V.; Kanjilal, S.; Hamrick, M.R.; Li, L.L.; Whittam, T.S.; Sawyer, S.A.; Musser, Mol. Microbiol. 16, 509-519, 1995
A; Title: Molecular population genetic analysis of the streptokinase gene of Streptococcut A; Reference number: 877671; MUID:96037795; PMID:7565111
A; Accession: 877673
A; Status: translation not shown
A; Residues: 1-128 «KAP»
A; Residues: 1-128 «KAP»
A; Residues: 1-128 «KAP»
A; Residues: UNIPROT:Q54680; UNIPARC:UPI00000B5A01; EMBL:U25855; NID:9818912; PIE
C; Genetics:
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finger protein zfas8 - mouse (fragment)

(;Species: Mus musculus (house mouse)

C;Date: 28-way-1992 #sequence_revision 28-May-1992 #text_change 09-Jul-2004

C;Accession: D40984

R;Crossley, P.H.; Little, P.F.R.

A;Tritle: A cluster of related zinc finger protein genes is deleted in the mouse embryoni

A;Reference number: A40984; MUID:91376058; PMID:1680234

A;Accession: D40984
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A;Residues: 1-39 <CRO>
A;Cross-references: UNIPROT:Q9Z117; UNIPARC:UPI000017C663; GB:M74237
C;Keywords: DNA binding; zinc finger
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llarity 58.3%; Pred. No. 6.9;
Conservative 1; Mismatches
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22 RHQRVHTGEKNT 33
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267 TRTHNDEDNT 276
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Best Local Similarity
Matches 6; Conserva
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Matches 7; Conserve
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Gaps

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A;Cross-references: UNIPROT:Q9JWD3; UNIPARC:UDI00000C4986; GB:AL162753; GB:AL157959; NID
A;Experimental source: serogroup A, strain Z2491
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C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46226; S32501
R;Yamada, Y; Relsine, T.; Law, S.F.; Ihara, Y.; Kubota, A.; Kagimoto, S.; Seino, M.; Sr Mol. Endocrinol. 6, 2136-2142, 1992
Mol. Endocrinol. 6, 2136-2142, 1992
A;Title: Somatogratin receptors, an expanding gene family: cloning and functional charactal A;Reference number: A46226; MUID:93149123; PMID:1337145
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A;Residues: 1-418 <YAM.
A;Residues: 1-418 <YAM.
A;Cross-references: UNIPROT:P32745; UNIPARC:UPI000050435; GB:M96738; NID:g338498; PIDN
A;Cross-reference extracted from NCBI backbone (NCBIN:123665, NCBIP:123690)
A;Note: squence extracted from NCBI backbone (NCBIN:123665, NCBIP:123690)
R;Corness, J.D.; Demchyshyn, L.L.; Seeman, P.; van Tol, H.H.M.; Srikant, C.B.; Kent, G., FEBS Lett. 321, 279-284, 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Cross-references: UNIPROT:045146; UNIPARC:UP10000079E38; EMBL:AF047653; PIDN:AAC04459
A,Experimental source: strain Bristol N2; clone W02F12
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C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T32994
R;Du, Z.; Gattung, S.; Andrews, S.
submitted to the EMBL Data Library, February 1998
A;Description: The sequence of C. elegans cosmid W02F12.
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Reference number: A81775; MUID:20222556; PMID:10761919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein W02F12.3 - Caenorhabditis elegans
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Molecule type: DNA
Residues: 1-388 <DUZ>
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Pred. No. 79;
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70.0%;
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Similarity 54.5%;
6; Conservative 2
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Matches 7; Conservative
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A;Introns: 27/2; 118/3; 345/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167 RPCRLHNLRON 177
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Best Local Similarity
Matches 6; Conserv
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A;Residues: 1-418 <COR>
                                                                                       A;Molecule type: DNA
A;Residues: 1-375 <PAR>
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                                                                   Status: preliminary
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A;Gene: NMA0432
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C;Species: Pseudomonas syringae pv. glycinea
C;Species: Pseudomonas syringae pv. glycinea
C;Species: Dalabeck, D.; Staskawicz, B.; Keen, N.T.
J. Bacteriol. 170, 4846-4854, 1988
J. Bacteriol. 170, 4846-4854, 1988
J. A;Title: Characterization and expression of two avirulence genes cloned from Pseudomonas
A;Reference number: A41649; MUD:89008107; PMID:3049552
A;Accession: B43649
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-35 < TAM>
A;Residues: 1-35 < TAM>
A;Cross-references: UNIPROT:P13836; UNIPARC:UPI0000126683; GB:M22219; NID:g151052; PIDN:C;Superfamily: avirulence protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-101 -WIL>
A;Cross-references: UNIPROT:Q21274; UNIPARC:UPI0000079E5F; EMBL:Z71181; PIDN:CAA94895.1;
A;Experimental source: clone K07C5
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Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491.
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                                                                                                                                                                                                                                                     hypothetical protein KO7CS.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 05-Oct-2004
C;Accession: T23403
R;McMurray, A.
Submitted to the EMBL Data Library, April 1996
A;Reference number: Z19737
A;Accession: T23403
A;Stetus: preliminary; translated from GB/EMBL/DDBJ
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Pred. No. 72;
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              2; Indels
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                 Mismatches
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Pred. No.
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A;Introns: 68/3; 112/2; 152/1; 268/3
C;Superfamily: Aldehyde reductase
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Similarity 54.5%;
6; Conservative 3
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Best Local Similarity 53.8%;
Matches 7; Conservative
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259 PSRIHDNLHNT 269
                 6; Conservative
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52 PPRLHNSQVNS 62
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Best Local Similarity
Matches 6; Conserv
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A;Accession: G65076
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-492 <BLAT>
A;Cross-references: UNIPARC.: UNIPARC: UPI000013B07C; GB:AE000375; GB:U00096; NID:gl:A;Experimental source: Btrain K-12; substrain MG1655
C;Superfamily: acetyl-CoA hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Escherichia coli
C;Dates: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Dates: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.,
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DAR Res 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genor
A;Reference number: A99629; MUID:21156231; PMID:11258796
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R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew RiPerna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
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A;Residues: 1-492 <STO>
A;Cross-references: UNIPROT:Q8XD13; UNIPARC:UPI00000D01EF; GB:AE005174; NID:g12517452; P
A;Experimental source: strain O157:H7, substrain EDL933
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A;Cross-references: UNIPROT:Q8XD13; UNIPARC:UP100000D03EF; GB:BA000007; PIDN:BAB37213.1;
A;Experimental source: strain O157:H7, substrain RIMD 0509952
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C.Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
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1e+02;
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53.8%; Pred. No. 1e+02;
iive 2; Mismatches
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Pred. No. 1e+02;
2; Mismatches
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                                                                                                                                                                                                                                                                                                              Score 37;
Pred. No.
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C,Superfamily: acetyl-CoA hydrolase
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C, Superfamily: acetyl-CoA hydrolase
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53.88;
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Best Local Similarity 53.8%;
Matches 7; Conservative
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nes 7; Conserv
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A;Status: preliminary
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C; Species: Halobacterium Sp. NRC-1
C; Species: Halobacterium Sp. NRC-1
C; Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C; Accession: Halobacterium Sp. NRC-1
R; Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S. Jung, W.V.; Kennedy, S.P.; Mahairas, T.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablc Jung, K.H.; Alam, M.; Freitas, T. Jung, W.O.; Hough, D.W.; Maddocks, D.G.; Jablc Jung, K.H.; Alam, M.; Freitas, T. Jung, Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A; Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li, A; Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li, A; Accession: H84379
A; Accession: H84379
A; Residues: 1-491 <STO>
A; Residues: 1-491 <STO>
A; Conetics:
C; Genetics:
C; Genetics:
A; Genetics:
A; Gene: cat
C; Superfamily: acetyl-CoA hydrolase
                                                                                                                                                                  A,Map position: 22q13.1-2q13.1
A,IMap position: 22q13.1-2q13.1
A,IMatorons: #status absent
C,iMaywords: G procein-coupled receptor; glycoprotein; phosphoprotein; transmembrane predicted <TM1>
F,44-70/Domain: transmembrane #status predicted <TM2>
F,41-106/Domain: transmembrane #status predicted <TM3>
F,18-139/Domain: transmembrane #status predicted <TM4>
F,18-139/Domain: transmembrane #status predicted <TM4>
F,18-213/Domain: transmembrane #status predicted <TM4>
F,203-213/Domain: transmembrane #status predicted <TM6>
F,28-116/Domain: transmembrane #status predicted <TM7>
F,28-116/Domain: transmembrane #status predicted <TM6>
F,28-116/Domain: transmembrane #status predicted <TM7)
F,21/Anding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predic F,256/Binding site: phosphate (Thr) (covalent) (by protein kinase) #status predicted F,126/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted F,126/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted F,126/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted F,126/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted F,126/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted F,126/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted F,126/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted F,126/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted F,126/Binding site: phosphate (Thr) (covalent) (covalent) (covalent) (covalent) (covalent) (covalent) (cov
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C;Species: Escherichia coli
C;Species: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C;Accession: G6507 #nukett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; (A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
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48.7%; Score 37; DB 2; Length 418;
Best Local Similarity 53.3%; Pred. No. 86;
Matches 8; Conservative 3; Mismatches 4; Indels
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                                                                                                                                       A; Cross-references: GDB:134187; OMIM:182453
A;Cross-references: UNIPARC:UP1000050435
C;Genetics:
A;Gene: GDB:SSTR3
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Best Local Similarity 63.6
Local 7, Conservative
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338 VVLRPSNVSNA 348
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Riin, X.; Kaul S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L., euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Anture 402, 761-768, 1995
A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A; Reference number: A84420; MUID:20083487; PMID:10617197
A; Accession: B84802
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-732 <5TO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: UNIPROT: Q9SKE1; UNIPARC: UPI00000AB79C; GB: AE002093; NID: 94559381; PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species Yersinia pestis
C;Date: 02-Nov-2001 #text_change 05-Oct-2004
C;Accession: AC0403
A;Fillingworth, T; Cronin, A; Davies, R.M; Davis, P; Dougan, G; Il, M; Rutherford, K.; Simmonds, M.; Skelton, J; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cross-references: UNIPROT: Q9X6B0; UNIPARC: UPI0000127086; GB: AL590842; PIDN: CAC92551.1;
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C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T31994
                                                                                                    nypothetical protein At2g46380 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Peb-2001 #sequence_revision 02-Peb-2001 #text_change 09-Jul-2004
C;Accession: B84902
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 737;
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Pred. No. 1.6e+02;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Henkhaus, J.; Wohldmann, P.; Beck, C.
submitted to the EMBL Data Library, July 1997
A;Description: The sequence of C. elegans cosmid C49D10.
A;Reference number: Z21108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein C49D10.1 - Caenorhabditis elegans
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Pred. No. 1.6e+02;
3; Mismatches 2;
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54.5%;
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Best Local Similarity 58.3
Matches 7; Conservative
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LSPLRLHNIESN 51
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C,Superfamily: Catalase HPI
C,Keywords: oxidoreductase
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary A;Molecule type: DNA
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A,Map position: 2
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                                                                                                                                                                                                                                                              Listing process that Allege and the control of the 
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A. A. Reference number: Z21934
A. A. Reference number: Z21934
A. A. Reference number: Z21934
A. A. Residue: T40530
A. Status: preliminary; translated from GB/EMBL/DDBJ
A. Molecule type: DNA
A. Residues: 1-40. A. 42-544 < LXN>
A. Cross-references: UNIPARC: UP10000129903; EMBL: AL023634; PIDN: CAA19180.1; GSPDB: GN00067
A. Experimental source: strain 972h-; cosmid c530
C. Genetics:
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A; Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A; Reference number: AD3252; PMID:11756688
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A; Molecule type: DNA
A; Residues: 1-584 «KUR»
A; Cross-references: UNIPROT: Q8YD77; UNIPARC: UPI000005841B; GB: AE008918; PIDN: AAL53542.1;
A; Experimental source: strain 16M
C; Genetics:
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A;Map position: II
C;Superfamily: Bacillus subtilis probable ABC transporter yufO; ATP-binding cassette hom
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                                                                                                                                                                                                                            disl-suppressing protein kinase dsk1 - fission yeast (Schizosaccharomyces pombe)
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C,Superfamily: Protein kinase, CLK type; protein kinase homology
C,Keywords: serine/threonine-specific protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

48.7%; Score 37; DB 2; Length 544;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
Matches 8; Conservative 2; Mismatches 5; Indels
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Pred. No. 1.2e+02;
0; Mismatches 2; Indels
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Best Local Similarity 77.8%;
Matches 7; Conservative 0
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330 IVLRPQEISNNPE 342
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S gene family receptor
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C;Superfamily: S-locus receptor-like kinase SRK; protein kinase homology; S-locus-specifi
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase; signal tra:
F;32-427/Domain: S-locus-specific glycoprotein homology <SSG>
F;520-804/Domain: protein kinase homology <KIN>
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o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
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A;Molecule type: DNA
A;Residues: 1-196 «KAN»
A;Cross-references: UNIPROT: P72891; UNIPARC:UPI00000C0C38; EMBL:D90901; GB:AB001339; NID
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
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C:Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein; pyridoxal phosphate F;667/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor-like kinase (EC 2.7.1.-) SFR2 - wild cabbage
C;Species: Brassica oleracea (wild cabbage)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 31-Dec-2004
C;Accession: T14470; T14445
R;Pastuglia, M.; Roby, D.; Dumas, C.; Cock, J.M.
A;Title: Rapid induction by wounding and bacterial infection of an S gene fa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
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                                                                                                    Score 37; DB 2; Length 821;
Pred. No. 1.8e+02;
1; Mismatches 5; Indels
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rolecule type: DNA
A;Rosidues: 1-23,'S',25-622,'V',624-847 <STA>
A;Cross-references: UNIPARC:UDI00000A2F9E; EMBL:Y12530
A;Experimental source: strain S29
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Local Similarity 50.0%; Pred. No. 1.8e+02;
Ne 7; Conservative 3; Mismatches 4;
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A;Molecule type: mRNA
A;Residues: 1-847 <PAS>
                                                                                                    Query Match
Best Local Similarity 57.1%;
Matches 8; Conservative
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C;Species: Haemophilus influenzae
C;Species: Haemophilus influenzae
C;Species: Haemophilus influenzae
C;Species: B-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C;Accession: D64119
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A;Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: D64119
A;Status: nucleic acid sequence not shown; translation not shown
A;Accession: D64119
A;Status: acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-81 acids
A;Cross-references: UNIPROT:P45180; UNIPARC:UP10000131A14; GB:U32815; GB:L42023; NID:915
C;Superfamily: glucan phosphorylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: ADL2
A;Map position: 4
A;Map position: 4
A;Introns: 138/3; 233/1; 242/3; 276/3; 299/3; 319/3; 357/3; 374/1; 410/3; 441/3; 472/3;
A;Introns: 138/3; 233/1; 242/3; 276/3; 299/3; 319/3; 357/3; 374/1; 410/3; 441/3; 472/3;
A;Note: 116L1.140
C;Superfamily: dynamin-related protein VPS1
C;Keywords: P-loop; purine nucleotide binding
F;66-73/Region: nucleotide-binding motif A (P-loop)
F;168-173/Region: nucleotide-binding motif B
                                                                                                                                             A;Cross-references: UNIPROT:O16610; UNIPARC:UP1000007F7DE; EMBL:AF016665; PIDN:AAC71186.
A;Experimental source: strain Bristol N2; clone C49D10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dynamin-like protein ADD2 - Arabidopsis thaliana
dynamin-like protein ADD2 - Arabidopsis thaliana
dynamin-like protein T16L1.140
C;Alternate names: protein T16L1.140
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: T04982
R;Bevan, M; Obermaier, B.; Deutschenbaur, S.; Piravandi, E.; Hoheisel, J.; Mewes, H.W.
submitted to the Protein Sequence Database, November 1998
A;Reference number: Z15393
A;Accession: T04982
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A;Residues: 1-808 <BEV>
A;Residues: 1-808 <BEV>
A;Croser references: UNIPROT:081882; UNIPARC:UPI000009DDF4; EMBL:AL031394
A;Experimental source: cultivar Columbia; BAC clone T16L1
C;Genetics:
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48.7%; Score 37; DB 1; Length 808;
Best Local Similarity 50.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                     Length 758;
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Pred. No. 1.6e+02;
2; Mismatches 2;
                    A;Accession: T31994
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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nes 7; Conserv
                                                                                                                         A; Residues: 1-758 <HEN>
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A;Map position: 2
A;Introns: 438/2
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Best Local $
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D64119
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CjAccession: D97280
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, T. Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo A;Reference number: A96900; MUID:21359325, PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: UNIPROT: 097R96; UNIPARC: UPI0000051642; GB: AE005672; PIDN: AAK75053.1;
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R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; E
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; P
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; P
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R., A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rifettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E. Science 293, 498-506, 2001
Apauthors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae. A;Reference number: A95000; WUID:21357209; PMID:11463916
                                                                                                                                                                                                                                                                                                                                                                            GB:AE001437; PIDN:AAK81031.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Gene: CAC3091
C,Superfamily: iron-dependent tartrate dehydratase alpha chain; iron-dependent tartrate
        chain A (N-terminal domain of FumA E.coli) class I [imported]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - Streptococcus pneumoniae (strain TIGR4)
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CiDate: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Accession: D95107
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;pate: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
                                        C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
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A;Molecule type: DWA
A;Residues: 1-282 «KUR»
A;Cross.references: UNIPROT: Q97EL9; UNIPARC: UPI00000CA71C;
A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Superfamily: conserved hypothetical protein HI0176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 36; DB 2;
Pred. No. 86;
3; Mismatches
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Pred. No. 90;
3; Mismatches
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50.0%;
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209 LIRPIDVHNEDE 220
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Best Local Similarity
7; Conserva
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Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C;Accession: T49580
R;Schulet, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, May 2000
A;Reference number: Z2502
A;Accession: T49580
A;Accession: T49580
A;Residues: preliminary
A;Molecule type: DNA
A;Residues: 1-220 <SCH>A;Residues: 1-220 <SCH>A;CHAPARC:UPI00001265EB; EMBL:AL355930; GSPDB:GN00116;
A;Experimental source: BAC clone B208; strain OR74A
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                          probable oligomycin sensitivity conferring protein (ATP5) [imported] - Neurospora crassa N;Alternate names: protein B208.280 C;Species: Neurospora crassa C;Species: Neurospora crassa C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
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Pred. No. 82;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 220;
                                                          Length 196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                              Indels
C; Superfamily: uncharacterized conserved protein sll1186
                                                          5
                                                       47.4%; Score 36; DB
40.0%; Pred. No. 58;
ive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 66;
4; Mismatches
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Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47.4%;
77.8%;
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49 IVMSPSKAHEKAKST 63
                                                                                                                                                                      1 IVLRPSRVHNSEENT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :|||:|| |:: |
7 LLRPARVLNTQVRT 20
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Best Local Similarity 77.0
Tr.0
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                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: NCSP:B208.280
A;Map position: 6
A;Introns: 48/3; 152/3; 183/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135 IVLRPSQFH 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 IVLRPSRVH 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 7; Conserv
                                                       Query Match
Best Local Similarity
Matches 6; Conserv
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A;Molecule type: DNA
A;Residues: 1-269 <HEI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Accession: D82060
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6 RESULT us-10-774-242a-1.rpr

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A;Cross-references: UNIPARC:UPI00016F43B; GB:K01472; NID:g147463; PIDN:AAA24476.1; PID:gR:Hoover, T.A.; Roof, W.D.; Foltermann, K.F.; O'Donovan, G.A.; Bencini, D.A.; Wild, J.R. Proc. Natl. Acad. Sci. U.S.A. 80, 2462-2466, 1983
A;Title: Nucleotide sequence of the structural gene (pyrB) that encodes the catalytic poll A;Reference number: A21121; WUID:83195078; PMID:6302686
                                                                                                                                                                                                                                       A;Accession: A21121
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: UNIPARC:UPI0000172336; GB:V00323
R;Donahue, J.P.; Turnbough Jr., C.L.
B;Donahue, J.P.; Turnbough Jr., C.L.
A;Hitle: Chem. 265, 19091-19099, 1990
A;Title: Characterization of transcriptional initiation from promoters P-1 and P-2 of the A;Reference number: A36599; MUID:91035438; PMID:169940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPARC:UP1000016F43D; GB:M60508; NID:gl47469; PIDN:AAA24481.1; PID:gl87cross-references: UNIPARC:UP1000016F43D; GB:M60508; NID:gl47469; PIDN:AAA24481.1; PID:gl47cross-references: U.S.A. 80, 2467-2471, 1983
Proc. Natl. Acad. Sci. U.S.A. 80, 2467-2471, 1983
A;Title: Amino acid sequence of the catalytic subunit of aspartate transcarbamoylase from A;Reference number: A21120; MUID:83195079; PMID:6341995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein
A; Residues: 2-60, 0', 68-90, 'N', 92-129, 'N', 131-220, 'V', 222-256, 'D', 258-259, 'M', 'S,
A; Residues: 2-60, 0', 62-86, 0', 88-90, 'N', 92-129, 'N', 131-220, 'V', 222-256, 'D', 258-259, 'M', 'S,
A; Residues: 2-60, 0', 62-86, 0', 88-90, 'N', N',
B; References: UNIPARC: UD1000172337
B; Ref. H.; Honzatko, R.B.; Lipscomb, W.N.
A; Title: Structure of unligated aspartate carbamoyltransferase of Escherichia coli at 2.6 A; Reference number: A93993; MUID: 64448054; PMID: 6377306
A; Contents: annotation; X-ray crystallography, 2.6 angstroms; quaternary structure
A; Contents: annotation; X-ray crystallography, 2.6 angstroms; quaternary structure
B; Ref. S, 2105-2119, 1995
A; Title: Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1195, R, 197-311 <BUR>
A; Residues: 1195, R, 197-311 <BUR>
A; Cross-references: UNIPARC:UP1000016F6D0; EMBL:U14003; NID:g1263172; PIDN:AAA97142.1; PJ
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
C; Comment: The active enzyme contains two trimers of catalytic chains and three dimers of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: ornithine/aspartate carbamoyltransferase; aspartate/ornithine carbamoyltra
C;Keywords: heterododecamer; homohexamer; homotrimer; pyrimidine nucleotide biosynthesis.
F;8-305/Domain: aspartate/ornithine carbamoyltransferase homology <ACT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein pyrB [imported] - Bacherichia coli (atrain 0157:H7, substrain EDL93. C;Species: Escherichia coli C;Species: Escherichia coli C;Species: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Dec-2004 C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Dec-2004 C;Accession: G86122.

C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Dec-2004 C;Accession: G86122

Burland, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001

A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.

A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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A;Status: nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: S56314; MUID:95334362; PMID:7610040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 36; DB
Pred. No. 95;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 VLRPSRVHNSEEN 14
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A,Molecule type: DNA
A,Residues: 1-311 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        position: 97 min
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A, Residues: 1-18 < DON>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Accession: B36599
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R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc. A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A;Ttle: The complete genome sequence of Escherichia coli K-12.

A;Recession: H65236

A;Stetus: prellminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-311 < ABLAT>
A;Cession: H65236

A;Stetus: prellminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-311 < ABLAT>
A;Cross-references: UNIPROT: P00479; UNIPARC: UP10000111347; GB:AE000495; GB:U00096; NID:g
A;Cross-references: strain K-12, substrain M01655

R;Schachman, H.K.; Pauza, C.D.; Navre, M.; Karels, M.J.; Wu, L.; Yang, Y.R.
Proc. Natl. Acad. Sci. U.S.A. 81, 115-119; 1984
A;Reference number: A93985; MUID:84119419; PMID:6364131
A;Accession: A00561
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 43
E97160
probable pseudouridylate synthase, YLYB B. subtilis ortholog [imported] - Clostridium acciobable pseudouridylate synthase, YLYB B. subtilis ortholog [imported] - Clostridium acciobable pseudouridylicum
C;Species: Clostridium acetobutylicum
C;Species: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: E97160
R;Nolling, J.; Berton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Barteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: E97160
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-305 <RUR>
A;Cross-references: UNIPROT:Q97H99; UNIPARC:UPI00000CA400; GB:AE001437; PIDN:AAK80072.1;
A;Experimental source: Clostridium acetobutylicum ATCC824
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: F97975
A;Statuus: presiminary
A;Statuus: presiminary
A;Residues: 1-295 «KUR»
A;Residues: 1-295 «KUR»
A;Cross-references: UNIPROT:Q8DQ63; UNIPARC:UPI00000E3526; GB:AE007317; PIDN:AAK99634.1;
C;Genetics rlub
C;Superfamily: conserved hypothetical protein H10176
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C;Superfamily: conserved hypothetical protein H10176
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Pred. No. 94;
3; Mismatches
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Best Local Similarity 50.0%;
Matches 7; Conservative
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ilarity 50.0%;
Conservative
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Gaps

EMBL: L10990; NID: g156211; PID.

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Gaps

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Length 429

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Gaps

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Indels

Length 467;

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C;Superfamily: transcription factor unc-86; homeobox homology; POU domain homology C;Reywords: alternative splicing; DNA binding; homeobox; nucleus; transcription regulati F;234-304/Domain: POU domain homology <POU>
F;326-382/Domain: homeobox homology <HOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transcription factor unc-86, long splice form - Caenorhabditis elegans
NyAlternate names: C30A5.7 protein
C;Species: Caenorhabditis elegans
C;Species: Z8-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C;Accession: A30042; S44779
R;Finney, M.; Ruvkun, G.; Horvitz, H.R.
Cell 55, 757-76, 1988
A;Title: The C. elegans cell lineage and differentiation gene unc-86 encodes a protein w A;Reference number: A30042; MUID:89051866; PMID:2903797
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-C;Superfamily: transcription factor unc-86; homeobox homology; POU domain homology
K;Keywords: alternative splicing; DNA binding; homeobox; nucleus; transcription regulatz
F;272-342/Domain: POU domain homology <POU>
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                                                                               A;Cross-references: UNIPROT:P13528; UNIPARC:UPI000002B694;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, February 1993
A;Description: Sequence of the C. elegans cosmid C30A5.
A;Reference number: S44774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 36; DB 1; L
Pred. No. 1.5e+02;
3; Mismatches 4;
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46.2%; Pred. No. 1.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Intron8: 128/3; 253/3; 345/2; 382/2
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46.2%;
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LLRPSKISRGSEN 58
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Best Local Similarity
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A; Residues: 1-467 <FIN>
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Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-429 <AND>
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A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
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C;Species: Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Species: OS-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Oct-2004
C;Accession: T34873
R;Seeger, K.J.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, August 1999
A;Reference number: Z21560
A;Accession: T34873
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-392 <SEE>
A;Residues: 1-392 <SEE>
A;Residues: 1-392 <SEE>
A;Experimental source: strain A3(2)
A,Cross-references: UNIPARC:UPI00001659FA; GB:AE005174; NID:g12519253; PIDN:AAG59443.1;
A,Experimental source: strain 0157:H7, substrain EDL933
C,Genetics:
A,Gene: pyrs
C,Superfamily: ornithine/aspartate carbamoyltransferase; aspartate/ornithine carbamoylty
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53.8%; Pred. No. 95;
ive 3; Mismatches 3; Indels
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                                                                                                                                                                                                     2; Length 311;
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A;Gene: SCOEDB:SC3A3.08
C;Superfamily: ADP-ribosylglycohydrolase
                                                                                                                                                                                                         Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
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249 VLRASDLHNAKAN 261
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249 VLRASDLHNAKAN 261
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Best Local Similarity 53.8
Matches 7; Conservative
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281 RPSRLHAIEE 290
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A;Cross-references: UNIPROT:085872; UNIPARC:UPI000005C97C; EMBL:AF079317; NID:g3378261; I
C;Genetics:
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A;Residues: 1-620 <RIE>
A;Cross-references: UNIPROT:P53207; UNIPARC:UPI0000052FFB; EMBL:Z72798; NID:g1322975; PIII
A;Experimental source: strain S288C
C;Genetics: SGD:SNU71; MIPS:YGR013w
A;Genes: SGD:SNU71; MIPS:YGR013w
A;Genes: references: SGD:S0003245
A;Map position: 7R
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A;Molecule type: DNA
A;Molidus: 1-634 GMLA
A;Residuse: 1-634 GMLA
A;Cross-references: UNIPROT:046020; UNIPARC:UPI0000082CA1; EMBL:Z92822; PIDN:CAB07301.1;
A;Experimental source: clone ZK520
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N;Alternate names: hypothetical protein G4014
C;Species: Saccharomyces cerevisiae
C;Spate: 17-May-1996 #sequence_revision 17-May-1996 #text_change 09-Jul-2004
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C,Species: Caenorhabditis elegans
C,Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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A;Introns: 53/2; 75/2; 120/2; 187/1; 318/2; 341/1; 455/1; 530/3
                                                                                                                                                                                                                                                        47.4%; Score 36; DB 2; Length 595; 66.7%; Pred. No. 1.9e+02; tive 2; Mismatches 1; Indels
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S;Ritager, M.; Mueller-Auer, S.; Brueckner, M.; Schaefer, M.
submitred to the Protein Sequence Database, May 1996
A;Reference number: S64071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 36; DB 2;
Pred. No. 2e+02;
A,Accession: T31163
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Reaidues: 1-595 <ROM>
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47.4%; Score 36; DB 2;
Best Local Similarity 58.3%; Pred. No. 2e+02;
Matches 7; Conservative 2; Mismatches
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RjSteward, C.
submitted to the EMBL Data Library, March 1997
A;Reference number: 220434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              y Match
Local Similarity 62.5%;
hes 5; Conservative 3
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66 IHNSDQNT 73
                                                                                                                                                                                                                                                                                         Best_Local Similarity
Matches 6; Conserv
                                                                                                                                                                           A;Genome: plasmid pNL1
A;Note: orf347
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C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Accession: G75622
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, B.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma S; Saith, H.O.; Ventex, J.C.; Fraser, C.M.
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
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hypothetical protein orf347 - Sphingomonas aromaticivorans plasmid pNL1

hypothetical protein orf347 - Sphingomonas aromaticivorans plasmid pNL1

Species Sphingomonas aromaticivorans

C;Species Spin-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004

C;Accession: T31163

R;Romine, M.F.; Stillvell, L.C.; Wong, K.K.; Thurston, S.J.; Sisk, E.C.; Sensen, C.W.; G

B;Dandict to the EMBL Data Library, July 1998

A;Description: Complete sequence of a 184 kb catabolic plasmid from Sphingomonas aromati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: DNA
A;Reaidues: 1-578 «WHI>
A;Creaidues: references: UNIPROT:Q9RZS2; UNIPARC:UPI0000D3B45; GB:AE001826; NID:g6460827; PI
A;Experimental source: strain Rl
C;Genetics:
                                                  dihydroxy-acid dehydratase [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 05-Oct-2004 C;Accession: H97289 R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Baly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001 A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld A;Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:Q97EE3; UNIPARC:UP1000012D573; GB:AE001437; PIDN:AAK81107.1;
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Genetics:
A;Genetics:
C;Superfamily: Dihydroxy-acid dehydratase/phosphogluconate dehydratase
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Pred. No. 1.8e+02;
1; Mismatches 1; Indels
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Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 77.8
Matches 7; Conservative
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A,Map position: megaplasmid
A,Genome: plasmid
A,Note: plasmid MP1
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A Molecule type: DNA
A;Residues: 1-552 <KUR>
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R;Toda, T.; Niwa, H.; Nemoto, T.; Dhut, S.; Eddison, M.; Matsusaka, T.; Yanagida, M.; Hi J. Cell Sci. 109, 2331-2342, 1996
A;Title: The fission yeast sts5+ gene is required for maintenance of growth polarity and A;Reference number: Z22956; MUID:97041712; PMID:886983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Wolecule type: DNA
A;Residues: 1-1066 <TOD>
A;Cross.references: UNIPROT:074454; UNIPARC:UPI00001688DC; EMBL:D58421; NID:g2645172; PI
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1066 cPUR>
A;Cross=references: UNIPROT:074454; UNIPARC:UPI0000136150; EMBL:AL031535; PIDN:CAA20748.
A;Experimental source: strain 972h-; cosmid c16C4
                                                                                                            A;Map position: 3
A;Introns: 31/3; 74/2; 124/3; 161/2; 189/2; 205/3; 236/2; 278/3; 305/2; 757/1; 794/1
A;Note: F9K21.210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   growth polarity maintenance protein sts5 - fission yeast (Schizosaccharomyces pombe)
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C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Schizosaccharomyces pombe
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 09-Jul-2004
                 A;Cross-references: UNIPROT:Q9M1E4; UNIPARC:UP100000A8243; EMBL:AL138657
A;Experimental source: cultivar Columbia; BAC clone F9K21
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R;Purnelle, B.; Goffeau, A.; Wood, V.; Rajandream, M.A.; Barrell, B.G. Babmitted to the EMBL Data Library, September 1998
A;Reference number: Z21964
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Pred. No. 3.5e+02;
1; Mismatches 6;
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Pred. No. 3.5e+02;
1; Mismatches 6,
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Pred. No. 3.38+02;
                                                                                                                                                                                                                                                                              4; Mismatches
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Best Local Similarity 46.7%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                      1 IVLRPSRVHNSEENT 15
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C,Keywords: signal transduction
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Best Local Similarity
Matches 7; Conserva
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A;Residues: 1-989 <JOR>
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A; Status: preliminary
A; Coss. preliminary
A; Cross. references: UNIPROT: P43602; UNIPARC: UPI0000036C46; EMBL: D50617; NID: g936685; PIC
Genetics:
A; Cross. references: SGD: S0001918
A; Map position: 6R
A; Map position: 6R
C; Superfamily: Saccharomyces cerevisiae probable membrane protein YFR022w
C; Superfamily: Saccharomyces revisiae probable membrane protein
F; 382-398/ Domain: transmembrane #status predicted < TVM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Species: Saccharomyces cerevisiae
C; Species: Saccharomyces cerevisiae
C; Date: 02-Sep-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C; Accession: S56277
R; Murakami, Y:, Naitou, M.; Hagiwara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sasanu submitted to the EMBL Data Library, May 1995
A; Description: Analysis of the nucleotide sequence of chromosome VI from Saccaromyces ce
                                                                                                                                                                                                                                                                                                                                            A;Accession: T34573
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-691 <MUR>
A;Cross-references: UNIPROT:O54098; UNIPARC:UPI0000DABC8; EMBL:AL021529; PIDN:CAA16437.
C;Genetics:
C;Genetics:
A;Gene: SCOEDB:SC10A5.05
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A;Reference number: Z24467
A;Accession: T47503
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Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
                                                                                                                                       probable membrane protein - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C;Accession: T34573
S;Murphy, L; Harris, D; Parkhill, J; Barrell, B.G.; Rajandream, M.A.
Submitted to the EMBL Data Library, January 1998
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47.4%; Score 36; DB 2; Length 733;
Best Local Similarity 50.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 3; Mismatches 3: Indels
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Pred. No. 2.2e+02;
3; Mismatches 0; Indels
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Best Local Similarity 66.7
Matches 6; Conservative
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        LRLHRIRNSEDN 501
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512 MVRPSRVHS 520
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A, Molecule type: DNA

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A39578
SSD1 protein - yeast (Saccharomyces cerevisiae)
SSD1 protein - yeast (Saccharomyces cerevisiae)
SSD2 protein D9819.4; protein YDR293c; suppressor protein SRK1
C; Species: Saccharomyces cerevisiae
C; Date: 07-Feb-1992 #sequence_revision 07-Feb-1992 #text_change 09-Jul-2004
C; Date: 07-Feb-1992 #sequence_revision 07-Feb-1992 #text_change 09-Jul-2004
C; Accession: A39578; A40263; $70122; S14774; S16805
R; Sutton, A.; Immanuel, D.; Arndt, K.T.
Mol. Cell. Biol. 11, 2133-2148, 1991
A; Reference number: S14773; MUD:91172202; PMID:1848673
A; Reference number: S14773; MUD:91172202; PMID:1848673
A; Residues: 1-1250 <8UT>
A; Residues: 1-1250 <8UT>
A; Residues: 1-1250 <8UT>
A; Residues: UNIPROT:P24276; UNIPARC:UPI0000135FBA; GB:M60318; NID:9172611; PIDN: A; Title: The Saccharomyces cerevisiae SRK1 gene, a suppressor of bcyl and insl, may be in A; Reference number: A40263; MUID:91246207; PMID:1645449
A; Reference number: A40263; MUID:91246207; PMID:1645449
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A; Residues: 1-1550 < WIL:
A; Residues: 1-1550 < WIL:
A; Residues: 1-1550 < WIL:
A; Croser-references: UNIPARC: UPI0000135FBA; GB: M63004; NID: g172696; PIDN: AAA35089.1; PID:
B; Pubmitted to the EMBL Data Library, May 1996
A; Ap Bearciption: The sequence of S. cerevisiae cosmid 9819.
A; Reference number: S70114
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-1250 < FUL.
A; Croser-references: UNIPARC: UPI0000135FBA; EMBL: U51031; NID: g1332635; PID: g1230657; MIPS
C; Genetics:
A; Gene: SGD: SSD1; SRX1
A; Croser-references: SGD: S0002701; MIPS: YDR293C
A; Map position: 4R
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47.4%; Score 36; DB 2; Length 1250;
Best Local Similarity 53.8%; Pred. No. 4.2e+02;
Matches 7; Conservative 3; Mismatches 3; Indels
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Job time : 37.6842 secs
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561 LLRPSQQANSDNN 573
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bacteroides
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G68121 HUWAN

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073G36_WOLPM

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06FW28_CANGA

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10X12_FIG

07PLS7_POME

X.1024_WOUSE

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09CGA7_WOUSE

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2 O6GGC8 STAAR 2 O5HF18—STAAC 2 Q7A5C6_STAAN 2 Q99T54_STAAN 2 Q99T54_STAAN 2 Q6DX0_METCA 2 Q6DX0_METCA 2 Q6CAD9_METCA 2 Q6CAD9_METCA 2 Q6CAD9_METCA 2 Q6CAD9_METCA 2 Q6CAD9_METCA 3 Q6CAD9_METCA 4 Q6CAD9_BACT 4 MURB_FUSNN 5 Q6ESS8_STRA3 5 Q6ESS8_STRA3 5 Q6ESS8_STRA3 6 Q5CGC8_STRA3 6 Q5CGC8_STRA3 6 Q5CGC8_STRA3 6 Q6CGC8_STRA3 6 Q6CGC8_ST	SEPR HUMAN STANDARD; PRT; 760 AA. 0128FR HUMAN STANDARD; Geteled) 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last sequence update) 13-SEP-2005 (Rel. 48, Last annotation protein membrane serine protease) (170-kDa melanoma membrane- gelatinase).  Name-FAP; metazoa; Chordata; Craniata; Vertebrata; E Mammalia; Eutheria; Euarchontoglires; Primates; Catar Mammalia; Eutheria; Euarchontoglires; Primates; Catar NCBI_TaxID=9606; [1]  NUCLEOTIDE SEQUENCE (ISOFORM 1). 11SSUE=Fibroblast; MEDLINE=94261645; PubMed=7911242; MEDLINE=94261645; PubMed=7911242; MEDLINE=94261645; PubMed=7911242; MEDLINE=94261645; PubMed=7911242; MEDLINE=94261645; PubMed=7911242; MEDLINE=94261645; PubMed=7911242; MUCLEOTIDE SEQUENCE (ISOFORM 1), AND VARIANT THR-354. 12] Proc. Natl. Acad. Sci. U.S.A. 91:5657-5661(1994). 12] MUCLEOTIDE SEQUENCE (ISOFORM 1), AND VARIANT THR-354. 11SSUE=Melanoma; MOCLEOTIDE SEQUENCE (ISOFORM 1), AND PROTEIN SEQUENCE (ISOFORM 1), AN
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	STANDARD 10199; Q86229; 33 (Rel. 41, L. 15 (Rel. 44, L. 15 (Rel. 41, L. 16 (3.4.21) ( 16 (3.4.21) ( 16 (3.4.21) ( 17 (3.4.21) ( 18 SEQUENCE (IS 1261645; PubMeded, Rel. 16 (16 (16 (16 (16 (16 (16 (16 (16 (16
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Signal-anchor; Transmembrane
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13-SEP-2005 (TrEMBLrel. 31,
13-SEP-2005 (TrEMBLrel. 31,
Hypothetical protein FAP.
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Q53TP5;
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nes 15; Conservative
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WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altsuner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

D. Matchenco L., Marusina K.R., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahe S.S., Letteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smallus D.E.,

Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smallus D.E.,

Bronnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Bronnerch A.N. & Green E.D., Small Length human and manyer chan 15,000 full-length human and mouse chan a street of the stre
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MEDLINE=94327249; PubMed=7519584;

MEDLINE=94327249; PubMed=7519584;

MELLINE=94327249; PubMed=7519584;

Garin-Chesa P., Healey J.H., Old L.J.;

"Fibroblast activation protein: purification, epitope mapping and induction by growth factors.";

Int. J. Cancer 58:385-392(1994).

Int. J. Cancer 58:385-392(1994).

Int. J. Cancer 58:385-392(1994).

and wound healing, and may contribute to invasiveness in malignant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancers. CATALYTIC ACTIVITY: Degrades gelatin and heat-denatured type I and type IV collagen. but not native type I or type IV collagen. Does not cleave laminin, fibronectin, fibrin or caesin. SUBUNIT: Homodimer, or heterodimer with DPP4. The monomer is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INOCIONAL DESCRIPTION: In fibroblast specific.
-!- TISSUE SPECIFICITY: Fibroblast specific.
-!- INDUCTION: In fibroblasts at times and sites of tissue remodeling during development, tissue repair, and carcinogenesis.
-!- PTM: N-glycosylated.
-!- PTM: The N-terminus may be blocked.
-!- PTM: Belongs to the peptidase S9B family.
                                                                                                                                                                                                                                      Goldstein L.A., Chen W.-T.; "Identification of an alternatively spliced seprase mRNA that encodes a novel intracellular isoform.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Type II membrane protein. Found in cell surface lamellipodia, invadopodia and on shed vesicles. ALTERNATIVE PRODUCTS:
                                                                                               "Identification of the 170-kDa melanoma membrane-bound gelatinase (seprase) as a serine integral membrane protease.";
                                  MEDLINE=97218181; PubMed=9065413; DOI=10.1074/jbc.272.12.7595;
Pineiro-Sanchez M.L., Goldstein L.A., Dodt J., Howard L., Yeh Y.,
                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1), AND VARIANT
                                                                                                                                                                                                                    MEDLINE=20112818; PubMed=10644713; DOI=10.1074/jbc.275.4.2554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=1; Synonyms=L;
IsoId=012884-1; Sequence=Displayed;
Note=Major isoform;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=2; Synonyms=S, Truncated;
                                                                                                                                                                                                                                                                                           Biol. Chem. 275:2554-2559(2000).
                                                                                                                     (seprase) as a serine integral men
J. Biol. Chem. 272:7595-7601(1997)
                                                                                                                                                                              NUCLEOTIDE SEQUENCE (ISOFORM 2).
TISSUE=Melanoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and mouse cDNA sequences."
  461-472 AND 511-518.
                                                                                 Chen W.
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Signal-anchor for type II membrane protein (Potential).

Extracellular (Potential).

Charge relay system (By similarity).

N-linked (GLONAC...) (Potential).

N-linked (GLONAC...) (Potential).

N-linked (GLONAC...) (Potential).

N-linked (GLONAC...) (Potential).

Mishing (in isoform 2).

FridavSp 005367.
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InterPro; IPR001375; Peptidase S9.
InterPro; IPR001375; Peptidase S9.
InterPro; IPR001379; Ser estrs.
Pfam; PF0036; Peptidase S9. 1.
Pfam; PF0036; Peptidase S9; 1.
PROSITE; PS00708; PRO ENDOPPE SER; 1.
3D-structure; Alternative splicing; Direct protein sequencing; Glycoprotein; Hydrolase; Polymorphism; Protease; Serine protease;
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                                                                                                                                                                                                                                                                                                                                                                                                                    GO:0005887; C:integral to plasma membrane; TAS.
GO:0030027; C:lamellipodium; IDA.
GO:0005886; C:plasma membrane; NAS.
GO:0004274; F:dipoptidyl-peptidase IV activity; NAS.
GO:0004227; F:metalloendopeptidase activity; TAS.
GO:00042803; F:protein homodimerization activity; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /FTId=VAR_019691.
P -> A (in Ref. 2 and 5).
K -> T (in Ref. 2 and 5).
A0D34B4801BE07EA CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                 Ensembl; ENSG0000078098; Homo sapiens.
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                                                                                                                                                                                                                       EMBL; AF007822; AAF21600.1; -; mRNA.
EMBL; BC026250; AAH26250.1; -; mRNA.
PDB; 1268; X-ray; A=39-757, B=-.
MEROPS; S09.007; -.
                                                                                                                                                                         EMBL; U09278; AAB49652.1; -; mRNA
                                                                                                                                                                                                      EMBL; U76833; AAC51668.1; -; mRNA.
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761 AA.
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Pfam; PF00326; Peptidase S9; 1.
PROSITE; PS00708; PRO ENDOPEP_SER; 1.
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Interpro; IPR001375; PeptIdase_59.
Interpro; IPR002469; PeptIdase_599.
Interpro; IPR002469; PeptIdase_599.
Interpro; IPR00379; Ser_estrs.
Pfam; PF00930; DPPIV_N; I.
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Q8R492_RAT
ID Q8R492_RAT PRELIMINARY;
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Matches 11, Conservative
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                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                         TISSUE=Prostate;
                                                                                                                                                                                                                                                                                               NIH MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=Fap;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat)
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia, Eutheria, Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinee; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Wilson R.K.;
Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
REMBL, ACCONTSO; AAY2405-1;
GO; GO:0001824; F:catalytic activity; IEA.
GO; GO:0004274; F:dipptidyl-peptidase IV activity; IEA.
GO; GO:0004287; F:prolyl oligopetidiase activity; IEA.
GO; GO:0004287; F:prolyl oligopetidiase activity; IEA.
R InterPro; IPR001375; Peptidase_S9.
R InterPro; IPR001375; Peptidase_S9.
R InterPro; IPR001375; Peptidase_S9.
R Pfam: PF00930; DPPIV N; Prepress Pfam: PF00930; DPPIV N; PF00930; DPPIV 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 76; DB 2; Length 760; 100.0%; Pred. No. 8.1e-05; ive 0; Mismatches 0; Indels
                                                                            Cotton M., Maupin R., Hawkins M., Harkins R.;
"The sequence of Homo sapiens BAC clone RP11-576116.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                             to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                           to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        n; Transmembrane.
7FF817B5A4F75142 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         350 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical proteIn;
760 AA; 87713 MW; 7F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 IVLRPSRVHNSEENT 15
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Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QEP7D6_RAT PRELIMINARY;
Q6P7D6;
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                                                                                                                                                                                                                      Waterston R.H.;
Submitted (OCT-1999)
                                                                                                                                                                                                                                                                                                                              Waterston R.;
Submitted (OCT-2000)
                                                        NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                          NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE
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NCBI_TaxID=9606;
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δ d RESULT 3

OGPTOG RAP

OG POD OGPTOD O

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Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Kzzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Genezation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
69.7%; Score 53; DB 2; Length 350;
Best Local Similarity 73.3%; Pred. No. 0.55;
Matches 11; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (100-2003) to the EMBL/GenBank/DDBJ databases. EMBL; BC061713; AAH61713.1; -; mRNA. GO; GO:0016020; C:membrane; IEA. GO; GO:0006508; P:cimpeptidyl-peptidase IV activity; IEA. GO; GO:0006508; P:proteolygis and peptidolygis; IEA. InterPro; IRR002469; Peptidase_S9B. Pfam; PF00930; DPPLN N; 1. SEQUENCE 350 AA; 40869 MW; 49FF2846A9CF0F7F CRC64;
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Braembl; ENSRNGG00000005679; Rattus norvegicus.

RGD; G21253; Fap.
G0; G0:0004177; F:aminopeptidase activity; IEA.
G0; G0:0004274; F:dipeptidyl-peptidase IV activity; IEA.
G0; G0:0004287; F:hydrolase activity; IEA.
G0; G0:0004287; F:prolyl oligopeptidase activity; IEA.
G0; G0:0004580; F:prolyl oligopeptidase activity; IEA.
G0; G0:0006508; P:proteolygis and peptidolygis; IEA.
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Suckachwerdt K., Park J.E.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF493-182; AAM11677.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87843 MW; EB214BBE4BB14F2C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Fibroblast activation protein alpha subunit.
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-!- SIMILARITY: Belongs to the peptidase S9B family.
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Q73QP6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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ses 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPO DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Mammary gland;

MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Lischul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Lischul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Lischul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Dokins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Datchenow L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Lownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Dosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahesley J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.M., Mallysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse CDNA sequences.",
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: May have a role in tissue remodeling during development
and wound healing, and contribute to invasiveness in malignant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATALITIC ACTIVITY: Degrades gelatin and heat-denatured type I and type IV collagen, but not native type I or type IV collagen. Does not cleave laminin, fibronectin, fibrin or casein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isold=P97321:3; Sequence=VSP 005369; TISSUE SPECIFICITY: Detected in fibroblasts, in placenta, uterus, embryos from day 7-19 and in new-born mice (P1).
                                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Seprase (EC 3.4.21.-) (Fibroblast activation protein alpha) (Integral
                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Niedermeyer J., Scanlan M.J., Garin-Chesa P., Daiber C., Flebig H.H., Old L.J., Rettig W.J., Schnapp A., "Mouse fibroblast activation protein: molecular cloning, alternative splicing and expression in the reactive stroma of epithelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inactive (By similarity).
SUBCELLULAR LOCATION: Type II membrane protein (By similarity)
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: Homodimer, or heterodimer with DPP4. The monomer is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                    761 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=P97321-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ê
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE (ISOFORMS 1; 2 AND
                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=BALB/c; TISSUE=Embryo;
MEDLINE=97284459; Pubmed=9139873;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Int. J. Cancer 71:383-389(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Embryo;
       1 IVLRPSRVHNSEENT 15
                                  24 IVLRPSRVYSPEGNT 38
                                                                                                                                                                                                                                                                                                                  membrane serine protease)
                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                              musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancers.
                                                                                                                                                                      MOUSE
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=ATCC 35405 / DSM 14222;
PubMed=15064339; DOI=10.1073/pnas.0307639101;
Seshadri R., Myers G.S.A., Tettelin H., Eisen J.A., Heidelberg J.F.,
Dodson R.J., Davidsen T.M., DeBoy R.T., Fouts D.E., Haft D.H.,
Selengut J., Ren Q., Brinkac L.M., Madupu R., Kolonay J.F.,
Durkin S.A., Daugherty S.C., Shetty J., Shvartsbeyn A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal-anchor for type II membrane protein (Potential).

Charge relay system (By similarity). Charge relay system (By similarity). Charge relay system (By similarity). Charge relay system (By similarity). N-linked (GLONAC...) (Potential).                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema
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                                                                                                                                                                                                                                                           MEROPS; SON 500; MEROPS; SPRO01375; Peptidase S9.
InterPro; IPR001375; Peptidase S9.
InterPro; IPR001379; Ser_estrs.
Pfam; PF00930; DPPIV N; 1.
Pfam; PF00930; PEPVIV N; 1.
PFON; PF00930; PRO ENDOPER SE; 1.
PFON; PROSITE; PROFICING; GNDOPER SE; 1.
Alternative splicing; Glycoprotein; Hydrolase; Protease;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
011gopeptide/dipeptide ABC transporter, ATP-binding protein.
OrderedLocusNames=TDE0397;
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9174C3AEDA213B25 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Serine protease, Signal-anchor, Transmembrane TOPO DOM
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Pred. No. 2.1;
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EMBL; BC019190; AAH19190.1; -; mRNA.
HSSP; P27487; 1PPQ.
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761 AA; 87945 MW;
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Whitehead Institute Centre for Genome Research;

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HDC14087.
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Maucell E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Micaud S., Jaffe Do., Fischer S., Lutfalla G., Dossat C., Segurens B.,
Micaud S., Jaffe Do., Fischer S., Lutfalla G., Dossat C., Segurens B.,
Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Blemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
Arthouard V., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
Rellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Mincker P., Lander E.S., Weissenbech J., Roset Crollius H.;
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
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Gebregeorgis E., Geer K., Tsegaye G., Malek J.A., Ayodeji B., Shatsman S., McLeod M.P., Smajs D., Howell J.K., Pal S., Amin A., Vashisth P., McNeill T.Z., Xiang Q., Sodergren E., Baca E., Weinstock G.M., Norris S.J., Fraser C.M., Paulsen I.T., "Comparison of the genome of the oral pathogen Treponema denticola with other spirochete genomes.", Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651 (2004).
-!-SIMILARITY: Belongs to the ABC transporter family.
EMBL, ABC17247, AAS10892.1, -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Terracdon nigroviridis (Green puffer).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;

Actinopteryydi; Neopterygii, Teleostei, Buteleostei; Neoteleostei,

Acanthomorpha, Acanthopterygii, Percomorpha; Tetraodontiformes;

Tetradontoidea, Tetraodontidae, Tetraodon.
                                                                                                                                                                                                                                                                                          GO; GO: 0016020; C:membrane; IEA.

R GO; GO: 0016802; F:ATP binding; IEA.

R GO; GO: 0016802; F:ATPabe activity; IEA.

GO; GO: 0016802; F:ATPabe activity; IEA.

GO; GO: 000685; F: 013gopeptide transporter activity; IEA.

GO; GO: 000685; P: 013gopeptide transporter activity; IEA.

R GO; GO: 000685; P: 013gopeptide transporter activity; IEA.

R InterPro; IPR003439; ABC_transporter; IEA.

R InterPro; IPR003439; ABC_transporter; I.

R PROBOUS; ABC_transporter; I.

R PROBOUS; ABC_transporter; I.

R PROBITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.

R PROSITE; PS0031; ABC_TRANSPORTER_2; I.

M ATP-binding; Complete proteome; Membrane; Nucleotide-binding; Peptide transport; Protein transport; Transport.

S EQUENCE 325 AA; 36788 MW; 04Al0601D8PAC7CF CRC64;
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome 14 SCAF15003, whole genome shotgun sequence.
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116 ILLRPLKIHNIAEN 129
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Q4RR26;
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Matches 8; Conservative
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NUCLEOTIDE SEQUENCE

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"An integrated gene annotation and transcriptional profiling approach towards the full gene content of the Drosophila genome.";
Genome Biol. 5.RESEARCH0003.1-RESEARCH0003.17(2003).
-!- NISCELLANGEOUS: The sequence shown here is derived from an EMBL/GenBank/DDBJ third party annotation (TPA) entry.
EMBL, BK002601; DAA04107.1; -; Genomic_DNA.
SEQUENCE 81 AA; 9217 MW; D73008A7E41527F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
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Bubmda=14709175; DOI=10.1186/gb-2003-5-1-r3;
Hild M., Beckmann B., Haas S.A., Koch B., Solovyev V., Busold C.,
Fellenberg K., Boutros M., Vingron M., Sauer F., Hoheisel J.D.,
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.

NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                   2; Length 277;
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Pred. No. 4.4;
4; Mismatches 1; Indels
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Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                       277 AA; 31740 MW; F5C479D3D0811CC8 CRC64;
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Last annotation update)
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Last annotation update)
                                                                                                                  preliminary data.
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Pred. No.
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Best Local Similarity 61.5%;
Matches 8; Conservative
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222 VLEENKVHNSEDN 234
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Q61710;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 RPSRVHNSEENT 15
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RPSRLHSTNENS 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORFNames=HDC14087;
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11D 06

12D 06

13D 125

13D 12
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Matches

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Birren B.J. Musbaum C., Abouelleil A., Allen N., Anderson S., Aracherte, M. Musbaum C., Calvo S.E., Camarata J., Chang J., Arachchi H.M., Barna N., Eastien V., Bloom T., Boguslavkiy L., Anchchi H.M., Barna N., Calvo S.E., Camarata J., Chang J., Chopel Y., Collymore A., Cooke P., Cooke P., Corum B., DeArellano K., Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R., Erickson J., Farco S., Ferreira P., FitzGerald M., Gage D., Galagan J., Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N., Agree D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A., Affe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A., An L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J., Mathova T., Menga V., Murphy T., Naylor J., Nguyen C., Nicol R., Mielsen C.B., Norbu C., O'Connor T., O'Donnell B., O'Neil D., O'Connor T., O'Connor T., O'Connell S., Rechupka A., Ramasamy U., Raymond C., Retter R., Rise C., Rogov P., Rachupka A., Ramasamy U., Raymond C., Retter R., Rise C., Rogov P., Rahmas J., Tesfaye S., Theodore J., Topham K., Travers M., Vessiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B., Wallander E., Smith C., Zimmer A., Zody M., Lander E., Simner Y., Zimmer A., Zody M., Lander E., Simith C., Zimmer A., Zody M., Lander E., Stander E., Zalnoun J., Zimmer A., Zody M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Friedlin;
Peacock C.S., Murphy L., Ivens A.C., Berriman M., Blackwell J.,
Smith D., Collins M., Fosker N., Harris D., Oliver K., O'Neil S.,
Saunders D., Seeger K., Warren T., Rajandream M., and Barrell B.G.;
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; CT005271; CAJ07753.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The Sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
                                                                                                                                      Aspergillus nidulans FGSC A4.
Bukaryota, Fungi, Ascomycota, Pezizomycotina, Eurotiomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
SEQUENCE 1116 AA; 122163 MW; 18857D2CF3B47973 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-SEP-2005 (TrEMBLrel. 31, Last sequence update) 13-SEP-2005 (TrEMBLrel. 31, Last annotation update) Splicing factor ptsrl interacting protein, putative ORFNames-LmjF34.0495;
            10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 43; DB 2; I
Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           preliminary data.
,, AACD01000153; BAA67021.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genome Sequence of Aspergillus nidulans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                        Trichocomaceae; Emericella
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.6%;
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Q4Q3F8;
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                                                                                           Hypothetical protein.
ORFNames=AN8399.2;
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les 7; Conserv
                                                                                                                                                                                                               NCBI_TaxID=227321;
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A Arroya J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.,

B Bowyer P., Chen D., Collins M., Coulsen R., Davies R., Dyer P.S.,

R Bowyer P., Chen D., Collins M., Coulsen R., Davies R., Dyer P.S.,

R Farman M., Fedorova N., Fedorova N., Fediblyum T.V., Fischer R.,

R Fordman G.H., Gomik K., Garffith-Jonnes S., Gwilliam R., Haas B.,

RA Goldman G.H., Gomik K., Garffith-Jones S., Gwilliam R., Haas B.,

R Goldman G.H., Gomik K., Garffith-Jones S., Gwilliam R., Haas B.,

R Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,

R Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,

R Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.,

R Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.,

R Majoros W.H., May G.S., Miller B.L., Wolmend B.L., Quail M.A.,

R Rabbinowitsch E., Rawlins N., Parice C., Pritchard B.L., Quail M.A.,

R Rabbinowitsch E., Rawlins N., Rajandream M.-A., Reichard U.,

R Rabbinowitsch E., Salzberg S.L., Sanchez W.,

R Sanchez-Ferrero J.C., Saunder B., Sanchez M.,

R Sanchar P., Willer G., Vazquez de Aldana C.R., Weidman J.,

R Machida M., Hall N., Barrell B., Denning D.W.; Assai K.,

R Agencylia E., Willer C., Wolfyloshic and allergenic filamentous fungus

R Aspergillus fumigatus."

R Aspergillus fumigatus."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Fungi, Ascomycota, Pezizomycotina, Eurotiomycetes,
Eurotiales, Trichocomaceae, mitosporic Trichocomaceae, Aspergillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18
  CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Pred. No. 1.1e+02;
                                                                                                                                                                    57.9%; Score 44; DB 2; Length 809; 66.7%; Pred. No. 68;
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SEQUENCE 862 AA; 96297 MW; B050E61F036D7768 CRC64;
                                                                                                Hypothetical protein.
SEQUENCE 809 AA; 91832 MW; 00EB1442D461F33C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         preliminary data.
.; AAHF01000003; EAL91754.1; -; Genomic_DNA.
                                                  preliminary data.
EMBL; CAAC01000068; CAE68975.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAY-2005) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                862 AA.
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                                                                                                                                                                                             Pred. No. 68;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
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13-SEP-2005 (TrEMBLrel. 31, Le
13-SEP-2005 (TrEMBLrel. 31, Le
Hypothetical protein.
ORFNames-Afusgo8450;
Aspergillus fumigatus Af293.
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                                                                                                                                                                                                                                                                                                                 205 LRPSEVHNFHDN 216
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                                                                                                                                                                                                                         8; Conservative
                                                                                                                                                                                                                                                                    3 LRPSRVHNSEEN 14
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Best Local Similarity
9; Conserve
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                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=330879;
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QSATI1 EME
ID QSATI
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RESULT 10
044WHA
AC 044WHA
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Gaps

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257 AA

PRT; 1116 AA.

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Length 1116;

257 AA; 30326 MW; 968094356013F406 CRC64;

SEQUENCE

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Local Similarity
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RESULT 14
QGBYR6_DEBHA
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R Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

R Alachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhard N.K.,

Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhard N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

R Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Tochhyuki S., Carninci P., Prange C.,

R Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Wakernan R.J., Makek J.A., Guastarte P.H.,

R Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

R Hichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

R Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

R Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.

Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K.,
Nakajima Y., Mizuno T., Morinaga M., Ota T., Suzuki Y., Obayashi M.,
Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                   Gaps
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63.6%; Pred. No. 74;
ive 3; Mismatches 1; Indels
  55.3%; Score 42; DB 2; Length 257; 66.7%; Pred. No. 41;
                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ll protein.
425 AA; 49647 MW; F8288E143A3FF764 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Hypothetical protein FLJ20291.
                                                                                                                                                                                                                                                                   425 AA.
                                                   3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, AK000298; BAA91065.1; -; mRNA.
EMBL; BC008833; AAH08833.1; -; mRNA.
Ensembl; ENSG0000108296; Homo sapiens.
                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                               212 RSSRVHSSEESS 223
                                                                                                                                                                                                                                                                 QONXEB HUMAN PRELIMINARY;
QONXEB;
                          Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         segnences.
                                                                                                 4 RPSRVHNSEENT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 RPSRVHNSEEN 14
                                                                                                                                                                                                                                                                                                                                                                                                            Name=FLJ20291;
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
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       Query Match
                                                                                                                                                                                                                                             HUMAN
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CONKER HUM
CONKER HUM
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DT 01-00
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NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC PURAINATICC 36239 / CBS 767;

RY Pubmed=1522552; DOI=10.1038/nature02579;

RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,

RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,

RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,

RA Lafontaine I., Bandul L., Aigle M., Anthouard V., Babour A., Barbe V.,

RA Barnay S., Banchin S., Beckerich J.-M., Beyne E., Bleykasten C.,

RA Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruar A.,

Rosisame A., Roszul R., Lamine M., Joyet P., Kachouri R.,

RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,

RA Micaud J.-M., Nikolski M., Oztaer M. Joyet P., Kachouri R.,

RA Nicaud J.-M., Nikolski M., Oztaer B., Straub M.-L., Suleau A.,

Rellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,

Rennen D., Tekais F., Wesolowski-Louvel M., Westhof E., Wirth B.,

Renniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,

Rennicker P., Souciet J.-L...

RA Mincker P., Souciet J.-L...
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                                                                        25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Debaryomyces hansenii chromosome A of strain CBS767 of Debaryomyces
                                                                                                                                                                                                                                                                                    Debaryomyces hansenii (Yeast) (Torulaspora hansenii).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Debaryomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
MEDLINE=211555286; PubMed=11759840;
Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anabaena sp. (strain PCC 7120).
Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Nostoc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50090; MYB 3; 1.
Complete proteome; Nuclear protein; Repeat.
SEQUENCE 435 AA; 46322 MW; 335C478038777657 CRC64;
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Last annotation update)
   435 AA
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                                                                                                                                                                                                                                                             OrderedLocusNames=DEHA0A07634g;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome evolution in yeasts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            All1802 protein.
OrderedLocusNames=all1802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8YW14_ANASP PRELIMINARY;
QEBYR6 DEBHA PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
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403 PNKTHNSQKNT 413
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547 VLNPSQISNNEDN 559

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Annotation of the Genome of Candida albicans.";
"Annotation of the Genome of Candida albicans.";
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
Bhali, AGC01000199; EXK92203.1;
GO; GO:0005634; C:nuclaus; IEA.
GO; GO:0001700; F:ranscription factor activity; IEA.
GO; GO:0001700; F:ranscription factor activity; IEA.
GO; GO:0008270; F:rancion binding; IEA.
GO; GO:0008350; P:ranscription of transcription, DNA-dependent; IEA.
GO; GO:0006350; P:ranscription; IEA.
DNA-binding; Metal-binding; Nuclear protein; Transcription;
Transcription requiation; Zinc.
SEQUENCE 787 AA; 89731 MW; 74515755568D6C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S., Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T., Davis R.W., Scherer S., Thorstenson Sequence of Candida albicans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
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Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yabata S.; Tabata S.; "Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 787;
                                                                                                                                                                                                                                                                                                                                                                                                                                   55.3%; Score 42; DB 2; Length 444; 63.6%; Pred. No. 78; 2; Indels ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55.3%; Score 42; DB 2; Length 78, 53.8%; Pred. No. 1.58+02; Landels
                                                                                                                                                                                                                                                                                                                                                                                       729945E40614D03D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-MXY-2005 (TrEMBLrel. 30, Created)
10-MXY-2005 (TrEMBLrel. 30, Last sequence update)
10-MXY-2005 (TrEMBLrel. 30, Last annotation update)
Potential fungal zinc cluster transcription factor.
ORFNames-CaOl9.6680;
Candida albicans SC5314.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The diploid genome sequence of Candida albicans.";
Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
                                                                                                                                                                                           GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0008324; F:cation transporter activity; IEA.
GO; GO:0000812; P:cation transport; IEA.
InterPro; IPR003445; Cat transpt.
InterPro; IPR004772; K_transptTrk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=SC5314;
PubMed=15123810; DOI=10.1073/pnas.0401648101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         787 AA
                                                                                                                 DNA Res. 8:205-213(2001).
EMBL; BA000019; BAB73501.1; -; Genomic_DNA.
PIR; AD2031; AD2031.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                  444 AA; 48154 MW;
                                                                                                                                                                                                                                                                                                                    Pfam; PF02386; TrkH; 1.
TIGREAMB; TIGR00933; 2a38; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QS9NXS_CANAL PRELIMINARY;
QS9NXS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 63.6
Matches 7; Conservative
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430 RPTRIHYPEEN 440
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                        Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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Gaps
                                                                                                                                                                                                    Oryza sativa (japonica cultivar-group).
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:000521; F.ATP binding; IEA.
GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
GO; GO:000468; F:receptor activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
InterPro; IPR001480; B lectin.
InterPro; IPR0030019; PAN.
InterPro; IPR008271; Ser_thr_pkin_AS.
Pfam; PF00453; B lectin; l.
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EMBL; AP004384; BAC79932.1; -; Genomic_DNA.
EMBL; AP003753; BAD30190.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sasaki T., Matsumoto T., Yamamoto K.; "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, BAC clone:OJ1339 B08.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 837;
                                                                                                                                                                                                                                                                                                                                                                                           Sasaki T., Margumoto T., Yamamoto K.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases
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Last sequence update)
Last annotation update)
                                                         01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0FB-2005 (TrEMBLrel. 29, Last annotation update)
Putative S-receptor kinase.
Name=P0506C07.6; Synonyms=OJ1339_B08.15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATP-binding; Kinase; Nucleotide-binding; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55.3%; Score 42; DB 2; I
58.3%; Pred. No. 1.7e+02;
:ive 4; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Serine/threonine-protein kinase; Transferase.
SEQUENCE 837 AA; 92106 MW; 29ED3E7DBCDA9C
     837 AA
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        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00069; Pkinase; 1.
ProDom; PD000001; Prot kinase; 1.
SMART; SM00108; B_lectIn; 1.
PROSITE; PS50927; BULB_LECTIN; 1.
PROSITE; PS50948; PAN; 1.
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Q7NYT4;
Q7X125 ORYSA PRELIMINARY;
Q7X125;
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Best Local Similarity 58.3
Matches 7; Conservative
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270 LLKPAYVHNNEE 281
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                                                                                                                                                                                                                                                                                                                    NCBI TaxID=39947;
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Trypanosoma brucei
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NA SECONGE 12472 / DSM 30191;

ANDER SECONGE S. PubMed=14500782; DOI=10.1073/pnas.1832124100;

ANDER SECONGE J.A., Andrade E.M., Aratipe J., de Araujo M.F.F.,

ANDER S. Azevedo V., Baptiera A.J., Baraus L.A.M.,

Batiera J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,

Camargo A.A., Cardoso D.D.P., Carneiro N.P., Carraro D.M.,

Caravalho C.M.B., Caccardo J.C.M., Cavada B.S., Chucire L.M.O.,

Creczynski-Pasa T.B., Cunha-Junior N.C., Fagundes N., Falcao C.L.,

A Fantinatur F., Farias I.P., Felipe M.S.S., Ferrari L.P., Ferro J.A.,

Rantinatur F., Farias I.P., Felipe M.S.S., Ferrari L.P., Ferro J.A.,

Razinelli R.T., Gomes E.A., Goncalves P.R., Grangeiro T.B.,

Gazzinelli R.T., Gomes E.A., Goncalves P.R., Grangeiro T.B.,

Gazzinelli R.T., Gomes E.A., Manna E.S., Jardin L.R.,

Leoi L.C.T., Lima L.F.A., Loureiro M.F., Lyra M.C.C.P.,

Madeira H.M.F., Manifo G.P., Maranhao A.O., Martins W.S.,

A di Mauro S.M.Z., de Medeiros S.R.B., Meisener R.V., Moreira M.A.,

A paixao R.F.C., Parente J.A., Pedrosa F.O., Pena S.D.J., Pereira J.O.,

Ramalho-Neto C.E., Reis A.M.M., Rigo L.U., Rondinelli E.,

A santos E.B.P., Santos F.R., Schneider M.P.C., Seuanez H.N.,

Silva A.M.R., da Silva A.M.C., Silva E.M., Souza E.M., Souza K.R.L.,

Sund R.C., Steffens M.B.R., Scares R.B.A., Souza E.M., Souza K.R.L.,

Nettore A., Wassen R.S., Saha A., Simpson A.J.G., Unimenyi T.,

Nettore A., Wassen R.S., Saha A., Simpson A.J.G., Unimenyi T.,

Nettore A., Wassen R.S., Saha A., Simpson A.J.C., Seuanez H.N.,

Sunda R.C., Steffens M.B.R., Saha A., Simpson A.J.C., Seuanez H.N.,

Sunda R.C., Steffens M.B.R., Scares R.B.A., Souza E.M., Souza E.M., Shanna E.M., Manna E.M., Shanna E.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
Bacteroidaceae; Bacteroides.
NCBI_TaxID=272559;
                                               Chromobacterium violaceum.
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Chromobacterium.
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01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Putative CoA transferase (EC 2.8.3.-).
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437 VVLRDSEVHNNVE 449
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    OrderedLocusNames=CV1188;
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Best Local Similarity
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X PubMed=15466707; DOI=10.1073/pnas.0404172101;

R UbMed=15466707; DOI=10.1073/pnas.0404172101;

A Kuwahara T., Yamashita A., Hirakawa H., Nakayama H., Toh H., Okada N.,

Kuhara S., Hatori M., Hayashi T., Ohnishi Y.;

"Genomic analysis of Bacteroides fragilis reeveals extensive DNA

"Genomic analysis of Bacteroides fragilis reeveals extensive DNA

"Inversions regulating cell surface adaptation.";

In Proc. Natl. Acad. Sci. U.S.A. 101:14919-14924 (2004).

E EMBL, APO66841; BAD46775.1; -, Genomic DNA.

GO; GO:0016740; F:transferse activity; IEA.

GO; GO:0016740; F:transferse activity; IEA.

R O; GO:0016709; R:ceryl-CoA hydro.

R InterPro; IPR037702; ActCoA hydro.

R Fami, PR02550; AcetylCoA hydro.

R Promic R Prossion R Prossion R Pransferses

W Complete proteome; Transferses

W Complete Proteome; Transferses

N SEQUENCE 499 AA; 54063 MW; EB6F72A2BBB39295 CRC64;
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Ghedin E., Blandin G., Bartholomeu D., Caler E., Haas B., Hannick L.,
Shallom J., Hou L., Djikeng A., Feldblyum T., Hostetler J.,
Johnson J., Jones K., Koo H.L., Larkin C., Pai G., Peterson J.,
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NCBI_TaxID=5691;
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Bacteroidaceae; Bacteroides.
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                                                                                                                                                                                                 Score 41; DB 2; Length 499;
Pred. No. 1.4e+02;
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                                                                                                                                                54064 MW; EB6F72A2B8B39295 CRC64;
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Last annotation update)
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Last annotation update)
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Science 307:1463-1465(2005).

EMBL; CR626927; CAH05804.1; -; Genomic_DNA.

InterPro; IPR003702; ActCoA hydro.

Pfam; PF025050 AcetylCoA hydro; 1.

Complete protecom; Transferase.

SEQUENCE 499 AA; 54064 MW; EB6F72A2B8B3
                                                                                                                                                                                                                                                              3; Mismatches
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25-0CT-2004 (TrEMBLrel. 28, Last seq
25-0CT-2004 (TrEMBLrel. 28, Last ann
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                                                                                                                                                                                                             53.9%;
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ID Q650P9 BACFR PRELIMINARY;
AC Q650P9;
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QSTVP6;
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Best Local Similarity 55...
T; Conservative
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ORFNames=Tb927.5.680;
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Best Local Similarity
7, Conserve
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NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=Pm70;
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        SO THE SERVICE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
    Khalak H.G., Salzberg S., Simpson A.J., Tallon L., Van Aken S., Wanless D., White O., Wortman J., Fraser C.M., El-Sayed N.M.A.; Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; ACIS9441; AAX70413.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Pasteurellaceae, Pasteurella.
NCBI_TaxID=747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O9T238:gei.4; NbExp=1; IntAct=EBI-326898, EBI-329192; Q22174:T04H1.2; NbExp=1; IntAct=EBI-326898, EBI-311938; Q22227:T05C12.6a; NbExp=1; IntAct=EBI-326898, EBI-316403; EMBL; 283069; CAB04906.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The C. elegans sequencing consortium; "Genome sequence of the nematode C. elegans: a platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53.9%; Score 41; DB 2; Length 740;
46.2%; Pred. No. 2.2e+02;
ive 5; Mismatches 2; Indels
                                                                                                                                               53.9%; Score 41; DB 2; Length 585; 61.5%; Pred. No. 1.7e+02; tive .1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome; Hypothetical protein.
SEQUENCE 740 AA; 84732 MW; C0363C58EE7EDDE2 CRC64;
                                                                                      Hypothetical protein.
SEQUENCE 585 AA; 65263 MW; 86BBA31FD82073E5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                 OLNOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-UON-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein W04A8.6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]...
STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-MAR-2004 (Rel. 43, Created)
29-MAR-2004 (Rel. 43, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Glycopen phosphorylase (EC 2.4.1.1).
Pasteurella multocida.
                                                                                                                                                                                                                                                                                                                                                                                 740 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       818 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ensembl; W04A8.6; Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WormBase; WBGene00012241; W04A8.6.
WormPep; W04A8.6; CE16540.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 investigating biology.";
Science 282:2012-2018(1998).
-!- INTERACTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OSTUMO CAEEL PRELIMINARY;
                                                                                                                                                                                                                                                             :|| ||| |||
23 LLRRKRVHKEEEN 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 46.2
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 VLRPSRVHNSEEN 14
                                                                                                                                                                                                                                    2 VLRPSRVHNSEEN 14
                                                                                                                                                                      Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IntAct; Q9XUMO; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PASMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 23
PHSG_PASMU
ID PHSG_PASN
AC Q9CN90;
                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                            CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                  Q9XUM0
                                                                                                                                                                                                                                                                                                                                       RESULT 22
Q9XUM0_CAE
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pyridoxal phosphate (covalent) (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TICRFAMB; TICR02093; P.ýlasē; Ī.
PROSITE; PS00102; PHOSPHORYLASE; 1.
Allosteric enzyme; Carbohydrate metabolism; Complete proteome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycogen metabolism; Glycosyltransferase; Pyridoxal phosphate;
MEDLINE=21145866; PubMed=11248100; DOI=10.1073/pnas.051634598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
Waterston R.;
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        818 AA; 94037 MW; 89E7643EDD48D5B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 41; DB 1; I
Pred. No. 2.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                887 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE006090; AAK02629.1; -; Genomic_DNA
HSSP; P06737; 1EM6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR011833; Glycg_phsphrylas.
InterPro; IPR000811; Glyco_trans_35.
PARTHER: PTR11468; Glyco_trans_35: 1.
Pfam; PF00343; Phosphorylase: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIRSF, PIRSF000460; Pprylas GlgP; 1.
TIGRFAMB; TIGR02093; P_ylase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |: | |:||: ||
IIYRHKRIHNTMEN 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 IVLRPSRVHNSEEN 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O9ZSB6_ARATH PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JAN-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LaPlant Y., Spalding
Submitted (JAN-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE
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Gaps

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2; Indels

2; Mismatches

Score 41; DB 2; Length 910; Pred. No. 2.8e+02;

53.9%;

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910 AA; 102648 MW; E01B0AD928A8EE71 CRC64;
                                                                                                                                            6; Conservative
                                                                                                                                                                                                                                                     639 PSKIHNGSEN 648
                                                                                                                                                                                                              14
                                                                                                                                                                                                           5 PSRVHNSEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE
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Best Local Similarity
                                                                         Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=3702;
          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                   RESULT 26
Q9T0B8_ARA
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Kim C.J., Chen H., Cheuk R., Shinn P., Bowser L., Carninci P.,

Bale J.M., Hayashizaki Y., Ishida J., Jones T., Kamiya A.,

Rarlin-Neumann G., Kawai J., Lam B., Lin J., Miranda M., Narusaka M.,

Karlin-Neumann G., Rawai J., Lam B., Lin J., Miranda M., Narusaka M.,

Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Sacou M.,

Seki M., Southwick A., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G.,

Shinozaki K., Davis R.W., Theologis A., Ecker J.R.,

Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, AY054463; AAK96655.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M., Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H., Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J., Kim C., Lin J., Liu S.X., Narrusaka M., Pham P.K., Sakano H., Eakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K., Scker J., Theologis A., Davis R.W.; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2005 (TrEMBLrel. 29, Last sequence update)
Hyporhetical protein At4g10590; T4F9.50 (At4g10590).
Name-At4g10590/T4F9.50;
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; cosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
R EMBL; AF118222; AAD03434.1; -; Genomic_DNA.
HSSP; Q93009; 1NBF.
GG; GG:0004197; F:cysteine-type endopeptidase activity; IEA.
GG; GG:0004221; F:ubiquitin thiolesterase activity; IEA.
GG; GG:0006512; F:ubiquitin cycle; IEA.
GG; GG:0006512; P:ubiquitin cycle; IEA.
R GG; GG:0006512; P:ubiquitin-dependent protein catabolism; IEA.
R GG; GG:0006512; P:ubiquitin-dependent protein catabolism; IEA.
R InterPro; IPR001394; Pept C19. N .
R InterPro; IPR00460; Pept C19. N .
R PROSTIT: PR0043; UCH; 1.
R PROSTITE; PS00972; UCH; 2.
R PROSTITE; PS00972; UCH 2. 1; 1.
R PROSTITE; PS00973; UCH 2. 2; 1.
R PROSTITE; PS00973; UCH 2. 3; 1.
C PROSTITE; RS00253; UCH 2. 3; 1.
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GO; GO:0004221; F:ubiquitin thiolesterase activity; IEA.
GO; GO:0006512; F:ubiquitin cycle; IEA.
GO; GO:0006511; P:ubiquitin-dependent protein catabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53.9%; Score 41; DB 2; Length 887; 60.0%; Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          910 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PS00972; UCH 2 1; 1.
PS00973; UCH 2 2; 1.
PS50235; UCH 2 3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q93Y01 ARATH PRELIMINARY;
Q93Y01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 60.0
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PROSITE;
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093Y01_ARATH

OG 93Y01_ARATH

OG 93Y01_ARATH

OI - DEC - 20
DT 01 - DEC - 20
DT 02 - 20
DT 02 - 20
DT 02 - 20
DT 03 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bevan M., Wedler H., Wedler B., Wambutt R., Bancroft I., Mewes H.W. Mayer K.F.X., Schueller C.; Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                       OLIMAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
1-FBB-2006 (TrEMBLrel. 29, Last annotation update)
Hypothetical protein T4F9.50 (Hypothetical protein AT4g10590).
Name-T4F9.50; Synonyma-AT4g10590;
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Subrayopa, Virialplantae; Streptoophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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EU VALDAJILDS SAUGANCE.

EU VALDAJICOPSIS SEGQUENCING PROJECT;

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

R EMBL, AL161517; CAB78182.1; -; Genomic_DNA.

R EMBL, AL161517; CAB78182.1; -; Genomic_DNA.

R EMBL, T04194; T04194.

R FSP, Q39009; 1NB8.

GO; GO:0004127; F:cysteine-type endopeptidase activity; IEA.

GO; GO:0004127; F:cysteine-type endopeptidase activity; IEA.

GO; GO:0006512; F:ubiquitin cycle; IEA.

R GO; GO:0006511; P:ubiquitin cycle; IEA.

R InterPro; IPR001394; Peptidase_C19.

R InterPro; IPR01394; Peptidase_C19.

R InterPro; IPR00465; Pept_C19_N_1.

R Pfam; PF00437; DUCH; 1.

R Pfam; PF00437; DUCH; 1.

R PROSITE; PS00972; UCH; 2.

R PROSITE; PS00972; UCH; 2.

R PROSITE; PS00973;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
EU Arabidopsis sequencing project;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
937 AA
     PRT;
Q9T0B8 ARATH PRELIMINARY;
Q9T0B8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
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666 PSKIHNGSEN 675
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Q9NR99 HUMAN
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Query Match
Best Local Similarity
---- 8; Conserv?
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmid pBF9343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-MAY-2005
                                                                                                                       Fauch A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                       nomo, apprens indimani.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
13-SEP-2005 (TrEMBLrel. 21, Last annotation update)
14-SEP-2005 (TrEMBLrel. 31, Last annotation update)
15-SEP-2005 (TrEMBLrel. 31, Last annotation update)
15-SEP-2005 (TrEMBLrel. 31, Last annotation update)
17-SEP-2005 (TrEMBLrel. 31, Last annotation update)
18-SEP-2005 (TrEMBLrel. 318)
18-SEP-2005 (TrEMBLrel. 31)
18-SEP-2005 (TrEMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 41; DB 2; Length 2828;
Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
PubMed=12948626; DOI=10.1016/S0168-1656(03)00154-8;
Kalinowski J., Bathe B., Bartels D., Bischoff N., Bott M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ensembl; ENSGO0000101825; Homo sapiens.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005021; F:vascular endothelial growth factor rece
GO; GO:0006468; P:protein amino acid phosphorylation; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunoglobulin domain; Leucine-rich repeat; Repeat.
SEQUENCE 2828 AA; 312294 MW; A18377D8554F1FE1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to the EMBL/GenBank/DDBJ databases.
                                                                                          Last sequence update)
Last annotation update)
PRT; 2828 AA
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35.7%; Pred. No. ...
7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Crowl R.M., Luk D.;
Submitted (MAR-2000) to the EMBL/Gen
EMBL; AF745505; AAF86402.1; -; mRNA.
HSSP; Q9BZR6; 10ZN.
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LRR Nterm.
LRR typ.
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Pfam; PF00056; LRR_1; 6.
PRINTS; PR01832; VEGFRECEPTOR.
SMART; SM00408; IGC2; 10.
SMART; SM00369; LRR_TYP; 3.
SMART; SM00082; LRR_TYP; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR007110; Ig-like.
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2238 VVMKPAKIEHKEEN 2251
                                                         (TrEMBLrel. 15, (TrEMBLrel. 15, (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PR003598; Ig c2.
PR001611; LRR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 IVLRPSRVHNSEEN 14
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QBNPCO; Q6M4C5;
   Q9NR99_HUMAN PRELIMINARY;
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InterPro, IPR009134;
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                                                                                                                                                                                    Homo sapiens (Human)
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Best Local Similarity
                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nakagawa S.;
                                                                                          01-OCT-2000
01-MAR-2004
                                                             -OCT-2000
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Burkovski A., Dusch N., Eggeling L., Eikmanns B.J., Gaigalat L.,
Goesmann A., Hartmann M., Howhmacher K., Kraemer R., Linke B.,
McHardy A.C., Meyer F., Mockel B., Pfefferle W., Puehler A.,
Rey D.A., Rueckert C., Rupp O., Sahm H., Wendisch V.F., Wiegraebe I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=15746427; DOI=10.1126/science.1107008; Cerdeno-Tarraga A.-M., Patrick S., Crossman L.C., Blakely G., Abratt V., Lennard N., Poxton I., Duerden B., Harris B., Quail M.A., Barron A., Clark L., Corton C., Doggett J., Holden M.T.G., Larke N., Line A., Lord A. Norbertczak H., Ormond D., Price C., Rabbinowitsch E., Woodward J., Barrell B.G., Parkhill J.; "Extensive DNA inversions in the B. fragilis genome control variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                              "The complete Corynebacterium glutamicum ATCC 13032 genome sequence and its impact on the production of L-aspartate-derived amino acids and vitamins"; or tamins"; or tamins"; or tamins"; or tamins"; or the production of L-aspartate-derived amino acids and vitamins"; or tamic lows.

EMBL; BA000036; BAB92287.1; -; Genomic DNA.

EMBL; BA00036; BAB92287.1; -; Genomic DNA.

EMBL; BA000046; Hypothetical protein.

SEQUENCE 115 AA; 12094 MW; 6B04C4BB455ED70 CRC64;
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Bacteroidaceae; Bacteroides.
NCBI_TaxID=272559;
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
                                                                                                                                                                                                                                                                                                                                                                                 Length 115;
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EMBL, CRC46928, CAH05754.1; -; Genomic_DNA.

Complete proteome; Plasmid.

SEQUENCE 143 AA; 16767 MW; 26DB2019C4DC6F03 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OrderedLocusNames=pBF9343.40c;
Bacteroides fragilis (strain ATCC 25285 / NCTC 9343).
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Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                 52.6%; Score 40; DB 2; 72.7%; Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143 AA.
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47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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10-MAY-2005 (TEEMBLrel. 30, Last and
Putative integral membrane protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 IVMRPSRKAMQVFNEEKN
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Q5CZC9_BACFN PRELIMINARY;
Q5CZC9;
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QBELX1;
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NCBI_TaxID=1392
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Matches
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0081UK7 BAG
0081UK7 BAG
0081UK7
DT 01-JU
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DE HYPOT
00 BACTE
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=14671098; DOI=10.1128/JVI.78.1.168-177.2004;
Delhon G., Tulman B.R., Afonso C.L., Lu Z.,
de la Concha-Bermejillo A., Lehmkuhl H.D., Piccone M.E., Kutish G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                Gaps
                                  MEDLINE-22220767; PubMed=12235376; DOI=10.1093/nar/gkf526; Takami H., Takaki Y., Uchiyama I.; "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya Ridge and its unexpected adaptive capabilities to extreme
                                                                                                                                                                                                                                                                                                                                                                                                Bovine papular stomatitis virus.
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
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Stomtatitis Virus.";
Virol. 78:168-177(2004).
EMBL; AY386265; AAX98477.1; -; Genomic_DNA.
Hypothetical protein.
                                                                                                                                                                    Query Match 52.6%; Score 40; DB 2; Length 174; Best Local Similarity 87.5%; Pred. No. 60; Matches 7; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 40; DB 2; Length 269;
Pred. No. 1e+02;
0; Mismatches 4; Indels
                                                                                         environments.";
Nucleic Acids Res. 30:3927-3935 (2002).
BMBL; BA000028; BAC15049.1; -; Genomic_DNA.
Complete proteome; Hypothetical protein.
SEQUENCE 174 AA; 20245 MW; C56966C4B5A4DEC5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 protein.
269 AA; 30567 MW; CC09C56720186501 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein FLJ46608.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                            05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                    269 AA.
            NUCLEOTIDE SEQUENCE.
STRAIN-HTEB31 / DSM 14371 / JCM 11309,
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66.7%;
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Q6ZR62;
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Best Local Similarity 66...
8; Conservative
                                                                                                                                                                                                                                                                                                                    QETV68_9POXV PRELIMINARY;
QGTV68;
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148 VHNNEENT 155
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TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=129727;
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0662862 HUM
066286
AC 066286
AC 066286
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DT 05-JU
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DE HYPOT
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Kanehori K., Ishibashi T., Chiba Y., Fujimori K., Hiraoka S., Tanai H., Watanabe S., Ishida S., Ono Y., Hotuta T., Watanabe M., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishi S., Yamanoto J., Isono Y., Kawai-Hio Y., Salto K., Nishikawa T., Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B. Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.; Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AK128465; BAC87451, J., PRNA.
GO, GO:0003676; F:nucleic acid binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K., Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R., Richardson D., Rubin B., Tice H.; "Complete genome sequence G Bacillus thuringiensis 97-27."; submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.

EMBL, ABGN1355, AAT62687.1; -; Genomic_DNA.

Complete protecome. 350 AA; 40704 MW; 2D55A7256C6972C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 310;
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Local Similarity 46.7%; Pred. No. 1.2e+02;
Les 7; Conservative 3; Mismatches 5; Indels
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Bacillus thuringienes; Bacillales; Bacillus;
Bacillus cereus group.
NCBI_TaxID=180856;
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Bacillus cereus group.
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Pfam; PF00098; Zf-CCHC; I.
PRINTS; PR00939; C2HCCHRINGER.
PROSITE; PS50158; ZF CCHC; I.
SEQUENCE 310 AA; 34669 MW; 6C8D18EAA7E9A2A0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein yhec.
Name=yheC; OrderedLocusNames=BT9727_076;
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4; Mismatches 2;
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Q6HMM1 BACHK
ID Q6HMM1 BACHK PRELIMINARY;
AC Q6HMM1;
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Best Local Similarity 50.0
Matches 6; Conservative
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Q4H676_9DEIO PRELIMINARY;
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145 IIIRPTNAHSSE 156
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nes 7, Conservative
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NUCLEOTIDE SEQUENCE.
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Best Local Similarity
Matches 6; Conserv
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Q8N4B4;
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                          MEDLINE-22608414; PubMed=12721629; DOI=10.1038/nature01586;
Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,
Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,
Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gills S.R.,
Holtzapple E.K., Okstad O.A., Helgason E., Rilatone J., Wu M.,
Rolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
DeBoy R.T., Madou R.J. Poop M., Khouri H.M., Radune D.,
Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman W.C.,
Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,
Salzberg S.L., Thomason B., Friedlander A.M., Koehler T.M.,
Hanna P.C., Kolstoe A.-B., Fraser C.M.;
The genome sequence of Bacillus anthracis Ames and comparison to
Closely related bacteria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
Hitchcock P., Jackbon P., Keilm P., Longmire J., Lucas S., Okinaka R.,
Richardson P., Rubin B., Tice H.;
"Complete genome sequence of Bacillus cereus ZK.";
Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.

EMBL, CP000001; AAU19484.1; -; Genomic_DNA.

Complete proteome; Hypothetical protein.

SEQUENCE 350 AA; 40708 MW; 913661EEA4ACSA96 CRC64;
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"Complete genome sequence of Bacillus anthracis Sterne.";
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.

EMBL, AB01734; AAT2997.1; -; Genomic_DNA.

EMBL, AB01725; AAT53145.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Federova N.B.
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NCBI_TaxID=288681;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Wilson M., Stanley S., Decker S., Read T.D., Salzberg S. Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Bacillus anthracis comparative genomics.";
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 350 AA; 40702 MW; 4642783DB7E578CD CRC64;
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Last annotation update)
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Q63FE9;
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145 ||IRPTNAHSSE 156
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NUCLEOTIDE SEQUENCE
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T., Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome assembly of Deinococcus geothermalis DSM 11300.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Larimer F., Land M.;
"Annotation of the draft genome assembly of Deinococcus geothermalis
"Annotation of the draft genome assembly of Deinococcus geothermalis
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
-!-CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gapa
                                                                          Gaps
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                        Length 350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein precursor.
OKFNames-DgeoDRAFT_2770;
Deinococcus geothermalis DSM 11300.
Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 40; DB 2; Length 414
Pred. No. 1.78+02;
2; Indels
Score 40; DB 2; Length 350
Pred, No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  414 AA; 45121 MW; C13BB6981624FD9A CRC64;
                                                                                                                                                                                                                                                                                                                                                                      13.SEP-2005 (TrEMBLrel. 31, Created)
13.SEP-2005 (TrEMBLrel. 31, Last sequence update)
13.SEP-2005 (TrEMBLrel. 31, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AAHE01000016; BAL81802.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         _5-OCT-2004 (Rel. 45, Created)
25-OCT-2004 (Rel. 45, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     442 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US DOE Joint Genome Institute (JGI-ORNL);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1] TOUCLEOTIDE SEQUENCE [LARGE SCALE MRNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Potential
                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein; Signal. SIGNAL 1 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52.6%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F-box only protein 39.
Name=FBXO39; Synonyms=FBX39;
Homo sapiens (Human).
                           52.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Deinococcaceae; Deinococcus
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Name=Fbxo39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BX39 RAT
                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                         removed.
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPENSOR SERVICE COCCOCCOCC
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     A Kausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Krausherg R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Krausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max G.I., Wang J., Hends P.,
RA Hopkins R.F., Jordan H., Moore T., Max G.I., Wang J., Heish F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Sapleton M., Soares M.B., Bonaldow M.F., Carannor T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Make S., Gararato P.H.,
RA Richards S., Worley K.C., Hales S., Garcia D., Mullahon D.K., Muzny D.M., Sodergen B.J., Lu X., Glibbs R.A.,
Rahes J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Blakesley R.W., Touchman J.W., Schwutz J., Myers R.M.,
B. Generation and initial analysis of more than 15,000 full-length human
Manner R. A. Scher L. M. R. A. Door, Konellonk M.A.
                                                                                                                                                                                                                                                                                                                                                                                   This Swiss-Prot entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                           between the Swiss Institute of Bioinformatics and the EMBL outstation-
the Buropean Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
--- FUNCTION: Substrate-recognition component of the SCF (SKPI-CULI-F-box protein)-type E3 ubiquitin ligase complex (By similarity).
--- SUBUNIT: Directly interacts with SKP1A and CULI (By similarity).
--- SIMILARITY: Contains 1 F-box domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Murokdea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 442;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          442 AA; 52646 MW; 32A1E4D69FA29C71 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52.6%; Score 40; DB 1; L
88.9%; Pred. No. 1.8e+02;
iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-MAY-2005 (Rel. 47, Created)
10-MAY-2005 (Rel. 47, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
P-box only protein 39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The mouse genome sequencing consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, BC034782, AAH34782.1; -; mRNA.
Ensembl; ENSG0000177294; Homo sapiens.
HGNC; HGNC:28565; FBXO39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F-box.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50181; FBOX; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEAM; PF00646; F-box; 1.
PRINTS; PR00019; LEURICHRPT.
SMART; SM00256; FBOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001810; F-box.
InterPro; IPR001611; LRR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 conjugation pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 88.5
hes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 RPSRVHNSE 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RPSRVHASE 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FBX39 MOUSE
QSNBU5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=Fbxo39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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-- SUBUNIT: Directly interacts with SKP1A and CUL1 (By similarity).
-- SIMILARITY: Contains 1 F-box domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gape
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52.6%; Score 40; DB 1; Length 443
88.9%; Pred. No. 1.8e+02;
iive 0; Mismatches 1; Indels
Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH - Mammalian Gene Collection (MGC) project;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 59 F-box.
443 AA; 52554 MW; 4F7D3B5F8B579213 CRC64;
                                                                                                                                                                                                                                                                                                                                                        EMBL; AL939071; CAI36035.1; ALT_INIT; Genomic_DNA. MGI; MGI:3505735; Fbxc39. InterPro; IPR001810; F-box. InterPro; IPR001611; LRR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 1-431.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; BC082089; AAH82089.1; ALT TERM; MRNA.
EMBL; BF542717; -; NOT ANNOTATED CDS; MRNA.
Ensembl; BNSNA000000014953; Rattus norvegicus.
InterPro; IPR001810; F.box.
InterPro; IPR001611; LRR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-MAY-2005 (Rel. 47, Created)
10-MAY-2005 (Rel. 47, Last sequence update)
MAY-2005 (Rel. 47, Last annotation update)
F-box only protein 39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                443 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00646; F-box; 1.
PRINTS; PR00019; LEURICHRPT.
PROSITE; PS50181; FBOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ubl conjugation pathway.
DOMAIN 13 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 RPSRVHNSE 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 RPSRVHASE 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10116;
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Southwick A., Nguyen M., Tripp M., Palm C.J., Jones T., Wu T.,
Carninci P., Chen H., Cheuk R., Chan M.M., Chang C.H., Dale J.M.,
Deng J.M., Hayashizaki Y., Hsuan V.W., Lee J.M., Ishida J., Kamiya A.,
Kawai J., Kim C.J., Narusaka M., Quach H.L., Sakurai T., Satou M.,
Seki M., Shinn P., Tang C.C., Toroumi M., Wallender B.K., Wong C.,
Wu H.C., Yamada K., Yu G., Yuan S., Shinozaki K., Ecker J.,
Theologis A., Davis R.W.;
                               Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                             Cheuk R., Chen H., Kim C.J., Shinn P., Ecker J.R.; Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.-!- SIMILARITY: Contains 1 RING-type zinc finger. EMBL; PA136427; AAM97093.1; -; mRNA. EMBL; BT0149665; AAT47817.1; -; mRNA.
                   (Mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :| | :|| |||:|
170 LVSRDARVSNSEQN 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 IVLRPSRVHNSEEN 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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                                                                                                               (1)
NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
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                                                                                         NCBI_TaxID=3702
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CDPK DAUCA
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Matches
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Whendeal5210978; DOI=10.1073/pnas.0305659101;

PubMeda=15210978; DOI=10.1073/pnas.0305659101;

A Alsmark U.C.M. Frank A.C., Karlberg E.O., Leganlt B.-A., Ardell D.H.,

A Alsmark U.C.M.; Frank A.C., Karlberg E.O., Leganlt B.-A., Huvet M.,

Canback B., Eriksson A.-S., Naeslund A.K., Handley S.A., Huvet M.,

La Scola B., Holmberg M., Andersson S.G.E.;

The louse-borne human pathogen Bartonella duintana is a genomic The derivative of the zoonocic agent Bartonella henselae.";

Proc. Natl. Acad. Sci. U.S.A. 101:9716-9721(2004).

REMBL; BKS97700; CAPE57931.j. -j Genomic_DAN.

GO; GO:0004445; F:glucose-6-phosphate I-dehydrogenase activity; IEA.

GO; GO:0016491; F:oxidoreductase activity; IEA.

RO; GO:0016975; P:carbohydrate metabolism; IEA.

InterPro; IPR001282; G6PD.

R Pfam; PPC0479; GGPD_N; 1.

R Pfam; PPC0479; GGPD_N; 1.

R PRES; PIRSP00110; G6PD, 1.

R PRINTS; PRSP000110; G6PD, 1.
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PROSITE; PS00069; G6P_DEHYDROGENASE; 1.
Carbohydrate metabolism; Complete proteome; Glucose metabolism; NADP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                          05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) (G6PD).
Name-zwf; OrderedLocusNames=BQ02930;
Bartonella quintana (Rochallmaea quintana).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bartonellaceae, Bartonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 40; DB 2; Length 491;
Pred. No. 2.1e+02;
                                                                                                                            52.6%; Score 40; DB 1; Length 443; 88.9%; Pred. No. 1.8e+02; cive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             491 AA; 56166 MW; 4F7F3A4E9EE8E107 CRC64;
                                                                                           SEQUENCE 443 AA; 52504 MW; 0A164BAC55B4B97F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2002 (TrEMBLrel. 22, Created)
1-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-FFB-2005 (TrEMBLrel. 29, Last annotation update)
RING finger-like protein (At5924870).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                             491 AA
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                                                                           F-box.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52.6%;
61.5%;
                 PRINTS, PRO0019, LEURICHRPT.
PROSITE, PS50181, PBOX, 1.
Ubl conjugation pathway.
DOMAIN 13 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    274 LMPLNVHNVEEHT 286
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Q8L775;
                                                                                                                                                                                                                                                                                                                 S BARQU
QGG155 BARQU PRELIMINARY;
QGG155;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                                       8; Conservative
 Pfam; PF00646; F-box; 1.
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                                                                                                                                                                                                            4 RPSRVHNSE 12
                                                                                                                                                                                                                                               66 RPSRVHASE 74
                                                                                                                                                    Best Local Similarity
Matches 8; Conser
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Q8L775 ARATH
D Q8L775 AR
AC Q8L775 D
DT 01-OCT-2
DT 01-OCT-2
DT 01-OCT-2
DE RING FEB-2
                                                                                                                                  Query Match
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Q6G155_BAR
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MEDLINE=92003674; PubMed=1912486;
Suen K.-L., Choi J.H.;
"Isolation and sequence analysis of a cDNA clone for a carrot calcium-
leolation and sequence thomology to calcium/calmodulin-dependent
protein kinases and to calmodulin.";
protein kinases and to calmodulin.";
Plant Mol. Biol. 17:581-590(1991).
-!- FUNCTION: May play a role in signal transduction pathways that
involve calcium as a second messenger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spermatophyta; Magnollophyta; eudicotyledons; core eudicotyledons;
asterids; campanulids; Apiales; Apiaceae; Apioideae; Scandiceae;
Daucinae; Daucus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 520;
GO; GO:00015; Timeral in ligase complex; IEA.
GO; GO:0046872; F:metal ion binding; IEA.
GO; GO:0046842; F:ubiquitin-protein ligase activity; IEA.
GO; GO:000270; F:zinc ion binding; IEA.
GO; GO:0016567; F:zinc ion binding; IEA.
InterPro; IPR001841; Znf xing.
Pfint: PF00097; Zf-C3HC4; 1.
SMO0184; RING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                           52.6%; Score 40; DB 2; Length 520
57.1%; Pred. No. 2.2e+02;
ive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Choi J.H.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                          PROSITE; PS50089; ZF RING 2; 1.
Metal-binding; Zinc, Zinc-finger.
SEQUENCE 520 AA; 56792 MW; 6BBEC00519AC886F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-1992 (Rel. 24, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Calcium-dependent protein kinase (EC 2.7.1.-) (CDPK).
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NCBI_TaxID=341;
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                                                                                    This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                 R INCEPTO; IPRO11992; EF-Hand type.
R INCEPTO; IPRO11992 EF-Hand Cabd.
Incerpro; IPR002048; EF-Hand Cabd.
Incerpro; IPR0020719; Prot kinase.
R Incerpro; IPR002290; Ser_thr_pkinase.
R Interpro; IPR002290; Ser_thr_pkinase.
R Pfan; PF00016; efhand; 4.
R Pfan; PF00012; EF-hand; 2.
R Probom; PD000012; EF-hand; 2.
R R PROSITE; PR00024; EFP; 4.
R PROSITE; PS00018; EF HAND 1; 4.
R PROSITE; PS00107; PROTEIN KINASE ATP; 1.
R PROSITE; PS00107; PROTEIN KINASE DOW; 1.
R PROSITE; PS00107; PROTEIN KINASE ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
ENZYME REGULATION: Activated by calcium. Autophosphorylation may play an important role in the regulation of the kinase activity. SIMILARITY: Belongs to the Ser/Thr protein kinase family. CAMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xanthomonas oryzae (pv. oryzae).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
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Proton acceptor (By similarity).
ATP (By similarity).
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Pred. No. 2.3e+02;
?; Mismatches 4; Indels
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein Khase.
EF-hand 1.
EF-hand 3.
EF-hand 4.
ATP (By similarity).
1 (Potential).
2 (Potential).
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STRAIN=KACC10331 / KXO85;
                                                        SIMILARITY: Contains 4 EF-hand domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                          EMBL; X56599; CAA39936.1; -; mRNA.
PIR; S17759; S17759.
PIR; T14335; T14335.
HSSP; Q63450; 1A06.
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QSGZ92;
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wes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACT SITE
BINDING
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CA_BIND
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PubMed=15673718; DOI=10.1093/nar/gki206;
Lee B.-M., Park Y.-J., Park D.-S., Kang H.-W., Kim J.-G., Song E.-S.,
Park I.-C., Yoon U.-H., Hahn J.-H., Koo B.-S., Lee G.-B., Kim H.,
A bark H.-S., Yoon K.-O., Kim J.-H., Xoo B.-S., Lee G.-B., Kim H.,
Go S.-J.;
The genome sequence of Xanthomonas oryzae pathovar oryzae KACC10331,
XT the bacterial blight pathogen of Tice.";
Nucleic Acids Res. 33:577-586(2008).
EMBL; AE013598; AAW7597-1; -; Genomic_DNA.
GO; GO:000156; F:two-component response regulator activity; IEA.
GO; GO:000160; P:two-component signal transduction system (p. .; IEA.
InterPro; IPR00163; BAL.
InterPro; IPR00160; P:two-component signal transduction system (p. .; IEA.
InterPro; IPR00160; P:two-component response regulator activity; IEA.
BR InterPro; IPR00160; P:two-component signal transduction system (p. .; IEA.
InterPro; IPR00160; P:two-component response regulator activity; IEA.
InterPro; IPR00160; P:two-component response regulator activity; IEA.
InterPro; IPR00160; P:two-component signal transduction system (p. .; IEA.
InterPro; IPR00160; P:two-component regulator activity; IEA.
InterPro; IPR00160; P:two-component regulator activity; IEA.
InterPro; IPR00160; P:two-component signal transduction system (p. .; IEA.
InterPro; IPR00160; P:two-component regulator activity; IEA.
InterPro; I
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PubMed-14642568; DOI=10.1128/JB.185.24.7092-7102.2003;

PubMed-14642568; DOI=10.1128/JB.185.24.7092-7102.2003;

PubMed-2 L., Thieme F., Gabler J., Buttner D., Bonas U.;

"XopC and XopJ, two novel type III effector proteins from Xanthomonas campestris pv. vesicatoria.";

J. Bacteriol. 185:7092-7102(2003).

EMBL, AX3085609; ARA23832.1; -; Genomic DNA.

EMBL, AX3085609; ARA23832.1; -; Genomic DNA.
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Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales,
Xanthomonadaceae, Xanthomonas.
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Pred. No. 3.5e+02;
1; Mismatches 4; Indels
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50.0%; Pred. No. 3.9e+02;
Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50883; EAL; 1.
PROSITE; PS50887; GGDEF; 1.
Complete proteome; Hypothetical protein.
SEQUENCE 771 AA; 85588 MW; B45DB7EFB918F9BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Type III_effector XopC.
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Best Local Similarity 61.5%;
Matches 8; Conservative 1
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220 LLRPTRDHYAEDST 233
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ID UME6_YEAST
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                   01-FEB-1995 (Rel. 31, Created)
10-CT-1996 (Rel. 34, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Transcriptional regulator UME6 (Negative transcriptional regulator
                                                                                                                                    Name=UME6; Synonyms=CAR80, CARGR1, NIM2; OrderedLocusNames=YDR207C;
                                                                                                                                                                                                                                                                                                                        STRAIN=Sigma 1278B;
Mart W.C., Park H.-D., Cooper T.G.;
"Sequence of the UMEs/CAR80 gene from Saccharomyces cerevisiae.";
Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                     Bukaryota, Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95011581; PubMed=7926768;
Strich R., Surosky R.T., Steber C., Messenguy F., Dubois E.
Easton Esposito R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UME6 is a key regulator of nitrogen repression and meiotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kumeno A.;
Submitted (DEC-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                               Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92253412; PubMed=1579492;
Park H.-D., Luche R.M., Cooper T.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97313263; PubMed=9169867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genes Dev. 8:796-810(1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=S288c / GRF88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AB972;
                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                              ORFNames=YD8142.04C;
                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                          NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-S288c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  development.
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GO; GO:0005634; C:nucleus; IPI.
GO; GO:0003677; F:DNA binding; IDA.
GO; GO:00030528; F:transcription regulator activity; IDA.
GO; GO:0007001; P:chromosome organization and biogenesis (sen. . .; IMP.
GO; GO:0007131; P:medotic recombination; IMP.
GO; GO:0007068; P:postive regulation of transcription, mitotic; IMP.
GO; GO:0030437; P:sporulation (sensu Fungi); IMP.
InterPro; IPR001138; Pungi_Trscrp_N.
PF00172; Zn_Clus; 1.
                                                                                                                                                                                                                                                                                                               expression.";
Nucleic Acids Res. 24:1322-1329(1996).
Nucleic Acids Res. 24:1322-1329(1996).
-!- FUNCTION: Binds to the UKS1 site (5'-AGCCGCCGA-3') and negatively regulates the expression of many genes including CAR1 (arginase), several required for sporulation, mating type switching, inositol metabolism, and oxidative carbon metabolism. Has both a positive and negative role in regulating phospholipid biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00463; ZN2 CY6 FUNGAL 1; 1.
PROSITE; PS50048; ZN2 CY6 FUNGAL 2; 1.
Activator; Complete proteome; DNA-binding; Metal-binding;
Nuclear protein; Repressor; Transcription; Transcription regulation;
                                                                                    Anderson S.F., Steber C.M., Easton Esposito R., Coleman J.E.;
Anderson S.F., Steber C.M., Easton Esposito R., Coleman J.E.;
"UMBG, a negative regulator of melosis in Saccharomyces cerevisiae,
contains a C-terminal Zn2Cys6 binuclear cluster that binds the URS1
DNA sequence in a zinc-dependent manner.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SUBCELLULAR LOCATION: Nuclear.
"The yeast UME6 gene product is required for transcriptional repression mediated by the CAR1 URS1 repressor binding site."; Nucleic Acids Res. 20:1909-1915(1992).
                                                                                                                                                                                                                                                         Jackson J.C., Lopes J.M.; "The yeast UME6 gene is required for both negative and posititranscriptional regulation of phospholipid biosynthetic gene
                                                                                                                                                                                                                       CHARACTERIZATION.
MEDLINE=96188868; PubMed=8614637; DOI=10.1093/nar/24.7.1322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 40; DB 1; Length 836; Pred. No. 3.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0DDA0A6B4A157182 CRC64;
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I -> V (in Ref. 1).
N -> T (in Ref. 1).
G -> D (in Ref. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; L32186; AAA34471.1; -; Genomic_DNA.
EMBL; L24539; AAC14472.1; -; Genomic_DNA.
EMBL; D2363; BAA04890.1; -; Genomic_DNA.
EMBL; Z68194; CAA92346.1; -; Genomic_DNA.
PIR; S61570; S1570.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSFAC; T01247; -.
Ensembl; YDR207C; Saccharomyces cerevisiae.
SGD; S000002615; UME6.
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Gaps

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1; Indels

Mismatches

VLRP--SRVHNSEE 13 Conservative

Local Similarity

6

Matches

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SOLUTION DE LA PRESENTATION DE L
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RR Amantalege For Scherer S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adamatides D.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,
Ra Brandon R.C., Barter E.G., Helf G., Nolson C.R., Miklos G.L.G.,
Ra Brandon R.C., Barter E.G., Helf G., Nolson C.R., Miklos G.L.G.,
Ra Ballew R.M., Baens P.V., Berman B.P., Bhandari D., Balahakvy S.,
Ballew R.M., Baens P.V., Berman B.P., Bhandari D., Bolahakvy S.,
Borkova D., Botchan M.R., Buller H., Cadieu E., Center A., Chandra I.,
Ra Cherry J.M., Cawley S., Dalike C., Davenport L.B., Downes R.A.
Borkova D., Botchan M.R., Buller H., Cadieu E., Center A., Chandra I.,
Ra Cherry J.M., Cawley S., Dalike C., Davenport L.B., Downes B.C.,
Durbin K.J., Evangelista C.C., Ferraz C., Ferricra S., Fleischman W.,
Ra Durbin K.J., Brongelista C.C., Ferraz C., Ferricra S., Fleischman W.,
Ra Harris N.L., Harvey D.A., Heiman T.J., Mei M.-H., Ibegam C.,
Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kalush F.,
Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Rechour K.A.,
Alali M., Kalush F., Karpen G.H., Ke Z., Kennison D.M., McPherson D.,
Ra Merkulov G. Milshina N.V., Mobarry C., Morris J., Mang Y., Lin X.,
Reiner K., Remington K.A., Murphy L., Murry D.M., Nelson D.L.,
Rainer K., Remington K.A., Murphy L., Murry D.M., Nelson D.K.,
Reiner K., Remington K., Sunders R.D.C., Scheeler F., Shen H.,
Rollos R., Peter S., Worley R., Weinstech B., Wallen R., Wolley R., Sunder S., Wall S., Wallen R., Wolley R., Weinstech B., Wallen S., Pollard J., Wang K., Wallesenbach J.,
Rainer R., Alexander S., Pander S., Pollard J., Wang X.,
Waller E., Spradling A.C., Stunders R.D.C., Scheeler F., Shen H.,
Rainer S.M., Woodage T., Worley K.C., Wu D., Yeh R., Shen B.,
Rainer S.M., Woodage T., Worley K., Wu D., Yeh S., Shirh H.,
Rainer S.M., Woodage T., Worley K., Wu D., Wang S., Zhu X., S
                                                                                                                                                                                                                                                                                               Importin-alpha re-exporter (Cellular apoptosis susceptibility protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22426069, PubMed=12537572;
Migra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21942515; PubMed=11944946; DOI=10.1006/dbio.2002.0612; Tekotte H., Berdnik D., Toeroek T., Buszczak M., Jones L.M., Cooley L., Knoblich J.A., Davis I.; "Dosa is required for importin-alpha3 nuclear export and mechanosensory organ cell fate specification in Drosophila."; Dev. Biol. 244:396-406(2002)
                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                               CSE1 DROME STANDARD; PRT; 975 AA. 09XZUJ; 09UB14; 09VJH4; 28-FEB-2003 (Rel. 41, Created) PFEB-2003 (Rel. 41, Last sequence update) 10-MAY-2005 (Rel. 47, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The genome sequence of Dro
Science 287:2185-2195(2000)
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571 VLRPILLRIHNSEQ 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
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Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P., Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                           STRAIN=Berkeley; TISSUE=Embryo; MEDLINE=20196012; PubMed=10731138; DOI=10.1126/science.287.5461.2222; Rubin G.M., Hong L., Brokstein P., Evans-Holm M., Frise E., Stapleton M., Harvey D.A.; A Drosophila complementary DNA resource."; Science 287:222-2224 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- FUNCTION: Export receptor for importin alpha. Mediates importinalpha reexport from the nucleus to the cytoplasm after import substrates have been released into the nucleoplasm (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- SUBUNIT: Binds with high affinity to importin-alpha only in the presence of RanGTP (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P23023-1:68x; NbExp=1; IntAct=EBI-126291, EBI-196732; Q9V9X8:Gcn2; NbExp=1; IntAct=EBI-126291, EBI-137454; I- SUBCLIULAR LOCATION: Nuclear and cytoplasmic (By similarity). -:- SIMILARITY: Belongs to the CSE1 family. -:- SIMILARITY: Contains 1 importin N-terminal domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                      "Annotation of the Drosophila melanogaster euchromatic genome:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 975;
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194 194 K -> T (in Ref. 2).
331 331 Q -> P (in Ref. 1).
589 590 AA -> GR (in Ref. 1).
975 AA, 110168 MW; 5C9BA11C08D49C11 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QBILYB PLAF7 PRELIMINARY; PRT; 2249 AA.
QBILYB;
QBILYB;
Q1.MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein PFD02000.
                                                                                                                                                                                                                                                               Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002)
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Ensembl; CG1328; Drosophila melanogaster.
ElyBase; FB90002213; Can.
GO; GO: 0006611; P: protein-ucleus export; IMP.
InterPro; IPR011989; ARM-like.
InterPro; IPR00494; Importinb_N.
Pfam; PF03178; CAS_CSEI; 1.
Pfam; PF03810; IBN_N; 1.
PROSITE; PS50166; IMPORTIN_B_NT; 1.
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54.5%; Pred. No. 4.7e+02;
iive 2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nuclear protein; Protein transport; Transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AJ238857; CAB42967.1; -; mRNA..
EMBL; AE003652; AAF53575.1; -; Genomic_DNA.
EMBL; AF132562; AAD27861.1; -; mRNA.
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PDRIHESDRNT 94
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                                                                                                                                                                                                                                              systematic review.";
                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                  Lewis S.E.;
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Q811Y8 PLAF7
1D Q811Y8-P1
AC Q811Y8,
DT 01-MAR-2(
DT 01-MAR-2D
DT 01-MAR-2D
DT HYDR-2(
DE HYDOCHAELS)
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Lectin_C
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es 7; Conserv
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                                                                                                                                                                                                ProDom;
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Q5R4S3_PON
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                                                                                                                          A Hall N., Pain A., Berriman M., Churcher C., Harris D.,

RA Hall N., Pain A., Berriman M., Churcher C., Harris D.,

RA Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,

RA Burkee C.O., Burrows C., Cherevach I., Chillingworth C.,

RA Chillingworth T., Christodoulou Z., Clark L., Clark E., Corton C.,

RA Chillingworth T., Gable A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,

R Feltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,

R Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,

R Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,

Line A., Maddison M., Mclean J., Mononey P., Moule S., Murphy L.,

A Diver K., Ormond D., Price C., Quail M.A., Rabbinowitsch E.,

R Rajandream M.A., Rutter S., Rutherford K.M., Sabbinowitsch E.,

R Rajandream S., Minkin E., Squares R., Squares S., Stevens K.,

R Sulston J.E., Craig A., Newbold C., Barrell B.G.;

Nature C. Plansmodium Falciparum chromosomes 1, 3-9 and 13.";

Nature A. 10.50-12-17000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100; Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T., Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R., Schlesner H., Amann R., Reinhardt R., Heitmann K., Reinhardt Schlesner Benome sequence of the marine planctomycete Pirellula sp. strain 1."; Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).

FEMBL: BX294135; CAD72214.1; -; Genomic_DNA.
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             Plasmodium falciparum (isolate 3D7).
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 40; DB 2; Length 2249;
Pred. No. 1.3e+03;
                                                                                                                 MEDLINE=22255708; PubMed=12368867; DOI=10.1038/nature01095;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
SEQUENCE 2249 AA; 271088 MW; 6EF04691C22FB787 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; 60:0016020; C:membrane; IEA.

GO; GO:0005509; F:calcium ion binding; IEA.

GO; GO:0005198; F:structural molecule activity; IEA.

GO; GO:0005529; F:sugar binding; IEA.

GO; GO:0007155; P:call adhesion; IEA.

GO; GO:0007156; P:homophilic cell adhesion; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein
OrderedLocusNames-RB1661;
Rhodopirellula baltica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 7716 AA
                                                                                                                                                                                                                                                                                                                                                                                                   Nature 419:527-531(2002).
EMBL; AL034557; CAD49133.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                h 52.6%;
Similarity 54.5%;
6; Conservative 4
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QTUWZ8 RHOBA PRELIMINARY;
QTUWZ8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
                                                                                    NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 6; Conserv
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      Name=PFD0200c
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EMBL, CR857776; CAH90040.1; -; mRNA.
Hypochetical protein.
SEQUENCE 113 AA; 13377 MW; CF0F91823777D34F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete protecome, HypoThetical protein.
SEQUENCE 7716 AA, 797868 MW; D391A25BD96405C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FBB-2005 (TrEMBLrel. 29, Created) 01-FBB-2005 (TrEMBLrel. 29, Last sequence update) 01-FBB-2005 (TrEMBLrel. 29, Last annotation update) Hypothetical protein DKFZp459G0119.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33 PONPY CORPY PRELIMINARY; PRT; 139 AA. Q5R433. PONPY PRELIMINARY; PRT; 139 AA. 05R483. 01-FEB-2005 (TrEMBLrel. 29, Created) 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52.6%; Score 40; DB 2; 1
63.6%; Pred. No. 5.5e+03;
ive 2; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50041; C TYPE LECTIN 2; 2. PROSITE; PS50025; LAM G DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
Interpro; PR006626; PbH1.
Interpro; IPR001759; Pentaxin.
Interpro; IPR001759; Pentaxin.
Pfam; PP02012; BNR; 5.
Pfam; PP02012; Chlam PMP; 7.
Pfam; PP0210; Chlam PMP; 7.
Pfam; PP0210; LaminIn G_2; 2.
                                                                                                                                                                                                                                                                              PD002153; Pentaxin; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Cortex;
The German cDNA Consortium;
                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00710; PbH1; 17.
TIGRFAMB; TIGR01376; POMP x
PROSITE; PS50268; CADHERIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pongo pygmaeus (Orangutan)
                                                                                                                                                                             Pfam; PF00059; Lectin C; 2
Pfam; PF00354; Pentaxin; 1
                                                                                                                                                                                                                            PRINTS; PR00205; CADHERIN.
PRINTS; PR00895; PENTAXIN.
                                                                                                                                                                                                                                                                                              SMART; SM00112; CA; 7.
SMART; SM00034; CLECT; 2.
SMART; SM00282; LamG; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 63.0
Eact Local 7; Conservative
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QSRDW7;
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and mouse
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                                                 Eukaryoča, Metazoa, Čhordata; Craniata; Vertebrata, Euteleostomi,
Mammalla, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pubmeda1702039; DOI=10.1038/ng1285;
Ota T. Survit Y. Nishikawa T., Otsuki T., Sugiyama T., Irie R., Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H., Sekine M., Obayashi K., Sato H., Shibahara T., Tanaka T., Ishii S., Yamanoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y., Abe K., Kamahara K., Katsuta N., Yamazaki M., Ishibashi T., Yamashita H., Murakawa K., Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y.,
                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Pituitary tumor;
Mao Y.F., Peng Y., Dai M., Huang Q.H., Song H., Zhang Q.H., Mao M.,
Pu G., Luo M., Chen J.H., Hu R.;
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                                                                                                                      VICLENCIPE.

TISSUB=Cortex;
The German cDNA Consortium;
Koehrer K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A., Robo G., Han M., Wiemann S.;
Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR861171; CAH93243.1; -; MRNA.
Hypothetical protein.

RROUENCE 139 AA; 16177 MW; 5137F6EBA9B8ACO5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                               09Y6G3; Q9F048; Q9P051;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Mitochondrial 288 ribosomal protein 532 (532mt) (MRP-532).
Name=WRP532; Synonyms=MRPL31, MRPL42; ORFNames=HSPC204, PTD007;
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21154917; PubMed=11230166; DOI=10.1101/gr.154701; Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S Ansorge W., Boecher M., Bloecker H., Bauersachber S., Blum H., Lauber J., Duestezhoeft A., Beyer A., Koehrer K., Strack N., Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D Wamburt R., Korn B., Klein M., Poustka A.; "Towards a catalog of human genes and proteins: sequencing and analysis of 500 novel complete protein coding human cDNAs.";
                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                            51.3%; Score 39; DB 2; Length 139; 70.0%; Pred. No. 70;
                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fu G., Luo M., Chen J.H., Hu R.;
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
 Last annotation update)
                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
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01-FEB-2005 (TrEMBLrel. 29, Last ar
Hypothetical protein DKFZp459F2016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome Res. 11:422-435(2001).
                                      Pongo pygmaeus (Orangutan)
                                                                                                                                                                                                                                 Query Match
Best Local Similarity 70.0°
                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                             4 RPSRVHNSEE 13
                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
                      Name=DKFZp459F2016;
                                                                                     NCBI_TaxID=9600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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Reservo. Y., Track-ground. S., Weathershe S., Yordsida M., Hourtea T., Kressno. V., Track-ground. S., Means M. T. Zake-drik K., Arita M., S., Mennes T. C., Mennes Y., Track-ground. S., Mennes T. C., Mennes T. S., Sasaki N., Sano S., Merry S. S., Sendhar S., Sano S., Merry S. S., Sendhar S., Sano S., Merry S. S., Sendhar S., Sano S., Merry S. S., Sendhar M., Sasaki N., Sano S., Merry S. S., Sendhar M., Sasaki N., Takani S., Palabara T., Merry S. Merry S. S., Sendhar M., Sano S., Merry S. S., Sendhar M., Sano S., Merry S. Merry S. Merry S. S., Merry S. Mer
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1 TETNG
QARF61 TETNG PRELIMINARY;
Q4RF61;
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RPSKPHNSKVN 94
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Matches
  LD DDT TD                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
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                                                                                                                                                                                                                                                                                This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
Koc E.C., Burkhart W., Blackburn K., Moseley A., Spremulli L.L., "The small subunit of the mammallan mitochondrial ribosome: "and protein of the full complement of ribosomal proteins present."; identification of the 19374 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                          -!- SUBUNIT: Component of the mitochondrial ribosome small subunit (285) which comprises a 125 rRNA and about 30 distinct proteins.-!- SUBCELLIULAR LOCATION: Mitochondrial.
-!- CAUTION: Was incorrectly assigned to be mitochondrial ribosomal protein L42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R EMBL; AKO00285; BAA91054.1; -; mRNA.
R EMBL; AL136659; CAB66594.1; -; mRNA.
R EMBL; AL131659; CAB66594.1; -; mRNA.
R EMBL; AL151038; AAF36124.1; -; mRNA.
R EMBL; BCG40240; AAH40240.1; -; mRNA.
R EMBL; AB051626; BAB54953.1; -; Genomic_DNA.
R Ensembl; RNGG0000198015; Homo sapiens.
R GO; GO:0005735; C:mitochondrial small ribosomal subunit; IDA.
R GO; GO:000543; P:protein biosynthesis; NAS.
R GO; GO:0006412; P:protein biosynthesis; NAS.
Mitochondrion; Ribonocleoprotein; Ribosomal protein.
SEQUENCE 142 AA; 16661 MW; AED9ECFA653F870A CRC64;
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Pred. No. 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 142;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF078860; AAD44492.1; -; mRNA.
EMBL; AF135160; AAF43784.1; -; mRNA.
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70.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QEFIDI HUMAN PRELIMINARY;
QEFIDI;
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Best Local Similarity 70.0
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10-MAY-2005 (TrEMBLrel.
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wes 7; Conserv
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Query Match

Matches

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RESULT 52
QGFIDI HUM
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RP REBELT
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RESULT 53 Q4R999 MAC ID Q4R99

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Maucell B., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., Maucell B., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Sequrens B., Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S., Anthouard V., Jubinn C., Castelli V., Katinka M., Vacherie B., Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V., Errand C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J., Reris M., Volff JN., Guigo R., Zody M.C., Mesirov J., McEwan P., Bosak S., Kallis M., Volff JN., Guigo R., Zody M.C., Mesirov J., McEwan P., Bosak S., Lindelad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M., Lindet V., Schachter V., Weissenbach J., Roest Crollius H.; Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.; Genome duplication in the teleost fish Tetraodon nigroviridis reveals
13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Testis cDNA clone: QCSA-10457, similar to human hypothetical protein
FLJ20291 (FLJ20291).
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        International consortium for macaque cDNA sequencing, analysis; "DNA sequences of macaque genes expressed in brain or testis and its evolutionary implications "; submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Bukaryota; Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Mepterygii; Teleostei; Buteleostei; Nocieleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Cercopithecidae, Cercopithecinae, Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VUCLEOTIDE SEQUENCE.
Osada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y.,
Osada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y.,
Osada N., Hashimoto K.,
Sugano S., Gojobori T., Shen J.C.-K., Wu C.I., Hashimoto K.,
Substitution rate and structural divergence of 5'UTR evolution:
Comparative analysis between human and cynomolgus monkey CDNAs.";
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AB168197; BAE00322.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
SEQUENCE 212 AA; 24772 MW; 175A63CB14E13C2A CRC64;
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
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63.6%; Pred. No. 1.2e+02;
tive 2; Mismatches 2;
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Nature 431:946-957(2004).
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Ait-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S., Arachchi H., Armbruster J., Bachanteang P., Baldwin J., Barry A., Bayul T., Blitshstepn B., Bloom T., Blyd., Boguslavskiy L., Boukhgalter B., Bloom T., Blyd., Boguslavskiy L., Boukhgalter B., Brunache A., Butler J., Campor K., Chang J., Chehatsang Y., Citroen M., Collymore A., Considine T., Cooke P., Cooke P., Corie P., Collymore A., Considine T., Cooke P., Cooke P., Corie P., Dorie E., Dorie K., Dorrie E., Dorie K., Dorrie K., Dorrie L., Defrey K., Golfe P., Elkins T., Engels R., Brickson J., Farina A., Faro S., Ferreira P., Elkins T., Engels R., Brickson J., Farina A., Faro S., Ferreira P., Elkins T., Engels R., Anix M., Poly K., Gage D., Galagan J., Garandols E., Gyalten K., Hafer N., Honde D., Hagos B., Hall J., Hatcher B., Haller A., Hagdins H., Honan T., Horn A., Houde N., Hudbes L., Hulme W., Hubby E., Illev I., Rangopian D., Hagos B., Hall J., Mardes L., Lowits B., Lowis B., Land D., Lander T., Luu X., Lowits D., Lowis B., Land D., Lander T., Luu X., Lowits B., Labutti K., Lama D., Lander T., Luu X., Lowits B., Labutti K., Lama D., Lander T., Luu X., Lowis B., Lowis D., Ludin D., Mandel M., Mabbit R., Maru K., Matthews C., Maucell E., Mallalev A., Malbour T., Michelen C., Malong V., Malhalev A., Minova T., Mikkelsen T., Meneus L., Mayven T., Micol R., Mayche T., Michelen C., Mizzari M., Noryuen T., Minova T., Mikhelsen T., Mizzari M., Noryuen T., Minova D., Phunkhang P., Patanin D., Phunkhang P., Patanin D., Phunkhang P., Patanin D., Saman C., Settigali S., Rachupka T., Ramasamy U., Ramesu R., Ray V., Raymond C., Ruchan M., Schupbach R., Saaman C., Settigali S., Sougnez C., Stone S., Studyer C., Sougnez C., Stone S., Studyer C., Sougnez C., Stenge-thomann M., Schupbach R., Saaman C., Settigali S., Rachipka S., Taender C., Settigali S., Rachipka S., Theodore J., Thollucasan Y., Topham K., Towey S., Tsaal T., Tower S., Tander E., Stone S., Studyer C., Spencer B., Studyer S., Tander S., Thollucasan S., Tophan R., Towey S., Tasal T., Tower S
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Arroya J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.,
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Aspergillus funigatus Af293.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eukaryota; Fungi; Ascomycota; mitosporic Trichocomaceae; Aspergillus.
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Pred. No. 1.7e+02;
5; Mismatches 2; Indels
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Last annotation update)
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EMBL; AACP01000002; EAK81573.1; -; Genomic_DNA.
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13-SEP-2005 (TrEMBLrel. 31, Last seq
13-SEP-2005 (TrEMBLrel. 31, Last ann
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ilarity 46.2%;
Conservative
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137 ILRTSRINNTRON 149
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Q4WQC4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 VLRPSRVHNSEEN 14
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Best Local Similarity
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PubMed=15305914; DOI=10.1111/j.1462-2920.2004.00665.x;

PubMed=15305914; DOI=10.1111/j.1462-2920.2004.00665.x;

Rabue R., Ruepp A., Fricky T., Rattel T., Fartmann B., Stark M.,

Rabue R., Albat A., Lombardot T., Becker I., Amann J., Gellner K.,

The ling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N., Amann R.,

Klenk H.-P.;

The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium from permanently cold Arctic sediments.";

Environ. Microbiol. 6:887-902(2004).

BRBL; CES22870; GAG36792.1; -; Genomic DNA.

GO; GO:0003700; F:transcription factor activity; IEA.

GO; GO:0003515; P:regulation of transcription, DNA-dependent; IEA.

GO; GO:000515; P:regulation of transcription, Complete protecome; Hypothetical protein.

GO SEQUENCE 226 AA; 24666 MW; 492206D2FD96A9BA CRC64;
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Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacterales;
Desulfobulbaceae; Desulfotalea.
                                                         -1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
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Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,
                                                                                                                                                                                                                                                                51.3%; Score 39; DB 2; Length 217; 61.5%; Pred. No. 1.2e+02; ive 2; Mismatches 3; Indels
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                            (FEB-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                       217 AA; 24829 MW; 4C59A115BE2D1DB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-OCT-2004 (TrEMBLrel. 28, Last sequence update) 25-OCT-2004 (TrEMBLrel. 28, Last annotation update) Hypothetical protein.
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Last annotation update)
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                                                                                                                                           EMBL; CAAE01015120; CAG12971.1; -; Genomic_DNA.
NON TER 217 217
SEQUENCE 217 AA; 24829 MW; 4C59A115BE2DIDBO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 226 AA.
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13-SEP-2005 (TrEMBLrel. 31,
13-SEP-2005 (TrEMBLrel. 31,
Hypothetical protein.
ORFNames=UM00188.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                  88 LRWSTLHGSEONT 100
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Best Local Similarity 61.3.
Best Local 8; Conservative
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Q4P175;
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QEALI3;
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                                                                                                                     preliminary data.
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04P175 UST
10 04P175 UST
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Bowyer P., Chen D., Collins M., Coulsen R., Davies R., Dyer P.S.,
Raman M., Fedorova N., Fedorova N., Feldblyum T.V., Fischer R.,
Rosker N., Eraser A., Garcia J.L., Garcia M.J., Goble A.,
Goldman G.H., Gomi K., Griffith J.Dones S., Gwilliam R., Haas B.,
Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J.,
Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,
Kumagai T., Lafton A., Latge J.-P., Li W., Lord A., Lu C.,
Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.,
Majoros W.H., May G.S., Murphy L., O'Neil S., Paulsen I.,
Rabbinowitsch E., Rawlins N., Price C., Pritchard B.L., Quail M.A.,
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White O., Woodward J., Yu J.-H., Fraser C., Galagan J.B., Asai K.,
Machida M., Hall N., Barrell B., Denning D.W.;
Agnares S.,
Machida M., Hall N., Barrell B., Denning C.M., Shagatus,
Rapperillus fumiquatus, M.,
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PubMed=1502419; DOI=10.1371/journal.pbio.0020069;

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"Phylogenomics of the reproductive parasite Wolbachia pipientis wMel:

a streamlined genome overrun by mobile genetic elements.";

EMBL, AE017260; AAS14782.1; -; Genomic_DNA.
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Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Wolbachieae; Wolbachia.
NCBL_TaxID=66077;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51.3%; Score 39; DB 2; Length 316; S0.0%; Pred. No. 1.9e+02; tive 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases
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SEQUENCE 316 AA; 35718 MW; B3D773BEA6BFB326 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .AAHF01000005; EAL89560.1; -; Genomic_DNA.
NCE 316 AA; 37064 MW; F9824E1C3F42BB86 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Pfam; PF01370; Epimerase; 1.
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165 VTLRPSLRHSTEED 178
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7; Conservative
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Q73G36;
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nes 7; Conservative
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073436 WOL
073433 AC
07343 AC
0734                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Spiegel L.A., Huang B.N., Nascimento L.U., de la Bastide M., Vil D.M., Preston R.R., Matero A., Shah R., O'Shaughnessy A., Rodriguez M., Shekhter M., Schutz K., See L.H., Swaby I., Habermann K., Dedhia N.N., Mawes H.W., Lemcke K., Mayer K.F.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brwinia carotovora (gubsp, atroseptica) (Pectobacterium atrosepticum).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Pectobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=SCRI 1043 / ATCC BAA-672;

PubMed=15263089; DOI=10.1073/pnas.0402424101;

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Holeva M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,

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Salmond G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;

"Genome sequence of the enterobacterial phytopathogen Erwinia
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                                                                                                                                                                             core eudicots, rosids,
                                                                                                                                                            Eukaryoča; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 333;
                                                                                                                                                                                                                                                                                                                                                                                                      EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ALIS1503; CAB81086.1; -; Genomic_DNA.
PIR; D85068; D85068.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR009772; D123.
Pfam; PF07065; D123; 1.
SEQUENCE 333 AA; 38777 MW; 85DBA4B4F38703D2 CRC64;
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EMBL; BX950851; CAG74953.1; -; Genomic_DNA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005524; F:ATP binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Putitive ABC-transporter ATP-binding protein.
                                                 Created)
Last sequence update)
Last annotation update)
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               333 AA
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1; Mismatches
                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).
                 PRT;
                                                 01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-MAR-2004 (TrEMBLrel. 26,
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               QMOV1_ARATH PRELIMINARY;
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Matches 7; Conservative
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NUCLEOTIDE SEQUENCE.
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                                                                                                              D123-like protein.
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                                                                                                                               Name=AT4g05440
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R GO; GO:0016887; F:ATPase activity; IEA.

R GO; GO:00166; F:nucleotide binding; IEA.

R GO; GO:0015417; F:polyamine transporting ATPase activity; IEA.

R GO; GO:0015846; F:polyamine transporting ATPase activity; IEA.

R InterPro; IPR003593; AAA ATPase.

R InterPro; IPR003493; ABC transp like.

R InterPro; IPR005933; Sp/ptABC_transpt.

R InterPro; IPR005933; Sp/ptABC_transpt.

R R InterPro; IPR005934 ABC transpt.

R R SMART; SM00180; AAA; I.

R RYART; SM00182; AAA; I.

R PROSITE; PS00211; ABC TRANSPORTER 1; 1.

R PROSITE; PS00931; ABC_TRANSPORTER 2; 1.

R ATP-binding; Complete proteome.

O SEQUENCE 364 AA; 41307 MW; 676CE6C1F284ABF1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                Query Match 51.3%; Score 39; DB 2; Length 364; Best Local Similarity 40.0%; Pred. No. 2.2e+02; Matches 6; Conservative 5; Mismatches 4; Indels
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Search completed: March 11, 2006, 12:24:37 Job time : 169.842 secs

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27405, 24931, 33410,

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Sequence 12, Appl
Sequence 2267, Ap
Sequence 7647, Ap
Sequence 21009, A
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Sequence 32, At
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Sequence 3, Ap
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	1 125 2 US-09-370-838-59 Sequence 59, 1 125 2 US-09-854-133-59	1 126 2 US-09-270-76788 Sequence 4678 1 128 2 US-09-370-838-61 Sequence 61,	1 128 2 US-09-252-991A-28235 Sequence 2823 1 128 2 US-09-854-133-61 Sequence 61.	1 132 2 US-09-270-767-33546 Sequence 3354	1 132 2 US-09-270-767-48763 sequence 1 149 2 US-09-270-767-32661 Sequence	1 149 2 US-09-270-767-47878 Sequence	1 159 2 US-09-618-259-5 1. 163 2 US-09-489-039A-10183 Sequence	1 163 2 US-09-902-540-10547 Sequence	1 164 2 US-09-518-046-25 sequence	1 174 2 US-09-270-767-35941 Sequence	1 174 2 US-09-270-767-51158 Sequence	1 180 2 US-09-252-991A-32665 Sequence	1 183 Z US-US-31Z-Z83C-383 Sequence	1 183 2 US-10-015-389A-68 Sequence	1 183 2 US-10-006-768A-68 Sequence	1 183 2 US-10-015-671A-68 Sequence	1 183 2 US-10-015-393A-68 Sequence	1 183 2 US-10-011-833A-68 Sequence	1 183 2 US-10-006-041A-68 sequence	1 183 2 US-10-012-054A-68 sequence	1 183 Z US-10-030-259A-Z Sequence Z,	1 197 1 03-00-309-209-1 3 264memee 1,	1	1 197 2 US-09-220-399-2	1 197 2 US-10-017-754-1904 Sequence 1904, A	1 216 2 US-09-270-767-44613 sequence 44	1 218 2 US-09-489-039A-10326 Sequence 103	1 222 2 US-10-101-464A-720 sequence 720	1 223 2 US-09-538-092-145 Sequence 145	1 226 2 US-09-107-532A-3696 sequence 352	1 231 2 US-09-487-558B-232 sequence 232	1 237 2 US-09-252-991A-21759 Sequence 217	1 255 2 US-08-944-483-67 sequence 67,	1 256 1 US-09-027-337-3 Sequence 3,	1 256 2 US-09-644-600-3 sequence 3,	1 256 2 US-09-654-60UA-3 sequence 3,	1 273 2 US-09-270-767-41185 sequence 411	1 273 2 US-09-270-767-56401 Sequence 56401,	1 280 1 US-08-312-3878-6 Sequence 6, Appl	1 280 1 US-08-683-426-6 Sequence 6, Appl	1 280 1 US-08-683-458-6 Sequence 6, Appl	.1 280 1 US-08-878-360-6 Sequence 6,	1 280 2 US-08-478-140B-6 Sequence 6,	1 280 2 US-09-333-412-6 Sequence 6,	1 280 2 US-09-338-943-6 Sequence 6,	1 280 2 US-10-007-267A-6 Sequence b, Appl	.1 283 2 US-09-252-991A-22824 Sequence 22824,	1 296 2 US-US-101-101-391/U Sequence 331/U,	T. 200 2 US-01-01-01-01-01 2 062 T. 20-00-01 C 00C T.	1 311 2 11S-09-270-767-42099 Sequence 420	1 317 2 US-09-746-801A-57 Sequence 57,	.1 317 2 US-10-719-885-57 Sequence 57,	.1 . 326 2 US-09-248-796A-16985 Sequence 169	.1 349 2 US-10-300-819B-25 Sequence 25,	.1 353 2 US-09-107-532A-7032 Sequence 703	1 355 2 US-09-252-991A-32375 Sequence 323	1 356 2 US-09-248-796A-15198 Sequence 151	1 370 2 US-09-252-991A-24608 Sequence 246	1 370 2 US-08-311-731A-203 Sequence 203	.1 376 2 US-09-820-002-2 Sequence 2,	.1 386 2 US-09-086-483A-2 Sequence 2,	.1 386 2 US-08-875-082-2 Sequence 2,	1 386 2 US-09-130-491-6 Seguence 6,	.1 386 2 US-09-580-212-2 Sequence 2,	7-217-000-00-00 7 000 T	
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	2.1 125 2 US-09-370-838-59 Sequence 59, 2.1 125 2 US-09-854-133-59 Sequence 59,	42.1 126 2 US-09-270-767-46788 Sequence 4678 42.1 128 2 US-09-370-838-61 Sequence 61,	42.1 128 2 US-09-252-991A-28235 Sequence 2823 42.1 128 2 US-09-854-133-61 Sequence 61.	42.1 132 2 US-09-270-767-33546 Sequence 335	42.1 132 2 US-09-270-767-48763 Sequence	42.1 149 2 US-09-270-767-47878 Sequence	42.1 159 2 US-09-618-259-5 Sequence 42.1 163 2 US-09-489-039A-10183 Sequence	42.1 163 2 US-09-902-540-10547 Sequence	42.1 164 2 US-U9-518-046-25 sequence	42,1 174 2 US-09-270-767-35941 Sequence	42.1 174 2 US-09-270-767-51158 Sequence	42.1 180 2 US-09-252-991A-32665 Sequence	42.1 183 2 08-09-312-283C-583 Sequence	42.1 183 2 US-10-015-389A-68 Sequence	42.1 183 2 US-10-006-768A-68 Sequence	42.1 183 2 US-10-015-671A-68 Sequence	42.1 183 2 US-10-015-393A-68 Sequence	42.1 183 2 US-10-011-833A-68 Sequence	42.1 183 2 US-10-006-041A-68 sequence	42.1 183 2 US-IO-012-054A-58 Sequence	42.1 183 2 US-10-030-269A-2 Sequence 2,	42.1 19/ 1 US-US-203-203-1 Sequence 1,	12.1 107 2 00-03-220-000 7 12 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	42.1 I37 2 US-U3-22U-399-2 Seduence 2,	42.1 197 2 US-10-01/-/54-1904 Sequence 1904, A	42.1 216 2 US-09-270-767-44613 Sequence 44	42.1 218 2 US-09-489-039A-10326 Sequence 103	42.1 222 2 US-10-101-464A-720 Sequence 720	42.1 223 2 US-09-538-092-145 Sequence 145	42.1 226 2 US-09-107-532A-3696 sequence 353	42.1 231 2 US-09-487-5588-232 Sequence 232	42.1 237 2 US-09-252-991A-21759 Sequence 217	42.1 255 2 US-08-944-483-67	42.1 256 1 US-09-027-337-3 Sequence 3,	42.1 256 2 US-09-644-600-3 Sequence 3,	42.1 256 2 US-09-654-60UA-3 Sequence 3,	42.1 273 2 US-09-270-767-41185 Sequence 411	42.1 273 2 US-09-270-767-56401 Sequence 56401,	42.1 280 1 US-08-312-387B-6 Sequence 6, Appl	42.1 280 1 US-08-683-426-6 Sequence 6, Appl	42.1 280 1 US-08-683-458-6 Sequence 6, Appl	42.1 280 1 US-08-878-360-6 Sequence 6,	42.1 280 2 US-08-478-140B-6 Sequence 6,	42.1 280 2 US-09-333-412-6 Sequence 6,	42,1 280 2 US-09-338-943-6 Sequence 6,	42.1 280 2 US-10-007-26/A-6 Sequence 6, Appr	42.1 283 2 US-09-252-99IA-22824 Sequence 22824,	14.1	42.1 236 2 US-US-2/0-/01-240 2 247 T.24	42.1 2.1 2 US-09-270-767-42099 Sequence 420	42.1 317 2 US-09-746-801A-57 Sequence 57,	42.1 317 2 US-10-719-885-57 Sequence 57,	42,1 . 326 2 US-09-248-796A-16985 Sequence 169	42.1 349 2 US-10-300-819B-25 Sequence 25,	42.1 353 2 US-U9-I0/-53ZA-/03Z sequence /03	42.1 355 2 US-09-252-991A-32375 Sequence 323	42.1 356 2 US-09-248-796A-15198 Sequence 151	42.1 370 2 US-09-252-991A-24608 Sequence 246	42.1 370 2 US-08-311-731A-203 Sequence 203	42,1 376 2 US-09-820-002-2 Sequence 2,	42.1 386 2 US-09-086-483A-2 Seguence 2,	42.1 386 2 US-08-875-082-2 Sequence 2,	42.1 386 2 US-09-130-491-6 Sequence 6,	42.1 386 2 US-09-580-212-2 Sequence 2,	7-217-000-00 7 000 T:25	

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Length 760;
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Patent No. 5965373
GENERAL INFORMATION:
APPLICANT: Zimmermann, Rainer; Park, John E.;
APPLICANT: Rettig, Wolfgang; Old, Lloyd J.
TITLE OF INVENTION: ISOLATED DIMERIC FIBROBLAST ACT
TITLE OF INVENTION: PROTEIN ALPHA, AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIE: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 2.0 MB st
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOCTWARE: Wordberfect
CURBENT APPLICATION NUMBER: US/08/940,391
FILING DATE: 01-007-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 76;
100.0%; Pred. No. 1
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                            LUD 5330.1
                                   APPLICATION NUMBER: US/06/01/2009

CLASSIFICATION: 435

RIOR APPLICATION 435

PRIOR APPLICATION AUGUST

APPLICATION NUMBER: 08/230,491

FILING DATE: 20-APRIL-1994

ATTORNEY/ABRIT INFORMATION:
NAME: Hanson, No. 5767242mn D.
REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: LUD 5330

TELECHONNICATION INFORMATION:
TELECHONE: (212) 688-9200

TELEPAX: (212) 688-9200

TELEPAX: (212) 688-9201

TELEPAX: (212) 838-3894

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 760 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/619,280
FILING DATE: 18-MARCH-1996
APPLICATION NUMBER: 06/230,491
FILING DATE: 20-APRIL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Hanson, No. 5965373man D. REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (212) 688-9200
TELEPAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 760 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 IVLRPSRVHNSEENT 38
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Best Local Similarity 100.
Matches 15; Conservative
CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
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Patent No. 5767242
GENERAL INFORMATION:
APPLICANT: Zimmermann, Rainer; Park, John E.;
APPLICANT: Rettig, Wolfgang; Old, Lloyd J.
TITLE OF INVENTION: ISOLATED DIMERIC FIBROBLAST ACTIVATION PROTEIN
TITLE OF INVENTION: ALPHA, AND USES THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
                                                                                                              GENERAL INFORMATION:
APPLICANT: Rettig, Wolfgang J.; Scanlan, Matthew J.;
APPLICANT: Garin-Chesa, Filar; Old, Lloyd J.
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE CODING FOR TITLE OF INVENTION: FIRROBLIST ACTIVATION PROTEIN AND USES TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 760;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE 3.5 inch 1.2 MB STORAGE
COMPUTER: IBM PSC.
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT - ASC II
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/230,491A
FILING DATE: 20-APRIL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HANSON, NO. 5587299man D.
REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Diskette, 3.5 inch, 2.0 MB storage
                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: FELFE & LYNCH
STREET: 805 THIRD AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Sco
100.0%; Pre
                                                                    Sequence 2, Application US/08230491A
Patent No. 5587299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Felfe Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: LI
FELECOMMUNICATION INFORMATION
TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                    NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                              USA
10022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         760 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.8
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wordperfect
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COMPUTER READABLE FORM:
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OPERATING SYSTEM: F
SOFTWARE: Wordberfe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                    NEW YORK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-230-491A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-619-280A-2
                                                     US-08-230-491A-2
                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                 CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
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US-09-248-796A-23053
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 | Sequence 2. Application US/09265606 | Sequence 2. Application US/09265606 | Sequence 2. Application US/09265606 | Sequence 2. Applicant No. 6846910 | GENERAL INFORMATION: APPLICANT: Zimmermann, Rainer; Park, John E.; APPLICANT: Rettig, Wolfgang; Old, Lloyd J. TITLE OF INVENTION: ISOLATED DIMERCE FIBROBLAST ACTIVATION PROTEIN TITLE OF INVENTION: ALPHA, AND USES THEREOF | VUMBER OF SEQUENCES: 10 | CORRESPONDENCE ADDRESS: ADDRESSEE: Felfe & Lynch | STREET: 805 Third Avenue | CITY: New York City | STATE: New York City | STAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Pred. No. 1.7e-05;
Mismatches 0; Indels
                                                                  100.0%; Score 76; DB 1; Length 760; 100.0%; Pred. No. 1.7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 2.0 MB
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Hanson, No. 6846910man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5330.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID No: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 760 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/619,280
FILING DATE: 18 MARCH-1996
APPLICATION NUMBER: 08/230,491
FILING DATE: 20-APRIL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265,606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
US-09-518-550-26
Second 26, Application US/09518550
Patent No. 6875851
GENERAL INFORMATION:
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BANBULA, Agnieszka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 IVLRPSRVHNSEENT 38
                                                                                                                                                                                                                                                                     24 IVLRPSRVHNSEENT 38
                                                                                                                                                                                                                      1 IVLRPSRVHNSEENT 15
                                                              Query Match
Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: TRAVIS,
APPLICANT: POTEMPI
APPLICANT: BANBULA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-265-606-2
US-08-940-391-2
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Sequence 3063, Application US/09248796A

Sequence 3063, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS.

TITLE OF INVENTION: NUMBER: US/09/248,796A

CURRENT PILING DATE: 1999-02-13

PRIOR PELLING DATE: 1998-02-13

PRIOR PELLING DATE: 1998-02-13

PRIOR FILING DATE: 1998-08-13

NUMBER PO SEQ ID NOS: 28208

SEQ ID NO 23053

LENGTH: 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: UNSURE

1 LOCATION: (2),(3),(21)

2 OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknow

US-09-248-7968-23053
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Patent No. 6753314
GENERAL INFORMATION:
APPLICANT: Giot, Loic
APPLICANT: Giot, Loic
APPLICANT: Mansieled, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: 2000-329
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
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                                                                                                                                                                                                                                                                                                                                                                                              Query Match 68.4%; Score 52; DB 2; Length 761; Best Local Similarity 73.3%; Pred. No. 0.43; Matches 11; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 42; DB 2; Length 327;
Pred. No. 11;
4; Mismatches 2; Indels
TITLE OF INVENTION: PROLYL PEPTIDASES AND METHODS OF USE
                    FILE REFERENCE: 235.00190101
CURRENT APPLICATION NUMBER: US/09/518,550
CURRENT FILING DATE: 2000-03-03
FRIOR APPLICATION NUMBER: 60/123,148
PRIOR FILING DATE: 1999-03-05
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 26
LENGTH: 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 IVLRPSRVHNSEENT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 55.3
Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Mus musculus
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GENERAL INFORMATION:
US-09-270-767-62451
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APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62217
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 62451
LENGTH: 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hart, Hope
APPLICANT: Warren, Gregory W.
APPLICANT: Warren, Gregory W.
APPLICANT: Dunn, Martha
APPLICANT: Dunn, Martha
APPLICANT: Chen, Jeng S.
TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS FROM PHOTORHABDU
TITLE OF INVENTION: AND NUCLEIC ACID SEQUENCES CODING THEREFOR
FILE REFERENCE: CGC1983/A
CURRENT APPLICATION NUMBER: US/09/251,645
CURRENT FILING DATE: 1999-02-17
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52.6%; Score 40; DB 2; Length 1584; 61.5%; Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                   52.6%; Score 40; DB 2; Length 836; 64.3%; Pred. No. 77;
                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                      NAME/KEY: misc_feature

: LOCATION: (0)...(0)

: OTHER INFORMATION: Polypeptide Accession Number YDR207C

US-09-538-092-173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.6e+02;
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                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
  PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuraPatSegFormatter Version 0.9
SEQ ID NO 173
LENGTH: 836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Photorhabdus luminescens
                                                                                                                                     TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/09251645
Patent No. 6281413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kramer, Vance C. APPLICANT: Morgan, Michael K. APPLICANT: Anderson, Arne R.
                                                                                                                                                                                                                                                                                                                                                                                                                                        |||| |:||||:
571 VLRPILLRIHNSEQ 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 61.5%
Matches 8; Conservative .
                                                                                                                                                                                                                                                                                                                                                                                                               2 VLRP--SRVHNSEE 13
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                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 64.3
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1584
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Sequence 306, Application US/09673395A

Sequence 306, Application US/09673395A

Patent No. 6620923

GENERAL INFORMATION:
PAPLICANT: SPECHT, THOMAS

APPLICANT: SCHMITT, ARMIN
APPLICANT: SCHMITT, ARMIN
APPLICANT: ROSENTHAL, ANDRE
TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM UTERUS TUMOR TISSUE
TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM UTERUS TUMOR TISSUE
CURRENT FILING DATE: 2000-10-17

NUMBER OF SEQ ID NOS: 637

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 306

LENGTH 144
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APPLICANT: HINZMANN, BERND
APPLICANT: HINZMANN, BERND
APPLICANT: SCHMITT, ARMIN
APPLICANT: SCHMITT, ARMIN
APPLICANT: DAHL, EDGAR
APPLICANT: DAHL, EDGAR
APPLICANT: ROSENTHAL, ANDRE
TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES PROM UTERUS TUMOR TISSUE
FILE REFERENCE: ALBRE-12
CURRENT FILLING NUMBER: US/09/673,395A
CURRENT FILLING DATE: 2000-10-17
NUMBER OF SEQ ID NOS: 637
SOFTWARE: Atentin Ver. 2.1
SEQ ID NO 588
LENGTH: 144
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Pred. No. 16;
1; Mismatches 2; Indels
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16;
Length 81;
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                                        1; Indels
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                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 39;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-673-395A-588
; Sequence 588, Application US/09673395A
; Patent No. 6620923
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70.0%;
  51.3%;
77.8%;
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Best Local Similarity 70.0
Matches 7; Conservative
  Query Match 51.3
Best Local Similarity 77.8
Matches 7; Conservative
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79 RPDPVHNNEE 88
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79 RPDPVHNNEE 88
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ORGANISM: Homo sapiens
US-09-673-395A-588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
CRGANISM: Homo sapiens
US-09-673-395A-306
                                                                              7 RVHNSEENT 15
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26 RVHNIEDNT 34
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Matches 7: Conserv
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Score 38; DB 2;
Pred. No. 71;
1; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , DB 2;
                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/212,247C
FILING DATE: 16-Dec-1998
CLASSIFICATION: <Unknown>
INFORMATION POR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50.0%; Score 38; DB 53.3%; Pred. No. 71; tive 1; Mismatches
                    NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSE: Keil & Weinkauf
STREET: 1101 Connecticut Avenue
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
synthesis
21
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Patent No. 6878536
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 371 amino acids TYPE: amino acid
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145 VVLNPSHVTQLERNT 159
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Best Local Similarity 53.33
Matches 8; Conservative
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, ORGANISM: Ashbya gossypii
US-10-076-157-6
                                                                                                                        STATE: D.C.
COUNTRY: USA
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Best Local Similarity
Matches 8; Conserv
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                                   Sequence 46824, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT PILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 46824
LENGTH: 389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Glot, Loic
APPLICANT: Glot, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT APPLICATION NUMBER: 00/10/3-29
RELOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR FILING DATE: 1999-04-01
NUMBER OF SEQ ID NOS: 1387
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CURAPALSeqFormatter Version 0.9
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Pred. No. 70;
                                                                                                                                                                                                                                                                                                                                                                    51.3%; Score 39; DB 2; Length 389; 77.8%; Pred. No. 49;
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; OTHER INFORMATION: Polypeptide Accession Number YGR173W

US-09-538-092-38
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                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
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US-09-212-247C-6
; Sequence 6, Application US/09212247C
; Detent No. 6391603
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-46824
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Best Local Similarity 50.0°
Local 6; Conservative
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207 MILRDYRIHNAE 218
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Best Local Similarity 77.5
Best Local Similarity 77.5
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LENGTH: 368
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APPLICANT: Pompedus, Markus
APPLICANT: Pompedus, Markus
APPLICANT: Suelberger, Harald
APPLICANT: Suelberger, Harald
APPLICANT: Suelberger, Harald
APPLICANT: Jose Luis Wolfgang
APPLICANT: Jimenez, Alberto;
APPLICANT: Jimenez, Alberto;
APPLICANT: Jimenez, Alberto;
APPLICANT: Jimenez, Alberto;
APPLICANT: Garcia, Maria Angeles Santos
TITLE OF INVENTION: in microbial riboflavin synthesis
TITLE OF INVENTION: in microbial riboflavin synthesis
FILE REFERENCE: 48684DIV
CURRENT APPLICATION NUMBER: US/10/076,157
CURRENT APPLICATION NUMBER: US 09/212,247
PRIOR APPLICATION NUMBER: US 09/212,247
PRIOR APPLICATION NUMBER: US 09/212,247
SROFWARE: WordPerfect v. 6.1
SSQ ID NO 6
IENGTH: 371
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TITLE OF INVENTION: Genes of purine biosynthesis from Ashbya Gossypii
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                                 and the use thereof in microbial riboflavin
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                                                                                                                                                                                                                                                                                               ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
COMPUTER: IBM AT-compatible, Pentium processor
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect version 6.1
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Sequence 61152, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 61152
LENGTH: 113
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TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
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                                                      Length 83;
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28;
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                                                                                                                3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                   Score 37;
Pred. No. 1
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Pred. No.
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Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-270-767-37828

; Sequence 37838, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , ORGANISM: Drosophila melanogaster
US-09-270-767-61152
                                                         48.7%;
53.3%;
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203 VICNPKQMSNSQENS 217
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16 VLLRPSRRVRSQEPT 30
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                                                         Query Match
Best Local Similarity 53.3
Matches 8; Conservative
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Best Local Similarity
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Best Local Similarity
Matches 5; Conserv
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US-08-499-676A-12
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                                                                                                                                           GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
APIC J.
APPLICANT:
APIC J.
APIC 
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Sequence 12, Application US/08499676A
Patent No. 5988154
GENERAL INFORMATION:
APPLICANT: AGNES SCHONBRUNN
TITLE OF INFORTION: SOMATOSTATIN RECEPTOR PEPTIDE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,676A
FILING DATE: July 7, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Pravel, Hewitt, Kimball & Krieger STREET: 1177 West Loop South, 10th Floor CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79247.3/A95175US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11arity 56.2%; Pred. No. 1. Conservative 2; Mismatche
                                                                                          Sequence 20733, Application US/09252991A
Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Krieger, Paul E.
REGISTRATION NUMBER: 25,886
REFERENCE/DOCKET NUMBER: 7924
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-850-0909
TELEFAX: 713-850-0165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25,886
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 83 amino acida
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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Best Local Similarity
Matches 9; Conserv
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                                 RESULT 17
US-09-252-991A-20733
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Gaps

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Sequence 1278, Application US/09489039A

Factor No. 6610836

GENERAL INFORMATION:
APPLICANT: GATY Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US 60/117,747
PRIOR PLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342

EENGTH: 414
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Score 37; DB 2; Length 375;
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTE: IBM PC compatible
COMPUTE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/816,283
FILING DATE: 19911211
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McDaniel, C. Steven
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: 713-787-1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10, Application US/07816283
Sequence 10, Application US/07816283
Sequence 10, Application US/07816283
Sequence 10, Application US/07816283
SEQUENCE 10, Graeme I.
APPLICANT: Yamada, Yuichiro
APPLICANT: Seino, Suamu
TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESSE:
ADDRESSE: ATNOIG, White & Durkee
STREET: PO BOX 4433
CITY: HOUBTON
STATE: Texar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12578
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TELEFAX: 79-0924
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
    48.78;
                                                                                                                   173 MVLHPDEIHDGEAGT 187
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Best Local Similarity 53.8%;
Matches 7; Conservative
                                                                                          1 IVLRPSRVHNSEENT 15
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                                              6; Conservative
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      Query Match
Best Local Similarity
Matches 6; Conserv
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ZIP: 77210
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APPLICANT: Gary Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 1999-01-29
RIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 7670
LENGTH: 375
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APPLICANT: AUJAME et al.
TITLE OF INVENTION: Nucleic acids and polypeptides specific for pathogenic TITLE OF INVENTION: Strains of the Neisseria genius FILE REFERENCE: P07180US00/BAS
CURRENT APPLICATION NUMBER: US/09/830, 433A
CURRENT FILING DATE: 2001-04-26
PRIOR FILING DATE: 1998-10-30
NUMBER OF SEQ ID NOS: 129
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 366
  TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 53045
LENGTH: 293
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Pred. No. 82;
6; Mismatches 4; Indels
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Pred. No. 1.1e+02;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                      ; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-53045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7670, Application US/09489039A Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09830433A Patent No. 6835384
                                                                                                                                                                                 TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Neisseria meningitidis
US-09-830-433A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7670
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54.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                   1 IVLRPSRVHNSEENT 15
                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 33.3'
Matches 5; Conservative
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Best Local Similarity 54.5.
Annual 6; Conservative
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US-09-830-433A-4
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TITLE OF INVENTION: No. 16806054-Endogenous, Constitutively Activated Known G TITLE OF INVENTION: No. 16806054-Endogenous, Constitutively Activated Known G TITLE OF INVENTION: Protein-Coupled Receptors
FILE REFERENCE: AREN-207
CURRENT APPLICATION NUMBER: US/09/826,509
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/195,747
PRIOR FILING DATE: 2000-04-05
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 589
SOFTWARE: Patentin Version 2.1
SEQ ID NO 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 37; DB 1; Length 544;
Pred. No. 1.7e+02;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               Length 418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7, Application US/08264002
Patent No. 5559019
GENERAL INFORMATION:
APPLICANT: GUI, JIAN-FANG
APPLICANT: GUI, XIANG-DONG
TITLE OF INVENTION: NOVEL PROTEIN SERINE KINASE, SRPK1
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPPRATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/08/264,002
FILING DATE: 22-JUN-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: SPENSLEY HORN JUBAS & LUBITZ
1880 Century Park East, Fifth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 37; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: TUMARKIN PH.D., LISA A.
REGISTATION NUMBER: P-38,347
REFERENCE/DOCKET NUMBER: PD35
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  48.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48.7%;
53.3%;
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327 VLLRPSRRVRSQEPT 341
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amino acid
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Best Local Similarity 53.34
Best Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 53.33
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein US-08-264-002-7
                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-09-826-509-573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Los Angeles
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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                                                                                                                                                                                                                                                                                                           LENGTH:
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                                                                                                                 DB 1; Length 418;
                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
UNRENT APPLICATION DATA:
                                                                                                                 Query Match 48.7%; Score 37; DB 1; Best Local Similarity 53.3%; Pred. No. 1.2e+02; Matches 8; Conservative 3; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bell, Graeme I.
APPLICANT: Yamada, Yuichiro
APPLICANT: Yamada, Yuichiro
APPLICANT: Seino, Susumu
TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arrold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/417,103
FILING DATE: 05-APR-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/816,283
FILING DATE: 01-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 573, Application US/09826509
Patent No. 6806054
                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/08417103
Patent No. 5723299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Wilson, Mark B. REGISTRATION NUMBER: 37,259 REFERENCE/DOCKET NUMBER: AR. TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (512) 418-3000
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327 VLLRPSRRVRSQEPT 341
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                                                                                                                                                                                                     1 IVLRPSRVHNSEENT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (512) 474-7577 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 418 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 53.3
Matches 8; Conservative
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                                                   MOLECULE TYPE: protein US-07-816-283-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OMPUTER READABLE FORM: MEDIUM TYPE: Floppy
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Houston
STATE: Texas
COUNTRY: United
ZIP: 77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
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US-09-826-509-573
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RESULT 32
US-09-248-796A-24931
Sequence 24931, Application US/09248796A
Fatent No. 6747137
GENERAL INFORMATION:
FAPLICATORY: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS.
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: WORDER: US/09/248,796A
TITLE OF INVENTION NUMBER: US 60/074,725
FRIOR PELING DATE: 1999-02-12
FRIOR PELING DATE: 1998-02-13
FRIOR PILING DATE: 1998-06-13
FRIOR FILING DATE: 1998-08-13
WUMBER OF SEQ ID NOS: 28208
SEQ ID NO 2431
LENGTH: 62
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Sequence 33410, Application US/09270767

Sequence 33410, Application US/09270767

Sequence 33410, Application US/09270767

Sequence 33410, Application US/09270767

GENERAL INFORMATION:

TITLE OF INVENTION:

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 33410

LENGTH: 172
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                                                                                                                                                                        Length 1021;
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                                                                                                                                                      Score 37; DB 2; Length Lu-Pred, No. 3.48+02;
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Best Local Similarity 58.3%; Pred. No. 68;
Matches 7; Conservative 3; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
47.4%; Score 36; DB 2;
Best Local Similarity 40.0%; Pred. No. 21;
Matches 6; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-33410
                                                                                          TYPE: PRT ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                           48.7%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 IVLRPSRVHNSEENT 15
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PRIOR FILING DATE: 1998-07-;
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 27405
LENGTH: 1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 LRPSRFYVTKEN 132
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407 IVLRPGDAHDAE 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Candida albicans
                                                                                                                                                                                        Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 LRPSRVHNSEEN 14
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                                                                                                                                US-09-252-991A-27405
                                                                                                                                                                               Query Match
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Patent No. 6551795
GENERAL INFORMATION: BOUCHEL BALL
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR PAPLICATION NUMBER: US 60/094,190
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Sequence 45640, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7226-094
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFFWARE: Patentin Ver. 2.0
SEQ ID NO 45640

LENGTH: 565
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48.7%; Score 37; DB 2; Length 544;
Best Local Similarity 53.3%; Pred. No. 1.7e+02;
Matches 8; Conservative 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48.7%; Score 37; DB 2; Length 565;
46.2%; Pred. No. 1.7e+02;
tive 4; Mismatches 3; Indels
                                                                                                                       Sequence 15, Application US/09457040B
Patent No. 6387641
GENERAL INFORMATION:
APPLICANT: Vertex Pharmaceuticals Incorporated
APPLICANT: Ballon, Steve
TITLE OF INVENTION: Crystallized P38 Complexes
FILE REFERENCE: VPI/99-11
CURRENT APPLICATION NUMBER: US/09/457,040B
CURRENT FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 41
SEQ ID NO 15
LENGTH: 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , ORGANISM: Drosophila melanogaster US-09-270-767-45640
    316 ISLRDSQKHNSHPNS 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         316 İSLRDSOKHNSHPNS 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 VLRPSRVHNSEEN 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 46.2
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 31
US-09-252-991A-27405
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US-09-270-767-45640
                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Human
                                                                                                                US-09-457-040B-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-457-040B-15
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APPLICANT: MACOUNTAINS

APPLICANT: MACOUNTAINS

APPLICANT: MACOUNTAINS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196_136

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER: OS 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 25916

LENGTH: 219
                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
TITLE OF INVENTION: Nucleic 2326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 48657
LENGTH: 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 36; DB 2; Length 219;
Pred. No. 90;
2; Mismatches 3; Indels
                                                                                Length 212;
                                                                                                                             3; Indels
                                                                                  DB 2;
87;
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Pred. No. 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                             2; Mismatches
                                                                                     Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-252-991A-29516
; Sequence 29516, Application US/09252991A
; Patent No. 6551795
                                                                                                                                                                                                                                                                                                                         Sequence 48657, Application US/09270767 Patent No. 6703491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-48657
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-33440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29516
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54.5%;
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Similarity 54.5%;
6; Conservative 5
                                                                                     47.4%;
54.5%;
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Best Local Similarity 54.5-
Local Similarity 6.2-
Local Similarity
Local Similarity
                                                                                                                             Conservative
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42 PARVHPGDHNT 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 PSRVHNSEENT 15
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                                                                                                                                                                        5 PSRVHNSEENT 15
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Best Local Similarity
                                                                                     Query Match
Best Local Similarity
Matches 6; Conserv
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US-09-134-000C-5252
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Patent NO. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REPERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT APPLICATION NUMBER: US/09/270,767

NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 36; DB 2; Length 191;
Pred. No. 77;
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                                                                                                                                               APPLICANT: Black, w. APPLICANT: Hodgson, John APPLICANT: Knowles, David APPLICANT: Nicholas, Richard APPLICANT: Stoola, Robert TITLE OF INVENTION: No. 6348328el Compounds TITLE OF COMPANIES: 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OFERATING SYSTEM: DOS
SOFTWARE: FaetSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/858,207A
FILING DATE: 09-MAY-1997
                                                                                                                                                                                                                                                                                                                                ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                       Sequence 381, Application US/08858207A
Patent No. 6348328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/017670
FILING DATE: 14-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISCRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: 950475
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 381:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: No. 6348328e
US-08-858-207A-381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 50.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |||| || :::|
122 VLRPGIVHRIDKDT 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 610-270-5090
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                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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Patent No. 6800744
GENERAL INTELEMENTION: NUCLEIC AND AMINO ACID
TITLE OF INVENTION: RELATING TO STREPTOCOCCUS PNEUMONIAE
THERAPEUTICS
                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                 Score 36; DB 2; Length 295;
Pred. No. 1.3e+02;
                                                                                                                                                                                       4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: GENOME THERAPEUTICS CORPORATION STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SIGLE...
SOFTWARE: CURNIOWADS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
APPLICATION NUMBER: 60/085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
APPLICATION NUMBER: 60/051553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...295
SEQUENCE DESCRIPTION: SEQ ID NO: 3370:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: July 2, 1997
ATTORNEY/ASENT INFORMATION:
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: «Unknown»
OPERATING SYSTEM: «Unknown»
                                ; LENGTH: 295
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-5136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 3370:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 295 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 5206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                        Query Match
Best Local Similarity 50.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME
                                                                                                                                                                                                                                                                          122 VLRPGIVHRIDKOT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                   2 VLRPSRVHNSEENT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VLRPSRVHNSEENT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                       US-09-107-433-3370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-107-433-3370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE
           ; SEQ ID NO 5136
                                                                                                                                                                                                                                                                                                                                                    RESULT 41
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Parent No. 6699703

GRNERAL INFORMATION:
GRNERAL INFORMATION:
GRNERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: NUMBER: US/09/583,110
CURRENT APPLICATION NUMBER: US 09/107,433
PRIOR PLING DATE: 1998-06-30
PRIOR FILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-05-12
PRIOR PLING DATE: US 60/051,553
PRIOR PLING DATE: 1997-07-02
| Sequence 5252, Application US/09134000C
| Patent No. 6617156
| GENERAL INFORMATION:
| APPLICANT: Lynn Doucette-Stamm et al
| TITLE OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
| TITLE OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
| TITLE OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
| TITLE OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES AND THERAPEUTICS
| CURRENT APPLICATION NUMBER: US/09/134,000C
| CURRENT APPLICATION NUMBER: US 60/055,778
| PRIOR PLILING DATE: 1997-08-15
| NUMBER OF SEQ ID NOS: 6812
| SEQ ID NO 5252
| LENGTH: 269
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Pred. No. 1.1e+02;
6; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09190824A
Fatent No. 6361965
GENERAL INPORMATION:
TITLE OF INVENTION: Yfil pseudouridine synthase
FILE REFERENCE: GM10181
CURRENT APPLICATION NUMBER: US/09/190,824A
CURRENT FILING DATE: 1998-11-12
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47.4%; Score 36; DB 2; 1 50.0%; Pred. No. 1.3e+02; tive 3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , ORGANISM: Streptococcus pneumoniae US-09-190-824-2
                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                            47.4%;
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122 VLRPGIVHRIDKDT 135
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Best Local Similarity 40.0°
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Best Local Similarity
7; Conserva
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US-09-190-824-2
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Gaps
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Sequence 10, Application US/09934868

Patent No. 6689601

GENERAL INFORMATION:

APPLICANT: Koffas, Mattheos

APPLICANT: Schenzle, Andreas J

TITLE Odom, James M

TITLE REFERENCE: C11596 US NO.

FILE REFERENCE: C1000-01

NUMBER OF SEQ ID NOS: 81

SEQ ID NO 10

LENGTH: 501
                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INTOCATION:
APPLICANT: KOffas, Mattheos
APPLICANT: Odom, J. Martin
APPLICANT: Odom, J. Martin
APPLICANT: No. 65535310n, Kelley C.
APPLICANT: Ye, Rick
TITLE OF INVENTION: DENITRIFYING METHANOTROPHIC BACTERIAL STRAIN
FILE REFERENCE: CL1619 US NA
CURRENT APPLICATION NUMBER: US/09/934,901
CURRENT FILING DATE: 2001.08-22
PRIOR APPLICATION NUMBER: 60/229,906
PRIOR APPLICATION NUMBER: 60/229,906
NUMBER OF SEQ ID NOS: 20
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Microsoft Office 97
SEQ ID NO 20
LENGTH: 501
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                                                                         Length 469;
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                                                                                                                       4; Indels
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Pred. No. 2.3e+02;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 36; DB 2;
Pred. No. 2.3e+02;
                                                                           Score 36; DB 1; 1
Pred. No. 2.2e+02;
4; Mismatches 4;
                                                                                                                                                                                                                                                                                                                     Sequence 20, Application US/09934901
Patent No. 6555353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative
                                                                                38.5%;
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                                                                                                                                                                  3 LRPSRVHNSEENT 15
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49.LKPRKIHNEANHT 61
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Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT; ORGANISM: METHYLOMONAS SP. US-09-934-901-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METHYLOMONAS SP
           , MOLECULE TYPE: protein US-08-477-451-23
                                                                             Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 45
US-09-934-868-10
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                                                                                                                                                                                                                                                                                                       US-09-934-901-20
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ORGANISM:
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                                                                                         sequence 4, Application US/09213053
; Sequence 4, Application US/09213053
; Patent No. 6159477
; GENERAL INFORMATION;
; APPLICANT: AUDONNET, Jean-Christophe
; APPLICANT: BAUDU, Philippe
; TITLE OF INVENTION: CANINE HERPESVIRUS BASED RECOMBINANT LIVE VACCINE, IN
; TITLE OF INVENTION: CANINE HERPESVIRUS BASED RECOMBINANT LIVE VACCINE, ITTLE OF INVENTION: PARTICULIAR AGAINST CANINE DISTEMPER, RABIES OR THE
; TITLE OF INVENTION: PARTICULIAR AGAINST CANINE DISTEMPER, RABIES OR THE
; TITLE OF INVENTION: PARTICULIAR AGAINST CANINE DISTEMPER, RABIES OR THE
; CURRENT APPLICATION NUMBER: 9608242
; EARLIER FILING DATE: 1996-12-16
; EARLIER FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PATENTIN VAI. 2.1
; SEQ ID NO 4
; LENGTH: 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPLY disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: DatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,451
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McClung, Barbara G.
REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 0335.002
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Covacci, Antonello
TITLE OF INVENTION: Helicobacter Pylori Cagi Region
TITLE OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 36;
Pred. No.
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Patent No. 5928865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 50.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Canine herpesvirus
US-09-213-053-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 469 amino acids
TYPE: amino acid
STRANDEDNESS: single
122 VLRPGIVHRIDKDT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 IVLRPSRVHNSEEN 14
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
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US-08-477-451-23
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                                                                                    -09-213-053-4
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Fatent No. 695822
GENERAL INFORMATION:
APPLICANT: Koffas, Mattheos
APPLICANT: Odom, James M
APPLICANT: Odom, James M
TITLE OF INVENTION: DENITRIYING METHANOTROPHIC BACTERIAL STRAIN
FILE REPERENCE: CL1596 US NA
CURRENT APPLICATION WUMBER: US/10/701,200
CURRENT FILING DATE: 2001-08-22
FRIOR FILING DATE: 2001-08-22
FRIOR FILING DATE: 2001-08-22
FRIOR APPLICATION NUMBER: 60/229,858
FRIOR FILING DATE: 2000-01
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Microsoft Office 97
SEQ ID NO 10
                                                  GENERAL INCOFFES, Mattheos
APPLICANT: KOFFES, Mattheos
APPLICANT: Odom, J. Martin
APPLICANT: Odom, J. Martin
APPLICANT: Vo. 6908992ton, Kelley C.
APPLICANT: Ye Rick
TITLE OF INVENTION: DENITRIFYING METHANOTROPHIC BACTERIAL STRAIN
FILE REFERENCE: CL1619 US NA
CURRENT APPLICATION NUMBER: US/10/320,924
CURRENT FILING DATE: 2001-08-22
PRIOR FILING DATE: 2001-08-22
PRIOR FILING DATE: September 1, 2000
NUMBER OF SEQ ID NOS: 20
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Microsoft Office 97
SEQ ID NO 20
LENGTH: 501
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; Patent No. 5641650
; GENERAL INFORMATION:
; APPLICANT: BTLLACH, Mary C.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 501;
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Pred. No. 2.3e+02;
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Pred. No. 2.3e+02
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Application US/10320924
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61.5%;
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Best Local Similarity 61.5.
Best Local Similarity 61.5.
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US-10-701-200-10
                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: METHYLOMONAS SP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 8; Conserv
                    Patent No. 6908992
GENERAL INFORMATION:
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US-10-701-200-10
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US-08-313-553-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20, Application US/10320874

Sequence 20, Application US/10320874

Patent No. 677305

GENERAL INFORMATION:

APPLICANT: Koffss, Mattheos

APPLICANT: No. 6773905ton, Kelley C.

PILE REFERENCE: CL1619 US NA

CURRENT PAPLICATION NUMBER: US/10/320,874

CURRENT FILING DATE: 2001-08-22

PRIOR PLICATION NUMBER: 60/22,906

PRIOR APPLICATION NUMBER: 60/22

PRIOR PLING DATE: September 1, 2000

NUMBER OF SEQ ID NOS: 20

SOFTWARE: Microsoft Office 97

SEQ ID NO 20

LENTH: 501
                                                                                                                                   GENERAL INFORMATION:

APPLICANT: KOffae, Mattheos

APPLICANT: Odom, J. Martin,

APPLICANT: Odom, J. Martin,

APPLICANT: Ye, Rick

TITLE OF INVENTION: DENITRIFYING METHANOTROPHIC BACTERIAL STRAIN

FILE REPERENCE: C1619 US NA

CURRENT APPLICATION NUMBER: US/10/321,210

CURRENT APPLICATION NUMBER: US/09/934,901

PRIOR FILING DATE: 2001-08-22

PRIOR PILING DATE: September 1, 2000

NUMBER OF SEQ ID NOS: 20

SOFTWARE: Mcrosoft Office 97

LENGTH: 501
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Pred. No. 2.3e+02;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 501;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 36; DB 2;
Pred. No. 2.3e+02;
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                                                                                                  Sequence 20, Application US/10321210 Patent No. 6767744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47.4%;
61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       283 LRPITVRNVEEKT 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            283 LRPITVRNVEEKT 295
  283 LRPITVRNVEEKT 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 LRPSRVHNSEENT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: METHYLOMONAS SP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) ORGANISM: METHYLOMONAS SP.
US-10-320-874-20
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Best Local Similarity
Then 8; Conservat
                                                            RESULT 46
US-10-321-210-20
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US-10-320-874-20
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US-10-320-924-20
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US-09-540-236-2083
US-09-540-236-2083
US-09-540-236-2083
US-09-540-236-2083
US-09-540-236-2083
Sequence 2083, Application US/09540236
Patent No. 6673910
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REFERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
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APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196-132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-13
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR APPLICATION NUMBER: US 60/096,409
RIOR APPLICATION NUMBER: US 60/096,409
SRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 20015
LENGTH: 653
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 559;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 36; DB 2;
Pred. No. 2.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47.4%; Score 36; DB 2;
35.7%; Pred. No. 3.1e+02;
iive 6; Mismatches 3
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Pred. No. 3.2e+02;
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-57669/WHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20015, Application US/09248796A Patent No. 6747137
                                                                                                                                                                                                                                                                                                                                                                                                                                                  53.8%;
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624 MIQPANITNHDENT 637
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                                                                                                                                                                                                                                               : 559 amino acids
amino acid
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496 VLRASDLHNAKAN 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 35.7
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 VLRPSRVHNSEEN 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein US-08-767-993-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: M.catarrhalis US-09-540-236-2083
                                                                                                                                                                                                                                                                                                                   linear
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Best Local Similarity
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Matches 7; Conserv
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US-09-248-796A-20015
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ORGANISM:
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Sequence 15, Application US/08767993

Sequence 15, Application US/08767993

Sequence 15, Application US/08767993

Settle 10.010882

APPLICANT: TURNER, George J.

APPLICANT: TURNER, George J.

TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS POLYPEPTIDES

TITLE OF INVENTION: IN HALOBACTERIA

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSED:

ADDRESSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 36; DB 1; Length 559;
Pred. No. 2.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,553
                                                             NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Walter H Dreger
STREET: 4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-57669/WHD
FELECOWNUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/767,993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION BATA:
APPLICATION NUMBER: US/08/038,662
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Dreger, Walter H.
                           TITLE OF INVENTION: IN HALOBACTERIA
                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53.8%;
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||| | :||:: |
496 VLRASDLHNAKAN 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 559 amino acids TYPE: amino acid
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Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-313-553-15
                                                                                                                                                                                        CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 51
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Gaps

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APPLICANT: Sherman, Amir
APPLICANT: Silva, Jeff
APPLICANT: Silva, Jeff
APPLICANT: Summers, Exic
APPLICANT: Summers, Exic
APPLICANT: Summers, Exic
APPLICANT: Summers, Exic
APPLICANT: Summers, Exic
APPLICANTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.130
CURRENT APPLICATION NUMBER: US/09/487,558
PRIOR APPLICATION NUMBER: US 60/487,558
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 446
SOFTWARE: PatentIn version 3.0
SEQ ID NO 364
LENGTH: 1250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2. Application US/09213053
Sequence 2. Application US/09213053
Patent No. 6159477
GENERAL INFORMATION:
APPLICANT: AUDONET, Jean-Christophe
APPLICANT: BAUDU, Philippe
TITLE OF INVENTION: CANINE HERPESVIRUS BASED RECOMBINANT LIVE VACCINE, IN
TITLE OF INVENTION: PARTICULAR AGAINST CANINE DISTEMPER, RABIES OR THE
TITLE OF INVENTION: PARAINFLUENZA 2 VIRUS
FILE REFERENCE: 454313-2220
CURRENT APPLICATION NUMBER: US/09/213,053
CURRENT FILING DATE: 1998-12-16
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                                                                                                                                                                                                                       Score 36; DB 1; Length 1250;
Pred. No. 6.6e+02;
3; Mismatches 3; Indels
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53.8%; Pred. No. 6.6e+02;
tive 3; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 364, Application US/09487558B Parent No. 6949356 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     No. 6949356man, Thea
Royer, John
                                                                                                                                                                                                                            Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
                                                                                          1250 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : | | | | : | | 561 LLRPSQQANSDNN 573
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                    TELEX: 230 901 SANS UR INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1250 amino acid
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Holtzman, Doug
Madden, Kevin
Maxon, Mary
Milne, Todd
                                                                                                                                                                                                                                                                                                                    2 VLRPSRVHNSEEN 14
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516-742-4366
                                                                                                             TYPE: amino acid
TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-441-139-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salama, Sofie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Busby, Robert APPLICANT: Cali, Brian
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    TELEFAX:
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APPLICANT: NO.C231753
APPLICANT: NO.C231753
APPLICANT: NO.CLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 20334
LENGTH: 1089
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         Gaps
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Pred. No. 5.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Wittrup, Dr. Karl D.
APPLICANT: Wittrup, Dr. Karl D.
APPLICANT: Robinson, Anne S.
TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF TITLE OF INVENTION: RECOMBINANTLY EXPRESSED PROTEINS NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSE: SCULLY, SCOTT, MURPHY & PRESSER STREET: 400 Garden City Plaza
CITY: Garden City
      3; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: DISP PC.COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,139
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47.4%; Scc. 50.0%; Pred. No. 5...
      Mismatches
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APPLICATION NUMBER: US 08/089,997
FILING DATE: 06-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: DiGIGIO, Frank S.
REGISTRATION NUMBER: 31,346
REFERNCE/DOCKET NUMBER: 8646
TELEPHONE: 516-742-4343
                                                                                                                                                                                                       Sequence 20334, Application US/09252991A Patent No. 6551795
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Patent No. 5773245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
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Best Local Similarity 50.04
Matches 9; Conservative
      6; Conservative
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500 KPSRGHKDQEN 510
                                                   4 RPSRVHNSEEN 14
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US-09-252-991A-20334
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STATE: NY
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         Matches
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Gaps

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Sequence 1285, Application US/09471276
Patent No. 6622072
Patent No. 6622072
APPLICANT: UnrorMATION:
APPLICANT: Dunas Milne Edwards, J.B.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6822072
FILE REPERENCE: GENSET.025CP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
                                    DB 2; Length 72;
39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/471,276
CURRENT FILING DATE: 1999-12-21
EARLIER APPLICATION NUMBER: 09/057,719
EARLIER APPLICATION NUMBER: 09/069,047
EARLIER FILING DATE: 1998-04-09
EARLIER FILING DATE: 1998-04-09
EARLIER FILING DATE: 1998-04-09
EARLIER FILING DATE: 1998-04-09
NUMBER OF SEQ ID NOS: 1622
SOFTWARE: PALCHE, PM
SOFTWARE: PALCHE, PM
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                                                                                     2; Mismatches
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Pred. No.
                                           Score 35;
Pred. No.
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Job time : 39.5526 secs
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58.3%;
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Best Local Similarity 58.3
Matches 7; Conservative
                                           Query Match
Best Local Similarity 58.3
Matches 7; Conservative
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40 LRPSRLLRTREN 51
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                                                                                                                                                            40 LRPSRLLRTREN 51
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: -18..-1
US-09-471-276-1285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: SIGNAL
US-09-513-999C-6876
                                                                                                                                                                                                                                          RESULT 60
US-09-471-276-1285
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pagenere 17657, Application US/09252991A

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pagenere 17657, Application US/09252991A

pagenere 17657, Application US/09252991A

pagenere 1000 NO 17657

pagenere 1000 NO 1762 NO DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 10799-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 1467
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Sequence 6876, Application US/09513999C

Patent No. 678361

APPLICANT: Ducas Milne Edwards, J.B.

APPLICANT: Duclert, J.Y.

APPLICANT: Glordano, J.Y.

TITE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

PATENTE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

PILE REFERENCE: 59.042.REG

CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT FILING DATE: 2000-02-24

PRIOR FILING DATE: 1999-02-26

PRIOR FILING DATE: 1999-02-26
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Pred. No. 9.8e+02;
1; Mismatches 3;
                                                                                                                                                                                                                                                                      Score 36; DB 2;
Pred. No. 7.5e+02;
                                                                                                                                                                                                                                                                                                                 Mismatches
                         EARLIER FILING DATE: 1996-06-27
EARLIER APPLICATION NUMBER: PCT/FR97/01115
EARLIER FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Var. 2.1
SEQ ID NO 2
LENGTH: 1394
    EARLIER APPLICATION NUMBER: 9608242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17657
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Best Local Similarity. 61.5%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 50.0%;
Matches 7; Conservative
                                                                                                                                                                                 TYPE: PRT
CRGANISM: Canine herpesvirus
US-09-213-053-2
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SOFTWARE: Patent.pm
SEQ ID NO 6876
LENGTH: 72
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US-09-252-991A-17657
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US-10-425-114-61210

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US-10-10-425-115-229873

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US-10-369-493-3910
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Sequence 2, Appli
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                                                                                                                                     March 11, 2006, 12:26:08 , Search time 117.632 Seconds (without alignments) 53.280 Million cell updates/sec
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(c) 1993 - 2006 Biocceleration Ltd.
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US-10-301-822-55
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US-10-425-115-320178
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US-09-905-129-21
US-09-91-630-21
US-10-176-847-54
US-10-177-293-110
US-10-301-822-49
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Maximum Match 100%
Listing first 500 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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5 46.1 374 4 US-10-176-757-406 Sequence 406, 5 46.1 374 4 US-10-176-483-406 Sequence 406, 5 46.1 374 4 US-10-176-749-406 Sequence 406, 5 46.1 374 4 US-10-176-749-406	35 46.1 374 4 US-10-176-914-406 Sequence 406,	35 46.1 374 4 US-10-176-915-406 Sequence 406, 35 46.1 374 4 US-10-173-706-406 Sequence 406,	35 46.1 374 4 US-10-175-738-406 Sequence 406,	35 46.1 374 4 US-10-175-752-406 Sequence 406,	35 46.1 374 4 US-10-176-482-406 sequence 406, 35 46.1 374 4 US-10-176-757-406 Sequence 406,	35 46.1 374 4 US-10-176-913-406 Sequence 406,	35 46.1 374 4 US-10-180-552-406 Sequence 406,	35 46.1 374 4 US-10-180-557-406 Sequence 406,	35 46.1 374 4 US-10-173-700-406 Sequence 406, 35 46.1 374 4 US-10-174-572-406 Sequence 406,	35 46.1 374 4 US-10-174-579-406 Sequence 406,	35 46.1 374 4 US-10-174-582-406 Sequence 406,	35 46.1 374 4 US-10-174-588-406 Seguence 406,	35 46.1 3/4 4 US-IO-I/5-/39-406 Sequence 406, 35 46.1 374 4 US-10-175-740-406 Sequence 406.	35 46.1 374 4 US-10-175-743-406 Sequence 406,	35 46.1 374 4 US-10-176-488-406 Sequence 406,	35 46.1 374 4 US-10-176-492-406 Sequence 406,	35 46.1 374 4 US-10-176-747-406 Sequence 406,	35 46.1 374 4 US-10-176-750-406 Sequence 406,	35 46.1 374 4 US-10-176-985-406 Sequence 406,	35 46.1 374 4 US-10-176-987-406 Sequence 406,	35 46.1 374 4 US-10-176-992-406 Sequence 406,	35 46.1 374 4 US-10-176-993-406 Sequence 406,.	35 46.1 374 4 US-10-184-658-406 Sequence 406,	35 46.1 374 4 US-10-176-991-406 Sequence 406,	35 40.1 374 4 03-10-1/3-035-406 364466166 400,	35 46.1 374 4 US-10-173-705-406 Sequence 406,	35 46.1 374 4 US-10-174-576-406 Sequence 406,	35 46.1 374 4 US-10-174-585-406 Sequence 406,	35 46.1 374 4 US-10-174-586-406 Sequence 406,	35 46.1 3/4 4 US-10-1/5-/4/-406 Sequence 406,	35 46.1 374 4 US-10-176-485-406 Sequence 406,	35 46.1 374 4 US-10-176-487-406 Sequence 406,	35 46.1 374 4 US-10-176-493-406 Sequence 406,	35 46.1 374 4 US-10-176-756-406 Sequence 406,	35 46.1 374 4 US-10-176-919-406 Sequence 406.	35 46.1 374 4 US-10-176-925-406 Sequence 406,	35 46.1 374 4 US-10-176-978-406 Sequence 406,	35 46.1 374 4 US-10-179-510-406 Sequence 406,	35 46.1 374 4 US-10-180-543-406 Sequence 406,	35 46.1 374 4 US-10-180-544-406 Sequence 406	35 46.1 374 4 US-10-180-540-406 Sequence 406.	35 46.1 374 4 US-10-180-549-406 Sequence 406,	35 46.1 374 4 US-10-180-555-406 Sequence 406,	35 46.1 374 4 US-10-180-559-406 Sequence 406,	35 46.1 374 4 US-10-181-000-406 sequence 406,	35 46.1 374 4 US-10-183-012-406 Sequence 406,	35 46.1 374 4 US-10-184-614-406 Sequence 406,	35 46.1 374 4 US-10-184-623-406 Sequence 406,	35 46.1 374 4 US-10-184-635-406 Sequence 406,	35 46.1 374 4 US-10-184-637-406 Sequence 406,	35 46.1 3/4 4 US-IO-IO4-0400 SEQUENCE 400,	35 46.1 374 4 US-10-184-652-406 Sequence 406,	35 46.1 374 4 US-10-187-594-406 Sequence 406,	35 46.1 374 4 US-10-187-596-406 Sequence 406,	35 46.1 374 4 US-10-187-745-406 Sequence 406,	35 46.1 374 4 US-10-187-885-406 Sequence 406,	35 46.1 3/4 4 US-IO-IS/-888-408 SEQUENCE 409,

| Sequen          | Sequen                                    | Sequen  | Sequen  | Sequen   | Seguen   | Seguen   | Sequen   | Seguen  | Sequen   | Seguen  
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| US-10-188-775-4 | US-10-196-745-4                           | US-10-196-762-4   | US-10-195-894-4   | US-10-176-484-4  | US-10-1/6-/55-4<br>US-10-176-917-4   | US-10-176-982-4  | US-10-179-513-4  | US-10-179-514-4   | US-10-180-556-4  | US-10-180-560-4   
   | US-10-184-615-4  | US-10-184-620-4  | US-10-184-643-4<br>US-10-184-656-4   | US-10-192-010-4  | US-10-205-906-4<br>US-10-184-619-4  
  | US-10-187-599-4  | US-10-187-750-4<br>US-10-188-780-4   | US-10-192-015-4  | US-10-194-394-4<br>US-10-194-425-4   | US-10-194-485-4  
   | US-10-195-885-4<br>US-10-195-899-4   | US-10-196-748-4  | US-10-196-750-4<br>US-10-197-699-4   | US-10-197-700-4   | US-10-197-705-4<br>US-10-197-708-4   | US-10-198-764-4   
  | US-10-198-765-4   | US-10-198-769-4  | US-10-199-305-4   | US-10-199-306-4<br>US-10-199-310-4   | US-10-199-311-4   | US-10-199-317-4  
   | US-10-199-665-4   
   | US-10-199-669-4   | US-10-201-534-4   
   
  | US-10-201-855-4  | US-10-201-856-4   
   | US-10-202-470-4                       | US-10-202-476-4<br>US-10-202-934-4  | US-10-202-935-4   | US-10-202-936-4<br>US-10-202-939-4  | US-10-205-504-4   
   | US-10-205-509-4<br>US-10-205-895-4   | US-10-205-899-4   | US-10-205-900-4<br>US-10-205-909-4   | US-10-195-890-4   | US-10-183-002-4<br>US-10-184-621-4  | US-10-184-638-4 |
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   | 4 4  | 74  | 4.4  | 74  | 4 4   | 74              |
| 46.             | 46.                                       | 46.   | 4.6   | 46.  | 4. 4.<br>6. 6.   | 46.  | 46.  | 4.6   | 46.  | 46.   
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  | 46.  | 46.  | 46   | 46.  | 46.  
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   | 4. c   | 36   | 27   | 36  | 20   | 32  
  | 33  | 32   | 36  | 38 3   | 39  | 41   
   | 342   
   |   | 3.3   
   
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   | 200                                   | 51  | 3.60  | 4 th  | 39  
   | 57   | 29  | 60   | 62  | 5.3   | 30              |
|                 | 33 35 46.1 374 4 US-10-188-775-406 Sequen | 33 35 46.1 374 4 US-10-188-775-406 Sequen<br>14 35 46.1 374 4 US-10-194-462-406 Sequen<br>15 35 46.1 374 4 US-10-196-745-406 Sequen | 35 46.1 374 4 US-10-188-775-406 Sequen 35 46.1 374 4 US-10-194-462-406 Sequen 35 46.1 374 4 US-10-196-745-406 Sequen 35 46.1 374 4 US-10-196-745-406 Sequen 35 46.1 374 4 US-10-196-745-406 Sequen 35 46.1 374 4 US-10-196-762-406 Sequen | 35 46.1 374 4 US-10-188-775-406 Sequen 35 46.1 374 4 US-10-194-462-406 Sequen 35 46.1 374 4 US-10-196-745-406 Sequen 35 46.1 374 4 US-10-196-745-406 Sequen 35 46.1 374 4 US-10-196-762-406 Sequen 35 46.1 374 4 US-10-197-695-406 Sequen 83 46.1 374 4 US-10-195-894-406 Sequen | 35 46.1 374 4 US-10-188-775-406 Sequen 35 46.1 374 4 US-10-194-462-406 Sequen 35 46.1 374 4 US-10-196-745-406 Sequen 35 46.1 374 4 US-10-196-745-406 Sequen 35 46.1 374 4 US-10-195-894-406 Sequen 35 46.1 374 4 US-10-197-695-406 Sequen 37 4 US-10-197-694-406 Sequen 37 4 US-10-196-894-406 Sequen 37 4 US-10-1 | 35 46.1 374 4 US-10-188-775-406 Sequen 15 35 46.1 374 4 US-10-194-462-406 Sequen 15 35 46.1 374 4 US-10-196-745-406 Sequen 17 35 46.1 374 4 US-10-196-745-406 Sequen 17 35 46.1 374 4 US-10-197-695-406 Sequen 18 35 46.1 374 4 US-10-197-695-406 Sequen 18 35 46.1 374 4 US-10-176-484-406 Sequen 18 46.1 374 4 US-10-176-484-406 Sequen 18 46.1 374 4 US-10-176-753-406 Sequen 18 46.1 374 4 US-10-176-753-406 Sequen 19 35 46.1 374 4 US-10-176-917-406 Sequen 19 35 46.1 374 4 US-10-176-406 Sequen 19 35 46.1 374 4 US-10-176-406 Sequen 19 35 46 | 35 46.1 374 4 US-10-188-775-406 Sequen 35 46.1 374 4 US-10-198-462-406 Sequen 374 4 US-10-196-745-406 Sequen 374 4 US-10-196-745-406 Sequen 37 4 4 US-10-196-745-406 Sequen 37 4 4 US-10-195-894-406 Sequen 37 4 4 US-10-195-894-406 Sequen 37 4 US-10-176-484-406 Sequen 37 4 US-10-176-484-406 Sequen 37 4 US-10-176-484-406 Sequen 37 4 US-10-176-484-406 Sequen 37 4 US-10-176-917-406 Sequen 37 4 US-10 | 35 46.1 374 4 US-10-188-775-406 Sequen 35 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        US-10-188-775-406         Sequen           15         3.5         46.1         374         4         US-10-194-462-406         Sequen           16         3.5         46.1         374         4         US-10-196-762-406         Sequen           17         3.5         46.1         374         4         US-10-196-762-406         Sequen           18         3.5         46.1         374         4         US-10-196-762-406         Sequen           10         3.5         46.1         374         4         US-10-176-484-406         Sequen           11         3.5         46.1         374         4         US-10-176-912-406         Sequen           12         3.7         4         US-10-176-912-406         Sequen         Sequen           13         3.7         4         US-10-176-912-406         Sequen           14         13.7 | 13         46.1         374         4         US-10-188-775-406         Sequen           15         35         46.1         374         4         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Sequen Seq | 13         36.1         374         4         US-10-194-462-406         Sequen Se | 13         36         46.1         374         4         US-10-194-462-406         Sequen           16         35         46.1         374         4         US-10-194-462-406         Sequen           16         35         46.1         374         4         US-10-194-462-406         Sequen           18         35         46.1         374         4         US-10-196-762-406         Sequen           19         35         46.1         374         4         US-10-196-762-406         Sequen           10         35         46.1         374         4         US-10-196-762-406         Sequen           11         35         46.1         374         4         US-10-196-762-406         Sequen           12         374         4         US-10-196-762-406         Sequen         Sequen           13         46.1         374         4         US-10-176-404-406         Sequen           13         46.1         374         4         US-10-176-404-406         Sequen           14         US-10-176-404-406         Sequen         Sequen           15         46.1         374         4         US-10-176-404-406         Sequen <td< th=""><th>13         35         46.1         374         4         US-10-188-775-406         Sequen           16         35         46.1         374         4         US-10-196-745-406         Sequen           16         35         46.1         374         4         US-10-196-765-406         Sequen           18         46.1         374         4         US-10-196-765-406         Sequen           19         35         46.1         374         4         US-10-196-765-406         Sequen           10         35         46.1         374         4         US-10-196-765-406         Sequen           11         35         46.1         374         4         US-10-196-765-406         Sequen           12         35         46.1         374         4         US-10-196-765-406         Sequen           13         46.1         374         4         US-10-196-765-406         Sequen           14         US-10-196-765-406         Sequen         Sequen           15         35         46.1         374         4         US-10-196-768-406         Sequen           16         374         4         US-10-196-768-406         Sequen         Sequen</th><th>13         35         46.1         374         4         US-10-18B-775-406         Sequen           16         35         46.1         374         4         US-10-194-466-406         Sequen           16         35         46.1         374         4         US-10-195-695-406         Sequen           19         35         46.1         374         4         US-10-195-695-406         Sequen           19         35         46.1         374         4         US-10-195-695-406         Sequen           10         35         46.1         374         4         US-10-195-695-406         Sequen           11         35         46.1         374         4         US-10-195-695-406         Sequen           12         36         46.1         374         4         US-10-195-695-406         Sequen           13         46.1         374         4         US-10-195-695-406         Sequen           14         35         46.1         374         4         US-10-196-695-406         Sequen           15         46.1         374         4         US-10-196-695-406         Sequen           16         374         US-10-196-66-60         Sequen<th>13         35         46.1         374         4         US-10-188-775-406         Sequen           16         35         46.1         374         4         US-10-194-466-406         Sequen           16         35         46.1         374         4         US-10-195-695-406         Sequen           19         35         46.1         374         4         US-10-195-695-406         Sequen           10         35         46.1         374         4         US-10-195-695-406         Sequen           11         35         46.1         374         4         US-10-195-695-406         Sequen           12         36         46.1         374         4         US-10-195-695-406         Sequen           35         46.1         374         4         US-10-196-695-406         Sequen           36         46.1         374         4        
US-10-196-695-406         Sequen           37         4         US-10-196-695-406         Sequen         Sequen           38         46.1         374         US-10-196-695-406         Sequen           39         46.1         374         US-10-196-666         Sequen           30         46.1</th><th>13         46.1         374         4         US-10-184-75-406         Sequent           16         35         46.1         374         4         US-10-194-65-406         Sequent           16         35         46.1         374         4         US-10-195-69-406         Sequent           18         35         46.1         374         4         US-10-195-69-406         Sequent           19         35         46.1         374         4         US-10-195-69-406         Sequent           10         35         46.1         374         4         US-10-196-69-406         Sequent           11         35         46.1         374         4         US-10-196-69-406         Sequent           12         36         46.1         374         4         US-10-196-69-406         Sequent           13         46.1         374         4         US-10-196-69-406         Sequent           13         46.1         374         4         US-10-196-69-606         Sequent           13         46.1         374         4         US-10-196-69-606         Sequent           14         US-10-196-69-606         Sequent         Sequent         Sequent     <!--</th--><th>  1   1   1   1   1   1   1   1   1   1</th><th>13         46.1         374         4         US-10-188-775-406         Sequent           16         35         46.1         374         4         US-10-196-745-406         Sequent           16         35         46.1         374         4         US-10-196-745-406         Sequent           18         35         46.1         374         4         US-10-196-765-406         Sequent           19         35         46.1         374         4         US-10-196-765-406         Sequent           10         35         46.1         374         4         US-10-196-765-406         Sequent           10         35         46.1         374         4         US-10-176-759-406         Sequent           10         35         46.1         374         4         US-10-176-517-406         Sequent           11         35         46.1         374         4         US-10-176-517-406         Sequent           12         35         46.1         374         4         US-10-176-517-406         Sequent           13         46.1         374         4         US-10-176-517-406         Sequent           14         US-10-176-517-406         Sequent</th><th>13         46.1         374         4         US-10-198-775-406         Sequent           16         35         46.1         374         4         US-10-196-745-406         Sequent           16         35         46.1         374         4         US-10-196-745-406         Sequent           18         35         46.1         374         4         US-10-196-765-406         Sequent           19         35         46.1         374         4         US-10-196-765-406         Sequent           10         35         46.1         374         4         US-10-196-765-406         Sequent           10         35         46.1         374         4         US-10-196-766-406         Sequent           10         36         46.1         374         4         US-10-196-766-406         Sequent           10         36         46.1         374         4         US-10-196-766-406         Sequent           11         35         46.1         374         4         US-10-196-766-406         Sequent           12         35         46.1         374         4         US-10-196-766-406         Sequent           36         46.1         374</th><th>13         46.1         374         4 US-10-189-775-406         Sequent           16         35         46.1         374         4 US-10-196-75-406         Sequent           16         37         4 US-10-196-75-406         Sequent           18         35         46.1         374         4 US-10-196-75-406         Sequent           19         46.1         374         4 US-10-196-75-406         Sequent           10         35         46.1         374         4 US-10-196-75-406         Sequent           10         35         46.1         374         4 US-10-196-75-30-406         Sequent           10         37         4 US-10-176-97-406         Sequent         Sequent           11         37         4 US-10-176-97-406         Sequent           12         37         4 US-10-176-97-406         Sequent           13         46.1         374         4 US-10-176-97-406         Sequent           14         37         4 US-10-176-97-406         Sequent           15         46.1         374         4 US-10-176-97-406         Sequent           16         37         4 US-10-176-97-606         Sequent           17         4 US-10-176-97-606</th><th>13         46.1         374         4 US-10-188-775-406         Sequent           15         46.1         374         4 US-10-186-775-406         Sequent           16         35         46.1         374         4 US-10-196-775-406         Sequent           18         35         46.1         374         4 US-10-196-775-406         Sequent           19         46.1         374         4 US-10-196-775-406         Sequent           20         36         4 US-10-196-775-406         Sequent           21         374         4 US-10-196-786-406         Sequent           22         36         1374         4 US-10-196-786-406         Sequent           23         46.1         374         4 US-10-196-786-406         Sequent           24         41         US-10-196-786-406         Sequent           25         46.1         374         4 US-10-196-786-406         Sequent           26         37         4 US-10-196-786-406         Sequent           27         4 US-10-196-786-406         Sequent         Sequent           28         46.1         374         US-10-196-786-406         Sequent           28         46.1         374         US-10-196-786-406&lt;</th><th>35         46.1         374         4 US-10-189-775-406         Sequent           46         35         46.1         374         4 US-10-196-775-406         Sequent           56         37         4 US-10-196-775-406         Sequent           35         46.1         374         4 US-10-196-775-406         Sequent           36         46.1         374         4 US-10-196-775-406         Sequent           37         46.1         374         4 US-10-196-775-406         Sequent           38         46.1         374         4 US-10-196-775-406         Sequent           39         46.1         374         4 US-10-196-775-406         Sequent           31         46.1         374         4 US-10-196-775-406         Sequent           32         46.1         374         4 US-10-196-775-406         Sequent           32         46.1         374         4 US-10-196-775-406         Sequent           33         46.1         374         4 US-10-196-775-406         Sequent           34         40.1         40.10-10-196-746-706         Sequent           35         46.1         374         40.10-10-196-746-706         Sequent           36         40.1</th><th>35         46.1         374         4 US 10-188-775-406         Sequent           4         35         46.1         374         4 US 10-189-75-406         Sequent           7         35         46.1         374         4 US 10-197-659-406         Sequent           8         35         46.1         374         4 US 10-197-659-406         Sequent           9         35         46.1         374         4 US 10-197-659-406         Sequent           9         36         46.1         374         4 US 10-197-659-406         Sequent           9         36         46.1         374         4 US 10-197-659-406         Sequent           9         46.1         374         4 US 10-197-522-406         Sequent           9         46.1         374         4 US 10-197-522-406         Sequent           9         46.1         374         4 US 10-198-522-406         Sequent           9         46.1         10-</th><th>13         46.1         37.4         4 US-10-180-775-406         Sequent           15         46.1         37.4         4 US-10-180-775-406         Sequent           16         35         46.1         37.4         4 US-10-197-659-406         Sequent           17         4 US-10-197-659-406         Sequent         Sequent         Sequent           18         35         46.1         37.4         4 US-10-197-659-406         Sequent           19         36         40.1         37.4         4 US-10-197-659-406         Sequent           10         37         4 US-10-197-659-406         Sequent         Sequent           10         37         4 US-10-197-552-406         Sequent           10         37         4 US-10-197-552-406         Sequent           10         37         4 US-10-198-752-406         Sequent</th><th>3.3         46.1         374         4 B.10-188-765-406         Sequent           4.5         5.6         1.74         4 B.10-188-765-406         Sequent           6.6         3.74         4 B.10-188-765-406         Sequent           8.6         4.6         1.74         4 B.10-188-765-406         Sequent           9.5         4.6         1.74         4 B.10-188-765-406         Sequent           9.6         1.74         4 B.10-188-765-406         Sequent           9.6         1.74         4 B.10-188-765-406         Sequent           9.6         1.74         4 B.10-118-765-76-406         Sequent           9.6         1.74         4 B.10-118-76-76-74-606         Sequent           9.6         1.74         4 B.10-118-76-76-74-606         Sequent     <th>13         46.1         174         4 US.10-188-465-406         Sequent           14         15         46.1         174.4         4 US.10-188-465-406         Sequent           15         46.1         174.4         4 US.10-186-765-406         Sequent 
         16         15         46.1         174.4         4 US.10-186-765-406         Sequent           17         4 US.10-186-765-406         Sequent         Sequent         Sequent           18         3.5         46.1         174.4         4 US.10-186-765-406         Sequent           18         3.5         46.1         174.4         4 US.10-186-765-406         Sequent           18         3.5         46.1         174.4         4 US.10-1186-767-406         Sequent           18         3.5         46.1         174.4</th><th></th></th></th></th></td<> | 13         35         46.1         374         4         US-10-188-775-406         Sequen           16         35         46.1         374         4         US-10-196-745-406         Sequen           16         35         46.1         374         4         US-10-196-765-406         Sequen           18         46.1         374         4         US-10-196-765-406         Sequen           19         35         46.1         374         4         US-10-196-765-406         Sequen           10         35         46.1         374         4         US-10-196-765-406         Sequen           11         35         46.1         374         4         US-10-196-765-406         Sequen           12         35         46.1         374         4         US-10-196-765-406         Sequen           13         46.1         374         4         US-10-196-765-406         Sequen           14         US-10-196-765-406         Sequen         Sequen           15         35         46.1         374         4         US-10-196-768-406         Sequen           16         374         4         US-10-196-768-406         Sequen         Sequen | 13         35         46.1         374         4         US-10-18B-775-406         Sequen           16         35         46.1         374         4         US-10-194-466-406         Sequen           16         35         46.1         374         4         US-10-195-695-406         Sequen           19         35         46.1         374         4         US-10-195-695-406         Sequen           19         35         46.1         374         4         US-10-195-695-406         Sequen           10         35         46.1         374         4         US-10-195-695-406         Sequen           11         35         46.1         374         4         US-10-195-695-406         Sequen           12         36         46.1         374         4         US-10-195-695-406         Sequen           13         46.1         374         4         US-10-195-695-406         Sequen           14         35         46.1         374         4         US-10-196-695-406         Sequen           15         46.1         374         4         US-10-196-695-406         Sequen           16         374         US-10-196-66-60         Sequen <th>13         35         46.1         374         4         US-10-188-775-406         Sequen           16         35         46.1         374         4         US-10-194-466-406         Sequen           16         35         46.1         374         4         US-10-195-695-406         Sequen           19         35         46.1         374         4         US-10-195-695-406         Sequen           10         35         46.1         374         4         US-10-195-695-406         Sequen           11         35         46.1         374         4         US-10-195-695-406         Sequen           12         36         46.1         374         4         US-10-195-695-406         Sequen           35         46.1         374         4         US-10-196-695-406         Sequen           36         46.1         374         4         US-10-196-695-406         Sequen           37         4         US-10-196-695-406         Sequen         Sequen           38         46.1         374         US-10-196-695-406         Sequen           39         46.1         374         US-10-196-666         Sequen           30         46.1</th> <th>13         46.1         374         4         US-10-184-75-406         Sequent           16         35         46.1         374         4         US-10-194-65-406         Sequent           16         35         46.1         374         4         US-10-195-69-406         Sequent           18         35         46.1         374         4         US-10-195-69-406         Sequent           19         35         46.1         374         4         US-10-195-69-406         Sequent           10         35         46.1         374         4         US-10-196-69-406         Sequent           11         35         46.1         374         4         US-10-196-69-406         Sequent           12         36         46.1         374         4         US-10-196-69-406         Sequent           13         46.1         374         4         US-10-196-69-406         Sequent           13         46.1         374         4         US-10-196-69-606         Sequent           13         46.1         374         4         US-10-196-69-606         Sequent           14         US-10-196-69-606         Sequent         Sequent         Sequent     <!--</th--><th>  1   1   1   1   1   1   1   1   1   1</th><th>13         46.1         374         4         US-10-188-775-406         Sequent           16         35         46.1         374         4         US-10-196-745-406         Sequent           16         35         46.1         374         4         US-10-196-745-406         Sequent           18         35         46.1         374         4         US-10-196-765-406         Sequent           19         35         46.1         374         4         US-10-196-765-406         Sequent           10         35         46.1         374         4         US-10-196-765-406         Sequent           10         35         46.1         374         4         US-10-176-759-406         Sequent           10         35         46.1         374         4         US-10-176-517-406         Sequent           11         35         46.1         374         4         US-10-176-517-406         Sequent           12         35         46.1         374         4         US-10-176-517-406         Sequent           13         46.1         374         4         US-10-176-517-406         Sequent           14         US-10-176-517-406         Sequent</th><th>13         46.1         374         4         US-10-198-775-406         Sequent           16         35         46.1         374         4         US-10-196-745-406         Sequent           16         35         46.1         374         4         US-10-196-745-406         Sequent           18         35         46.1         374         4         US-10-196-765-406         Sequent           19         35         46.1         374         4         US-10-196-765-406         Sequent           10         35         46.1         374         4         US-10-196-765-406         Sequent           10         35         46.1         374         4         US-10-196-766-406         Sequent           10         36         46.1         374         4         US-10-196-766-406         Sequent           10         36         46.1         374         4         US-10-196-766-406         Sequent           11         35         46.1         374         4         US-10-196-766-406         Sequent           12         35         46.1         374         4         US-10-196-766-406         Sequent           36         46.1         374</th><th>13         46.1         374         4 US-10-189-775-406         Sequent           16         35         46.1         374         4 US-10-196-75-406         Sequent           16         37         4 US-10-196-75-406         Sequent           18         35         46.1         374         4 US-10-196-75-406         Sequent           19         46.1         374         4 US-10-196-75-406         Sequent           10         35         46.1         374         4 US-10-196-75-406         Sequent           10         35         46.1         374         4 US-10-196-75-30-406         Sequent           10         37         4 US-10-176-97-406         Sequent         Sequent           11         37         4 US-10-176-97-406         Sequent           12         37         4 US-10-176-97-406         Sequent           13         46.1         374         4 US-10-176-97-406         Sequent           14         37         4 US-10-176-97-406         Sequent           15         46.1         374         4 US-10-176-97-406         Sequent           16         37         4 US-10-176-97-606         Sequent           17         4 US-10-176-97-606</th><th>13         46.1         374         4 US-10-188-775-406         Sequent           15         46.1         374         4 US-10-186-775-406         Sequent           16         35         46.1         374         4 US-10-196-775-406         Sequent           18         35         46.1         374         4 US-10-196-775-406         Sequent           19         46.1         374         4 US-10-196-775-406         Sequent           20         36         4 US-10-196-775-406         Sequent           21         374         4 US-10-196-786-406         Sequent           22         36         1374         4 US-10-196-786-406         Sequent           23         46.1         374         4 US-10-196-786-406         Sequent           24         41         US-10-196-786-406         Sequent           25         46.1         374         4 US-10-196-786-406         Sequent           26         37         4 US-10-196-786-406         Sequent           27         4 US-10-196-786-406         Sequent         Sequent           28         46.1         374         US-10-196-786-406         Sequent           28         46.1         374         US-10-196-786-406&lt;</th><th>35         46.1         374         4 US-10-189-775-406         Sequent           46         35         46.1         374         4 US-10-196-775-406         Sequent           56         37         4 US-10-196-775-406         Sequent        
  35         46.1         374         4 US-10-196-775-406         Sequent           36         46.1         374         4 US-10-196-775-406         Sequent           37         46.1         374         4 US-10-196-775-406         Sequent           38         46.1         374         4 US-10-196-775-406         Sequent           39         46.1         374         4 US-10-196-775-406         Sequent           31         46.1         374         4 US-10-196-775-406         Sequent           32         46.1         374         4 US-10-196-775-406         Sequent           32         46.1         374         4 US-10-196-775-406         Sequent           33         46.1         374         4 US-10-196-775-406         Sequent           34         40.1         40.10-10-196-746-706         Sequent           35         46.1         374         40.10-10-196-746-706         Sequent           36         40.1</th><th>35         46.1         374         4 US 10-188-775-406         Sequent           4         35         46.1         374         4 US 10-189-75-406         Sequent           7         35         46.1         374         4 US 10-197-659-406         Sequent           8         35         46.1         374         4 US 10-197-659-406         Sequent           9         35         46.1         374         4 US 10-197-659-406         Sequent           9         36         46.1         374         4 US 10-197-659-406         Sequent           9         36         46.1         374         4 US 10-197-659-406         Sequent           9         46.1         374         4 US 10-197-522-406         Sequent           9         46.1         374         4 US 10-197-522-406         Sequent           9         46.1         374         4 US 10-198-522-406         Sequent           9         46.1         10-</th><th>13         46.1         37.4         4 US-10-180-775-406         Sequent           15         46.1         37.4         4 US-10-180-775-406         Sequent           16         35         46.1         37.4         4 US-10-197-659-406         Sequent           17         4 US-10-197-659-406         Sequent         Sequent         Sequent           18         35         46.1         37.4         4 US-10-197-659-406         Sequent           19         36         40.1         37.4         4 US-10-197-659-406         Sequent           10         37         4 US-10-197-659-406         Sequent         Sequent           10         37         4 US-10-197-552-406         Sequent           10         37         4 US-10-197-552-406         Sequent           10         37         4 US-10-198-752-406         Sequent</th><th>3.3         46.1         374         4 B.10-188-765-406         Sequent           4.5         5.6         1.74         4 B.10-188-765-406         Sequent           6.6         3.74         4 B.10-188-765-406         Sequent           8.6         4.6         1.74         4 B.10-188-765-406         Sequent           9.5         4.6         1.74         4 B.10-188-765-406         Sequent           9.6         1.74         4 B.10-188-765-406         Sequent           9.6         1.74         4 B.10-188-765-406         Sequent           9.6         1.74         4 B.10-118-765-76-406         Sequent           9.6         1.74         4 B.10-118-76-76-74-606         Sequent           9.6         1.74         4 B.10-118-76-76-74-606         Sequent     <th>13         46.1         174         4 US.10-188-465-406         Sequent           14         15         46.1         174.4         4 US.10-188-465-406         Sequent           15         46.1         174.4         4 US.10-186-765-406         Sequent           16         15         46.1         174.4         4 US.10-186-765-406         Sequent           17         4 US.10-186-765-406         Sequent         Sequent         Sequent           18         3.5         46.1         174.4         4 US.10-186-765-406         Sequent           18         3.5         46.1         174.4         4 US.10-186-765-406         Sequent           18         3.5         46.1         174.4         4 US.10-1186-767-406         Sequent           18         3.5         46.1         174.4</th><th></th></th></th> | 13         35         46.1         374         4         US-10-188-775-406         Sequen           16         35         46.1         374         4         US-10-194-466-406         Sequen           16         35         46.1         374         4         US-10-195-695-406         Sequen           19         35         46.1         374         4         US-10-195-695-406         Sequen           10         35         46.1         374         4         US-10-195-695-406         Sequen           11         35         46.1         374         4         US-10-195-695-406         Sequen           12         36         46.1         374         4         US-10-195-695-406         Sequen           35         46.1         374         4         US-10-196-695-406         Sequen           36         46.1         374         4         US-10-196-695-406         Sequen           37         4         US-10-196-695-406         Sequen         Sequen           38         46.1         374         US-10-196-695-406         Sequen           39         46.1         374         US-10-196-666         Sequen           30         46.1 | 13         46.1         374         4         US-10-184-75-406         Sequent           16         35         46.1         374         4         US-10-194-65-406         Sequent           16         35         46.1         374         4         US-10-195-69-406         Sequent           18         35         46.1         374         4         US-10-195-69-406         Sequent           19         35         46.1         374         4         US-10-195-69-406         Sequent           10         35         46.1         374         4         US-10-196-69-406         Sequent           11         35         46.1         374         4         US-10-196-69-406         Sequent           12         36         46.1         374         4         US-10-196-69-406         Sequent           13         46.1         374         4         US-10-196-69-406         Sequent           13         46.1         374         4         US-10-196-69-606         Sequent           13         46.1         374         4         US-10-196-69-606         Sequent           14         US-10-196-69-606         Sequent         Sequent         Sequent </th <th>  1   1   1   1   1   1   1   1   1   1</th> <th>13         46.1         374         4         US-10-188-775-406         Sequent           16         35         46.1         374         4         US-10-196-745-406         Sequent           16         35         46.1         374         4         US-10-196-745-406         Sequent           18         35         46.1         374         4         US-10-196-765-406         Sequent           19         35         46.1         374         4         US-10-196-765-406         Sequent           10         35         46.1         374         4         US-10-196-765-406         Sequent           10         35         46.1         374         4         US-10-176-759-406         Sequent           10         35         46.1         374         4         US-10-176-517-406         Sequent           11         35         46.1         374         4         US-10-176-517-406         Sequent           12         35         46.1         374         4         US-10-176-517-406         Sequent           13         46.1         374         4         US-10-176-517-406         Sequent           14         US-10-176-517-406         Sequent</th> <th>13         46.1         374         4         US-10-198-775-406         Sequent           16         35         46.1         374         4         US-10-196-745-406         Sequent           16         35         46.1         374         4         US-10-196-745-406         Sequent           18         35         46.1         374         4         US-10-196-765-406         Sequent           19         35         46.1         374         4         US-10-196-765-406         Sequent           10         35         46.1         374         4         US-10-196-765-406         Sequent           10         35         46.1         374         4         US-10-196-766-406         Sequent           10         36         46.1         374         4         US-10-196-766-406         Sequent           10         36         46.1         374         4         US-10-196-766-406         Sequent           11         35         46.1         374         4         US-10-196-766-406         Sequent           12         35         46.1         374         4         US-10-196-766-406         Sequent           36         46.1         374</th> <th>13         46.1         374         4 US-10-189-775-406         Sequent           16         35         46.1         374         4 US-10-196-75-406         Sequent           16         37         4 US-10-196-75-406         Sequent           18         35         46.1         374         4 US-10-196-75-406         Sequent           19         46.1         374         4 US-10-196-75-406         Sequent           10         35         46.1         374         4 US-10-196-75-406         Sequent           10         35         46.1         374         4 US-10-196-75-30-406         Sequent           10         37         4 US-10-176-97-406         Sequent         Sequent           11         37         4 US-10-176-97-406         Sequent           12         37         4 US-10-176-97-406         Sequent           13         46.1         374         4 US-10-176-97-406         Sequent           14         37         4 US-10-176-97-406         Sequent           15         46.1         374         4 US-10-176-97-406         Sequent           16         37         4 US-10-176-97-606         Sequent           17         4 US-10-176-97-606</th> <th>13         46.1         374       
 4 US-10-188-775-406         Sequent           15         46.1         374         4 US-10-186-775-406         Sequent           16         35         46.1         374         4 US-10-196-775-406         Sequent           18         35         46.1         374         4 US-10-196-775-406         Sequent           19         46.1         374         4 US-10-196-775-406         Sequent           20         36         4 US-10-196-775-406         Sequent           21         374         4 US-10-196-786-406         Sequent           22         36         1374         4 US-10-196-786-406         Sequent           23         46.1         374         4 US-10-196-786-406         Sequent           24         41         US-10-196-786-406         Sequent           25         46.1         374         4 US-10-196-786-406         Sequent           26         37         4 US-10-196-786-406         Sequent           27         4 US-10-196-786-406         Sequent         Sequent           28         46.1         374         US-10-196-786-406         Sequent           28         46.1         374         US-10-196-786-406&lt;</th> <th>35         46.1         374         4 US-10-189-775-406         Sequent           46         35         46.1         374         4 US-10-196-775-406         Sequent           56         37         4 US-10-196-775-406         Sequent           35         46.1         374         4 US-10-196-775-406         Sequent           36         46.1         374         4 US-10-196-775-406         Sequent           37         46.1         374         4 US-10-196-775-406         Sequent           38         46.1         374         4 US-10-196-775-406         Sequent           39         46.1         374         4 US-10-196-775-406         Sequent           31         46.1         374         4 US-10-196-775-406         Sequent           32         46.1         374         4 US-10-196-775-406         Sequent           32         46.1         374         4 US-10-196-775-406         Sequent           33         46.1         374         4 US-10-196-775-406         Sequent           34         40.1         40.10-10-196-746-706         Sequent           35         46.1         374         40.10-10-196-746-706         Sequent           36         40.1</th> <th>35         46.1         374         4 US 10-188-775-406         Sequent           4         35         46.1         374         4 US 10-189-75-406         Sequent           7         35         46.1         374         4 US 10-197-659-406         Sequent           8         35         46.1         374         4 US 10-197-659-406         Sequent           9         35         46.1         374         4 US 10-197-659-406         Sequent           9         36         46.1         374         4 US 10-197-659-406         Sequent           9         36         46.1         374         4 US 10-197-659-406         Sequent           9         46.1         374         4 US 10-197-522-406         Sequent           9         46.1         374         4 US 10-197-522-406         Sequent           9         46.1         374         4 US 10-198-522-406         Sequent           9         46.1         10-</th> <th>13         46.1         37.4         4 US-10-180-775-406         Sequent           15         46.1         37.4         4 US-10-180-775-406         Sequent           16         35         46.1         37.4         4 US-10-197-659-406         Sequent           17         4 US-10-197-659-406         Sequent         Sequent         Sequent           18         35         46.1         37.4         4 US-10-197-659-406         Sequent           19         36         40.1         37.4         4 US-10-197-659-406         Sequent           10         37         4 US-10-197-659-406         Sequent         Sequent           10         37         4 US-10-197-552-406         Sequent           10         37         4 US-10-197-552-406         Sequent           10         37         4 US-10-198-752-406         Sequent</th> <th>3.3         46.1         374         4 B.10-188-765-406         Sequent           4.5         5.6         1.74         4 B.10-188-765-406         Sequent           6.6         3.74         4 B.10-188-765-406         Sequent           8.6         4.6         1.74         4 B.10-188-765-406         Sequent           9.5         4.6         1.74         4 B.10-188-765-406         Sequent           9.6         1.74         4 B.10-188-765-406         Sequent           9.6         1.74         4 B.10-188-765-406         Sequent           9.6         1.74         4 B.10-118-765-76-406         Sequent           9.6         1.74         4 B.10-118-76-76-74-606         Sequent           9.6         1.74         4 B.10-118-76-76-74-606         Sequent     <th>13         46.1         174         4 US.10-188-465-406         Sequent           14         15         46.1         174.4         4 US.10-188-465-406         Sequent           15         46.1         174.4         4 US.10-186-765-406         Sequent           16         15         46.1         174.4         4 US.10-186-765-406         Sequent           17         4 US.10-186-765-406         Sequent         Sequent         Sequent           18         3.5         46.1         174.4         4 US.10-186-765-406         Sequent           18         3.5         46.1         174.4         4 US.10-186-765-406         Sequent           18         3.5         46.1         174.4         4 US.10-1186-767-406         Sequent           18         3.5         46.1         174.4</th><th></th></th> | 1   1   1   1   1   1   1   1   1   1 | 13         46.1         374         4         US-10-188-775-406         Sequent           16         35         46.1         374         4         US-10-196-745-406         Sequent           16         35         46.1         374         4         US-10-196-745-406         Sequent           18         35         46.1         374         4         US-10-196-765-406         Sequent           19         35         46.1         374         4         US-10-196-765-406         Sequent           10         35         46.1         374         4         US-10-196-765-406         Sequent           10         35         46.1         374         4         US-10-176-759-406         Sequent           10         35         46.1         374         4         US-10-176-517-406         Sequent           11         35         46.1         374         4         US-10-176-517-406         Sequent           12         35         46.1         374         4         US-10-176-517-406         Sequent           13         46.1         374         4         US-10-176-517-406         Sequent           14         US-10-176-517-406         Sequent | 13         46.1         374         4         US-10-198-775-406         Sequent           16         35         46.1         374         4         US-10-196-745-406         Sequent           16         35         46.1         374         4         US-10-196-745-406         Sequent           18         35         46.1         374         4         US-10-196-765-406         Sequent           19         35         46.1         374         4         US-10-196-765-406         Sequent           10         35         46.1         374         4         US-10-196-765-406         Sequent           10         35         46.1         374         4         US-10-196-766-406         Sequent           10         36         46.1         374         4         US-10-196-766-406         Sequent           10         36         46.1         374         4         US-10-196-766-406         Sequent           11         35         46.1         374         4         US-10-196-766-406         Sequent           12         35         46.1         374         4         US-10-196-766-406         Sequent           36         46.1         374 | 13         46.1         374         4 US-10-189-775-406         Sequent           16         35         46.1         374         4 US-10-196-75-406         Sequent           16         37         4 US-10-196-75-406         Sequent           18         35         46.1         374         4 US-10-196-75-406         Sequent           19         46.1         374         4 US-10-196-75-406         Sequent           10         35         46.1         374         4 US-10-196-75-406         Sequent           10         35         46.1         374         4 US-10-196-75-30-406         Sequent           10         37         4 US-10-176-97-406         Sequent         Sequent           11         37         4 US-10-176-97-406         Sequent           12         37         4 US-10-176-97-406         Sequent           13         46.1         374         4 US-10-176-97-406         Sequent           14         37         4 US-10-176-97-406         Sequent           15         46.1         374         4 US-10-176-97-406         Sequent           16         37         4 US-10-176-97-606         Sequent           17         4 US-10-176-97-606 | 13         46.1         374         4 US-10-188-775-406         Sequent           15         46.1         374         4 US-10-186-775-406         Sequent           16         35         46.1         374         4 US-10-196-775-406         Sequent           18         35         46.1         374         4 US-10-196-775-406         Sequent           19         46.1         374         4 US-10-196-775-406         Sequent           20         36         4 US-10-196-775-406         Sequent           21         374         4 US-10-196-786-406         Sequent           22         36         1374         4 US-10-196-786-406         Sequent           23         46.1         374         4 US-10-196-786-406         Sequent           24         41         US-10-196-786-406         Sequent           25         46.1         374         4 US-10-196-786-406         Sequent           26         37         4 US-10-196-786-406         Sequent           27         4
US-10-196-786-406         Sequent         Sequent           28         46.1         374         US-10-196-786-406         Sequent           28         46.1         374         US-10-196-786-406< | 35         46.1         374         4 US-10-189-775-406         Sequent           46         35         46.1         374         4 US-10-196-775-406         Sequent           56         37         4 US-10-196-775-406         Sequent           35         46.1         374         4 US-10-196-775-406         Sequent           36         46.1         374         4 US-10-196-775-406         Sequent           37         46.1         374         4 US-10-196-775-406         Sequent           38         46.1         374         4 US-10-196-775-406         Sequent           39         46.1         374         4 US-10-196-775-406         Sequent           31         46.1         374         4 US-10-196-775-406         Sequent           32         46.1         374         4 US-10-196-775-406         Sequent           32         46.1         374         4 US-10-196-775-406         Sequent           33         46.1         374         4 US-10-196-775-406         Sequent           34         40.1         40.10-10-196-746-706         Sequent           35         46.1         374         40.10-10-196-746-706         Sequent           36         40.1 | 35         46.1         374         4 US 10-188-775-406         Sequent           4         35         46.1         374         4 US 10-189-75-406         Sequent           7         35         46.1         374         4 US 10-197-659-406         Sequent           8         35         46.1         374         4 US 10-197-659-406         Sequent           9         35         46.1         374         4 US 10-197-659-406         Sequent           9         36         46.1         374         4 US 10-197-659-406         Sequent           9         36         46.1         374         4 US 10-197-659-406         Sequent           9         46.1         374         4 US 10-197-522-406         Sequent           9         46.1         374         4 US 10-197-522-406         Sequent           9         46.1         374         4 US 10-198-522-406         Sequent           9         46.1         10- | 13         46.1         37.4         4 US-10-180-775-406         Sequent           15         46.1         37.4         4 US-10-180-775-406         Sequent           16         35         46.1         37.4         4 US-10-197-659-406         Sequent           17         4 US-10-197-659-406         Sequent         Sequent         Sequent           18         35         46.1         37.4         4 US-10-197-659-406         Sequent           19         36         40.1         37.4         4 US-10-197-659-406         Sequent           10         37         4 US-10-197-659-406         Sequent         Sequent           10         37         4 US-10-197-552-406         Sequent           10         37         4 US-10-197-552-406         Sequent           10         37         4 US-10-198-752-406         Sequent | 3.3         46.1         374         4 B.10-188-765-406         Sequent           4.5         5.6         1.74         4 B.10-188-765-406         Sequent           6.6         3.74         4 B.10-188-765-406         Sequent           8.6         4.6         1.74         4 B.10-188-765-406         Sequent           9.5         4.6         1.74         4 B.10-188-765-406         Sequent           9.6         1.74         4 B.10-188-765-406         Sequent           9.6         1.74         4 B.10-188-765-406         Sequent           9.6         1.74         4 B.10-118-765-76-406         Sequent           9.6         1.74         4 B.10-118-76-76-74-606         Sequent           9.6         1.74         4 B.10-118-76-76-74-606         Sequent <th>13         46.1         174         4 US.10-188-465-406         Sequent           14         15         46.1         174.4         4 US.10-188-465-406         Sequent           15         46.1         174.4         4 US.10-186-765-406         Sequent           16         15         46.1         174.4         4 US.10-186-765-406         Sequent           17         4 US.10-186-765-406         Sequent         Sequent         Sequent           18         3.5         46.1         174.4         4 US.10-186-765-406         Sequent           18         3.5         46.1         174.4         4 US.10-186-765-406         Sequent           18         3.5         46.1         174.4         4 US.10-1186-767-406         Sequent           18         3.5         46.1         174.4</th> <th></th> | 13         46.1         174         4 US.10-188-465-406         Sequent           14         15         46.1         174.4         4 US.10-188-465-406         Sequent           15         46.1         174.4         4 US.10-186-765-406         Sequent           16         15         46.1         174.4         4 US.10-186-765-406         Sequent           17         4 US.10-186-765-406         Sequent         Sequent         Sequent           18         3.5         46.1         174.4         4 US.10-186-765-406         Sequent           18         3.5         46.1         174.4         4 US.10-186-765-406         Sequent           18         3.5         46.1         174.4         4 US.10-1186-767-406         Sequent           18         3.5         46.1         174.4 |                 |

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RESULT

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TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT, TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT, TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER FILE REFERENCE: MRI-038

FILE REFERENCE: MRI-039

CURRENT APPLICATION NUMBER: US/10/17,293

CURRENT FILING DATE: 2001-06-21

PRIOR PILING DATE: 2001-06-27

PRIOR PILING DATE: 2001-06-27

PRIOR FILING DATE: 2001-07-18

PRIOR FILING DATE: 2001-07-18

PRIOR FILING DATE: 2001-07-18

PRIOR PILING DATE: 2001-07-18

PRIOR PILING DATE: 2001-09-25

PRIOR PILING DATE: 2002-03-05

PRIOR PILING DATE: 2002-03-05

PRIOR PILING DATE: 2002-05-14

NUMBER OF SEQ ID NOS: 506

SOFTWARE: FASTSEQ FOR Windows Version 4.0
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APPLICANT: Monhan, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Thibodeau, Stephen N.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: THERAPY OF COLON CANCER
TITLE OF INVENTION: THERAPY OF COLON CANCER
FILE REFERENCE: MPMO1-0292RNM
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2001-12-10
PRIOR FILING DATE: 2001-03-05
PRIOR FILING DATE: 2001-03-05
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: PRESEQ for Windows Version 4.0
SEQ ID NO 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 76; DB 4; 100.0%; Pred. No. 0.00026
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 55, Application US/10301822 Publication No. US20030148410A1 GENERAL INFORMATION:
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Kamatkar, Shubhangi
Schlegel, Robert
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Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 100.
Matches 15; Conservative
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; ORGANISM: Homo Sapiens
US-10-301-822-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens
US-10-177-293-136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 136
LENGTH: 760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
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                                                                 APPLICANT: Zimmermann, Rainer, Park, John E.;
APPLICANT: Zimmermann, Rainer, Park, John E.;
APPLICANT: Rettig, Wolfgang; Old, Lloyd J.
TITLE OF INVENTION: ISOLATED DIMERIC FIBROBLAST ACTIVATION PROTEIN
TITLE OF INVENTION: ALPHA, AND USES THEREOF
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Filing Late.
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/619,280
FILING DATE: 18-MARCH-1996
APPLICATION NUMBER: 08/230,491
FILING DATE: 20-APRIL-1994
ATTORNEY/AGENT INPORMATION:
NAME: Hanson, No. US
                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 2.0 MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Wordperfect
URRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265,606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/10177293
Sequence 2, Application US/09265606
Patent No. US20020034789A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     annavarpu, Manjula
amatkar, Shubhangi
ertens, Maureen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lortobagyi, Gabriel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lu, Yongyao
Hoersch, Sebastian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US20030124128A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (212) 838-3884 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 760 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lillie, James APPLICANT: Glatt, Karen
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-265-606-2
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Gaps

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Gaps

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Query Match
Best Local Similarity 50.0%;
Matches 7; Conservative
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Best Local Similarity 63.0-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
US-10-435-696-95
                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Zea mays
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                                                                                                            US-10-723-860-4171

US-10-723-860-4171

Sequence 4171, Application US/10723860

Publication No. US20040253606A1

GENERAL INFORMATION:
APPLICANT: Aziz, Natasha

APPLICANT: Ginsburg, Wendy M.
APPLICANT: Zlotnik, Albert

TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators

TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators

FILE REFERENCE: 05882.0193.NPUS01

CURRENT APPLICATION NUMBER: US/10/723,860

CURRENT FILING DATE: 2002-11-26

PRIOR PELING DATE: 2002-11-26

NUMBER OF SEQ ID NOS: 8393

SEQ ID NO 4111

LENGTH: 760
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APPLICANT: Wolf, Beni B.
APPLICANT: Wu, Thomas D.
APPLICANT: Thomas D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND TITLE OF INVENTION: TREATMENT OF TUMOR.
FILE REFERENCE: P5036R1-US
CURRENT APPLICATION NUMBER: US/10/884,070A
CURRENT FILING DATE: 2004-07-02
PRIOR FILING DATE: 2003-07-02
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 13
LENGTH: 760
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 760;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 76; DB 5; Lilarity 100.0%; Pred. No. 0.00026; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 13, Application US/10884070A; Publication No. US20050170368A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
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                           1 IVLRPSRVHNSEENT 15
                                                24 IVLRPSRVHNSEENT 38
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Best Local Similarity 100.0
These 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polakis, Paul
Smith, Victoria
Wolf, Beni B.
Wu, Thomas D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Frantz, Gretchen
APPLICANT: French, Dorothy
APPLICANT: Gonzalez, Lino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Ashkenazi, Avi J. APPLICANT: Cairns, Belinda APPLICANT: Dowd, Patrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
CORGANISM: Homo sapiens
US-10-884-070A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
US-10-723-860-4171
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Matches 15; Conserva
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USACHOL 18 - 696-95

1 Sequence 95, Application US/10435696

2 Sequence 95, Application US/10435696

3 CENERAL INFORMATION:
3 CENERAL INFORMATION:
4 APPLICANT: Wirtz, Ralph
5 APPLICANT: Wirtz, Ralph
6 APPLICANT: Wirtz, Ralph
7 TILE OF INVENTION: METHODS AND COMPOSITIONS FOR THE PREDICTION, DIAGNOSIS, PROGNOSIS
7 TILE OF INVENTION: METHODS AND TREATMENT OF MALIGNANT NEOPLASIA
7 TILE OF INVENTION: WINBER: US/10/435,696
7 CURRENT APPLICATION NUMBER: EP03003112.4
7 PRIOR APPLICATION NUMBER: EP02010291.9
7 PRIOR APPLICATION NUMBER: EP02010291.9
7 PRIOR FILING DATE: 2002-05-21
7 PRIOR FILING DATE: 2002-05-21
7 PRIOR FILING DATE: 2002-05-21
7 PRIOR FILING DATE: 2002-05-31
7 PRIOR FILING DATE: 2002-05-31
7 PRIOR FILING DATE: 2003-02-31
7 PRIOR FILING DATE: 2002-05-31
US-10-425-115-320178

US-10-425-115-320178

Sequence 320178, Application US/10425115

Publication No. US20040214272A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT APPLICATION NUMBER: US/10/425,115

UNMBER OF SEQ ID NOS: 369326

SEQ ID NO 320178

LENGTH: 120
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Pred. No. 1.1e+02;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 48; DB 4; Length 120;
Pred. No. 2.5;
5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_55069C.l.pep
US-10-425-115-320178
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US-10-425-115-361324
; Sequence 361324, Application US/10425115
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Gaps

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APPLICANT: Libro, Yhuua APPLICANT: Libro, Yhuua APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Gao, Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 39-21 (53313)
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 64668
TYPE. ...
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Jeants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 239911
LENGTH: 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 53.9%; Score 41; DB 4; Length 458; Best Local Similarity 80.0%; Pred. No. 1.8e+02; Matches 8; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           Length 258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Clone ID: PAT_MRT3847_58665C.1.pep
US-10-424-599-239911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , OTHER INFORMATION: Clone ID: LIB4571-006-D12_FLI.pep
US-10-425-114-64668
                                                                                                                                                                                                                                                                                                                                                                                                                         53.9%; Score 41; DB 4;
57.1%; Pred. No. 94;
tive 2; Mismatches
                                                                                                                                                                                                                                                                                         LOCATION: (1)..(258)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-282-122A-48505
; Sequence 48505, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103 İVLMPETVHRSEQS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 IVLRPSRVHNSEEN 14
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 57.1x
Best Local 8; Conservative
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                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Zea mays
                                                                                                                                                                                                                                                                      NAME/KEY: unsure LOCATION: (1)..(
                                                                                                                                                                                                                                                                                                                                         FEATURE:
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Subjection No. US20040214272A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Co. Yonghan Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

TITLE OF INVENTION: US/10/425,115

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

SEQ ID NO 353380

LENGTH: 113
                           GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 361324
LENGTH: 108
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Pred. No. 38;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 53.9%; Score 41; DB 4; Length 108; Best Local Similarity 45.0%; Pred. No. 36; Matches 9; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
COTHER INFORMATION: Clone ID: MRT4577_92705C.1.pep
US-10-425-115-361324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Clone ID: MRT4577_85457C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (1)..(113)
OTHER INFORMATION: unsure at all Xaa locations
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Edou Yihua
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36 LLRPSAIPTHGRIHNTERTT 55
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63.6%;
           Publication No. US20040214272A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 53.9
Best Local Similarity 63.6
Matches 7; Conservative
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Zea mays
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US-10-424-599-239911
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Gaps

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GENERAL INFORMATION:

APPLICANT: Einat, et al

APPLICANT: Einat, et al

ITLE OF INVENTION: GENERAL SASOCIATED MITH MECHANICAL STRESS, EXPRESSION PRODUCTS THERE.

ITLE OF INVENTION: AND USES THEREOF

FILE REFERENCE: 540579-2007.2

CURRENT APPLICATION NUMBER: 05/09/05,129

CURRENT PILING DATE: 2001-03-08

PRIOR RILING DATE: 2000-05-30

PRIOR FILING DATE: 2000-05-30

PRIOR FILING DATE: 2000-05-30

PRIOR FILING DATE: 1998-05-11

PRIOR FILING DATE: 1998-05-11

PRIOR PILING DATE: 1998-05-15

NUMBER OF SEQ ID NOS: 25

SOFTWARE: PatentIn version 3.0

SEQ ID NO 21

LENGTH: 2028
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CURRENT APPLICATION NUMBER: US/09/905,129
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-08
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2001-12-04
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PATENTIN VERSION 3.0
FROM THE TOWN OF 2.18
SOFTWARE: PATENTIN VERSION 3.0
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   Indels
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6
   Mismatches
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Patent No. US20020137705A1
7;
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Best Local Similarity 35.7%;
Matches 5; Conservative
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ilarity 35.7%;
Conservative
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                                                               1 IVLRPSRVHNSEEN 14
      5; Conservative
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; ORGANISM: homo sapiens
US-09-991-630-21
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CRGANISM: homo sapiens
JS-09-905-129-21
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Best Local Similarity
Matches 5; Conserva
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      Matches
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Publication No. US20020086825A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: GENES ASSOCIATED WITH MECHANICAL STRESS, EXPRESSION PRODUCTS THERE
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 540579-2007.1
CURRENT APPLICATION NUMBER: US/09/802,318
CURRENT FILING DATE: 2001-03-08
PRIOR PELLING DATE: 2000-08-04
PRIOR PELLING DATE: 2000-08-04
PRIOR PELLING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Version 3.0
SEQ ID NO 21
                                                                                                                                       APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034
FULE REFERENCE: ELITRA.034
CURRENT APPLICATION NUMBER: 05/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR PLILORATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-10-23
PRIOR PAPLICATION NUMBER: 60/230,347
PRIOR PLING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/25,625
PRIOR APPLICATION NUMBER: 60/25,625
PRIOR APPLICATION NUMBER: 60/25,625
PRIOR APPLICATION NUMBER: 60/25,636
PRIOR APPLICATION NUMBER: 60/25,636
PRIOR APPLICATION NUMBER: 60/25,636
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PRIOR APPLICATION NUMBER: 60
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53.8%; Pred. No. 1.9e+02;
tive 3; Mismatches 3,
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35.7%;
                                                                                          Yamamoto, Robert
Forsyth, R.
Xu, H.
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      wall, Daniel
Trawick, John
Carr, Grant
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ORGANISM: homo sapiens
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Matches 7; Conserv
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Best Local Similarity
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US-10-282-122A-48505
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US-09-802-318-21
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APPLICANT:
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APPLICANT: Berger, Allison
APPLICANT: Guilemette, Tracy L.
APPLICANT: Goilemette, Tracy L.
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Thibodeau, Stephen N.
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE REFERENCE: MPMO1-029P2RNM
CURRENT APPLICANTON NUMBER: US/10/301,822
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Pred. No. 1.3e+03;
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                                                                                                                                                                                                                                      7; Mismatches
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PRIOR FILING DATE: 2001-12-10
PRIOR FILING DATE: 2001-12-10
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SEQ ID NO 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Millennium Pharmaceuticals, Inc.
NUMBER OF SEQ ID NOS: 506
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 110
LENGTH: 2828
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Publication No. US20030170630A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 49, Application US/10301822
Publication No. US20030148410A1
GENERAL INFORMATION:
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APPLICANT: Tehernev, Velizar J
PEPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A
                                                                                                                                                                                       53.9%;
35.7%;
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Grosse, William M
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Best Local Similarity 35.77
Conservative
5, Conservative
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                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
US-10-177-293-110
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Best Local Similarity
Matches 5; Conserva
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PPLICANT: Mills, Gordon B.
ITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
ITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
                                                                                                     Sequence 54, Application US/10176847

Sequence 54, Application US/10176847

Publication No. US20030068636A1

GENERAL INFORMATION

APPLICANT: Veiby, Petter Ole

TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR

TITLE OF INVENTION: AND OVARIAN CANCER

TITLE OF INVENTION: AND OVARIAN CANCER

TITLE OF INVENTION: AND OVARIAN CANCER

FILE REFERENCE: MRI-039

CURRENT FILING DATE: 2002-06-21

NUMBER OF SEQ ID NOS: 112

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 5-4
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CURRENT FILING DATE: 2002-06-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               URRENT FILING DATE: 2002-06-21
RIOR APPLICATION NUMBER: US 60/299,887
RIOR FILING DATE: 2001-06-21
RIOR APPLICATION NUMBER: US 60/301,572
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PRIOR APPLICATION NUMBER: US 60/306,501
PRIOR PILING DATE: 2001-07-18
PRIOR PELING DATE: 2001-09-25
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US 60/362,585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ku, Yongyao
Koersch, Sebastian
Monahan, John
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Mertens, Maureen
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2238 VVMKPAKIEHKEEN 2251
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2238 VVMKPAKIEHKEEN 2251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 IVLRPSRVHNSEEN 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Homo Bapiens
US-10-176-847-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LE REFERENCE: MRI-038
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Best Local Similarity
Matches 5; Conserva
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APPLICANT: Murray, Richard
APPLICANT: Matson, Susan R.
APPLICANT: Watson, Susan R.
APPLICANT: Ess Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer,
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
CURRENT PILING DATE: 2002-11-13
PRIOR PLING DATE: 2000-09-15
PRIOR PELING DATE: 2000-11-15
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR PILING DATE: 2001-11-13
PRIOR PELING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR PILING DATE: 2001-11-21
PRIOR PELING DATE: 2001-11-21
PRIOR PELING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/344,393
PRIOR PILING DATE: 2001-11-21
PRIOR PELING DATE: 2001-12-14
PRIOR PELING DATE: 2001-12-14
PRIOR PELING DATE: 2001-12-14
PRIOR PELING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR APPLICATION NUMBER: US 60/347,319
PRIOR PELING DATE: 2002-01-08
PRIOR PILING DATE: 2002-01-10
PRIOR PILING DATE: 2002-01-10
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APPLICANT: Afair, Daniel
APPLICANT: Ariz, Natasha
APPLICANT: Gish, Kurt C.
APPLICANT: Gish, Kurt C.
APPLICANT: Gish, Kurt C.
APPLICANT: Hevezi, Peter A.
APPLICANT: Hevezi, Peter A.
APPLICANT: Muxray, Richard
APPLICANT: Warenon, Susan R.
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APPLICANT: Warenon, Susan R.
APPLICANT: Ware
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US-10-295-027-1175
Sequence 1175, Application US/10295027
'; Bedication No. US2003023250A1
; GENERAL INFORMATION:
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Best Local Similarity
Matches 5; Conserv
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CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/257,495
PRIOR APPLICATION NUMBER: 60/259,740
PRIOR APPLICATION NUMBER: 60/259,171
PRIOR PILING DATE: 2000-12-20
PRIOR PILING DATE: 2000-12-20
PRIOR PILING DATE: 2000-13-20
PRIOR PILING DATE: 2001-03-09
PRIOR PILING DATE: 2001-03-09
PRIOR PILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 60/279,840
PRIOR PILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/292,981
PRIOR APPLICATION NUMBER: 60/282,981
PRIOR PILING DATE: 2001-04-11
PRIOR PILING DATE: 2001-04-13
PRIOR PILING DATE: 2001-04-13
PRIOR PILING DATE: 2001-04-13
PRIOR PILING DATE: 2001-04-13
PRIOR PILING DATE: 2001-08-17
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                                   Shimkets, Richard A
Grosse, William M
Szekeres, Edward S
Vernet, Corine A.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Afar, Daniel
APPLICANT: Atz, Nacasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Gish, Kurt C.
APPLICANT: Glynne, Richard
APPLICANT: Hevezi, Peter A.
APPLICANT: Mack, David H.
                                                                                                                                                                                                                                                                                                                                     Gorman, Linda
Gangolli, Esha A
Fernandes, Elma R
Rieger, Daniel K
Edinger, Shlomit R
Gunther, Erik
Millet, Isabelle
Sciore, Paul
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Boldog, Ferenc L
Gorman, Linda
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; ORGANISM: Homo sapiens
US-10-032-189-126
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LENGTH: 2828
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APPLICANT:
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Length 2828;

7; Mismatches

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Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 13191
SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/072,012
CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: 60/265,102
PRIOR FILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-31
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PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,395
PRIOR FILING DATE: 2001-01-31
                                                                               PRIOR FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/266,975
PRIOR FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/267,459
PRIOR FILING DATE: 2001-02-08
                                       FILING DATE: 2001-02-05
APPLICATION NUMBER: 60/267,057
                LICATION NUMBER: 60/266,767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Padigaru, Muralidhara
                                                                                                                                                                                                                                                                                                                                                                                                     53.9%;
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2238 VVMKPAKIEHKEEN 2251
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Shimkets, Richard
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                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 35.7
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
US-10-072-012-607
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                                                                                                                                                                                                                                                                     SEQ ID NO 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                    Remaining Prior Application data removed - See File Wrapper or PALM. WUMBER OF SEQ ID NOS: 1386 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 1175 LENGTH: 2828
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URRENT FILING DATE: 2002-01-31
                                       PRIOR APPLICATION NUMBER: US 60/340,376
PRIOR FILING DATE: 2001-12-14
PRIOR PELICATION NUMBER: US 60/347,211
PRIOR FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 60/347,349
PRIOR FILING DATE: 2002-01-10
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 60/355,250
PRIOR PILING DATE: 2002-02-08
PRIOR PILING DATE: 2002-02-13
                                                                 R FILING DATE: 2001-12-14
R APPLICATION NUMBER: US 60/347,211
R APPLICATION NUMBER: US 60/347,349
R FILING DATE: 2002-01-10
R FILING DATE: 2002-01-10
R FILING DATE: 2002-01-10
R FILING DATE: 2002-08
60/334,393
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RIOR APPLICATION NUMBER: 60/265,102
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PRIOR APPLICATION NUMBER: 60/265,395
PRIOR FILING DATE: 2001-01-31
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Burgess, Catherine E.
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atturajan, Meera
himkets, Richard
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2238 VVMKPAKIEHKEEN 2251
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rosse, William M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 IVLRPSRVHNSEEN 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 35.7
Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21402-258
                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
US-10-295-027-1175
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NAME/KEY: DOMAIN
LOCATION: (2586)...(2596)
OTHER INFORMATION: w KINASE ALPHA ADHESION T-CELL domain identified by eMATRIX,
OTHER INFORMATION: accession number DM00179, p-value=1.000e-10, raw score of 13.97
FRATURE:
NAME/KEY: DOMAIN
LOCATION: (628)...(2977)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTHER INFORMATION: Immunoglobulin domain identified by PFam, accession name ig, CTHER INFORMATION: E-value=1.3e-81, PFam score of 268.0 US-10-450-763-54243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                            Length 2828;
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APPLICATION NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

FILE REFERENCE: 790CIP3/US

FILE REFERENCE: 790CIP3/US

CURRENT FALING DATE: 2003-06-11

PRIOR APPLICATION NUMBER: DCT/US01/08631

PRIOR APPLICATION NUMBER: 09/540,217

PRIOR APPLICATION NUMBER: 09/540,217

PRIOR APPLICATION NUMBER: 09/649,167

PRIOR PLING DATE: 2000-03-31

PRIOR PLING DATE: 2000-08-23

NUMBER OF SEQ ID NOS: 60736

SOFTWARE: Custom

SEQ ID NO 54243

LENGTH: 2993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53.9%; Score 41; DB 5; ]
35.7%; Pred. No. 1.4e+03;
tive 7; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                     Score 41; DB 5;
Pred. No. 1.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                     Query Match 53.9%; Score 41; DB Best Local Similarity 35.7%; Pred. No. 1.3e Matches 5; Conservative 7; Mismatches
               CURRENT APPLICATION NUMBER: US/10/723,860
CURRENT FILING DATE: 2003-11-26
PRIOR PILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 8393
SOFTWARE: Patentin version 3.2
LENGTH: 2828
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 54243, Application US/10450763 Publication No. US20050196754A1 GENERAL INFORMATION:
FILE REFERENCE: 05882.0193.NPUS01
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2413 VVMKPAKIEHKEEN 2426
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2238 VVMKPAKIEHKEEN 2251
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Best Local Similarity 35.73
Matches 5; Conservative
                                                                                                                                                                                                                                                                TYPE: PRT CRGANISM: Homo sapiens US-10-723-860-554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens FEATURE:
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US-10-450-763-38920
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US-10-450-763-54243
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Sequence 21, Application US/10454351

Sequence 21, Application US/10454351

Sequence 21, Application No. US20040053301A1

GENERAL INFORMATION:

ADPLICATION OUATE Biotech Inc.; Paz Einat, et al

TITLE OF INVENTION: AND USES THEREOF

TITLE OF INVENTION: AND USES THEREOF

TITLE OF INVENTION: AND USES THEREOF

TITLE OF INVENTION: AND USES THEREOF

FILE REFERENCE: 010/PCT2-US2; EINAT=>E

CURRENT APPLICATION NUMBER: US/10/454,351

CURRENT FILING DATE: 2001-11-06

PRIOR PLING DATE: 2001-01-13-08

PRIOR PLING DATE: 2001-07-13

PRIOR PLING DATE: 2001-07-13

PRIOR PLING DATE: 2001-07-04

PRIOR PLING DATE: 2001-07-04

PRIOR PLING DATE: 2001-07-04

PRIOR PLING DATE: 2001-07-04

PRIOR PLING DATE: 2000-12-04

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Publication No. US200402536681
GENERAL INFORMATION:
APPLICANT: Aziz, Natasha
APPLICANT: Ginsburg, Wendy M.
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions & TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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   PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: 60/267,057
PRIOR FILING DATE: 2001-02-07
PRIOR PILING DATE: 2001-02-07
PRIOR PILING DATE: 2001-02-07
PRIOR PLING DATE: 2001-02-08
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1391
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53.9%; Score 41; DB 4; Length 2828; 35.7%; Pred. No. 1.3e+03; Live 7; Mismatches 2; Indels
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2238 VVMKPAKIEHKEEN 2251
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2238 VVMKPAKIEHKEEN 2251
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Best Local Similarity 35...
S. Conservative
S. Conservative
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Matches 5, Conservative
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ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
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US-10-723-860-554
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Score 40; DB 4; Length 90;
Pred. No. 44;
2; Mismatches 1; Indels
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TITLE OF INVENTION: PHENOTYPIC SCREEN OF CHIMERIC PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lee, Yangsoon
APPLICANT: Lee, Yangsoon
TITLE OF INVENTION: DIFFERENTIATION PROTEINS
FILE REFERENCE: 12279-007002
CURRENT APPLICATION NUMBER: US/10/669,861
CURRENT FILING DATE: 2003-09-24
PRIOR APPLICATION NUMBER: US 10/314,669
PRIOR FILING DATE: 2002-12-09
PRIOR FILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: US 60/336,441
PRIOR APPLICATION NUMBER: US 60/306,053
PRIOR APPLICATION NUMBER: US 60/400,904
PRIOR APPLICATION NUMBER: US 60/401,089
PRIOR FILING DATE: 2002-08-02
PRIOR FILING DATE: 2002-08-05
NUMBER OF SEQ ID NOS: 261
SEQ ID NO 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                  Score 40;
Pred. No. 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Saccharomyces cerevisiae US-10-314-669-133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52.6%;
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Best Local Similarity 64.3%;
Matches 9; Conservative
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GENERAL INFORMATION:
APPLICANT: Lee, Dong-Ki
                                                                                                                                                                                                                      FILE REFERENCE: 12279-007001
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                                                                                                                                                 Yang, Hyo-Young
Lee, Yangsoon
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-669-861-133
                                                                                                                                                                                                                                                                                                    LOCATION: (4839)..(4849)
OTHER INFORMATION: w KINASE ALPHA ADHESION T-CELL domain identified by eMATRIX,
OTHER INFORMATION: accession number DM00179, p-value=1.000e-10, raw score of 13.97
                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (628)..(5251)
OTHER INFORMATION: Immunoglobulin domain identified by PFam, accession name ig,
OTHER INFORMATION: E-value=1.4e-114, PFam score of 374.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 62671, Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
BAPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 62671
LENGTH: 81
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ed. No. 39;
Mismatches 5; Indels
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2 OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-38920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53.9%; Score 41; DB 5; I 35.7%; Pred. No. 2.6e+03; tive 7; Mismatches 2;
; OTHER INFORMATION: Clone ID: 18064519.pep
US-10-767-701-62671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 40;
Pred. No.
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; Sequence 133, Application US/10314669
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4676 VVMKPAKIEHKEEN 4689
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Best Local Similarity 42.9%;
Matches 6; Conservative
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Best Local Similarity 35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: DOMAIN
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Query Match 52.6%; Score 40; DB 4; Length 210; Best Local Similarity 64.3%; Pred. No. 1.1e+02; Matches 9; Conservative 2; Mismatches 1; Indels
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IIILE OF INVENTION: PHENOTYPIC SCREEN OF CHIMERIC PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-809-861-221

Publication No. US20040209277A1

GENERAL INFORMATION:

APPLICANT: Lee, Dong-Ki

APPLICANT: Lee, Yangsoon

TITLE OF INVENTION: UI-SOURCE

CURRENT APPLICATION UI-SOURCE

FILE REFERENCE: 12279-007002

CURRENT APPLICATION NUMBER: US/10/669,861

CURRENT APPLICATION NUMBER: US/10/669,861

CURRENT APPLICATION NUMBER: US 10/314,669

PRIOR APPLICATION NUMBER: US 60/338,441

PRIOR PILING DATE: 2001-12-07

PRIOR FILING DATE: 2001-12-07

PRIOR FILING DATE: 2001-12-07

PRIOR FILING DATE: 2001-12-07

PRIOR FILING DATE: 2001-04-26

PRIOR FILING DATE: 2002-04-26

PRIOR FILING DATE: 2002-08-05

PRIOR APPLICATION NUMBER: US 60/400,904

PRIOR APPLICATION NUMBER: US 60/400,904

PRIOR FILING DATE: 2002-08-05

PRIOR FILING DATE: 2002-08-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/314,669
CURRENT FILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: US 60/338,441
PRIOR PILING DATE: 2001-12-07
PRIOR PILING DATE: 2001-12-07
PRIOR PILING DATE: 2002-04-26
PRIOR PILING DATE: 2002-04-26
PRIOR FILING DATE: 2002-04-26
PRIOR PILING DATE: 2002-04-26
PRIOR PILING DATE: 2002-08-02
PRIOR PILING DATE: 2002-08-05
NUMBER: OF SEQ ID NOS: 266
SOFTWARE: FREUSEQ for Windows Version 4.0
SEQ ID NO 221
LENGTH: 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: plasmid sequence US-10-314-669-221
                                                                                                                                                   Sequence 221, Application US/10314669 Publication No. US20030194727A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
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184 VLRPILLRIHNSEQ 197
                                                                                                                                                                                                                        APPLICANT: Kim, Jin-Soo
APPLICANT: Park, Kyung-Soon
APPLICANT: Lee, Dong-Ki
                                                                                                                                                                                                                                                                                      Seol, Wongi
Lee, Horim
Lee, Seong-il
Yang, Hyo-Young
Lee, Yangsoon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 12279-007001
5 PSRVHNSEENT 15
                                       43 PLRVHASSENT 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 40; DB 5; Length 90;
Pred. No. 44;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                   US-10-732-620-119
; Sequence 119, Application US/10732620
; Publication No. US20050032186A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jin-Soo
; APPLICANT: Kim, Jin-Soo
; APPLICANT: Kwon, Heung-Sun
; TITLE OF INVENTION: REGULATORY ZINC FINGER PROTEINS
; FILE REFERENCE: 12279-009001
; CURRENT APPLICATION NUMBER: US/10/732,620
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/431,892
; PRIOR FILING DATE: 2002-12-09
; SOFTWARE: FREESE FOR WINDOWS VERSION 4.0
; SEQ ID NOS: 129
; LENGTH: 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 52.6%; Score 40; DB Best Local Similarity 72.7%; Pred. No. 58; Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 2000-12-18

PRIOR APPLICATION NUMBER: 19 99/377484

PRIOR FILING DATE: 1999-12-16

PRIOR APPLICATION NUMBER: 1P 00/159162

PRIOR APPLICATION NUMBER: JP 00/280988

PRIOR FILING DATE: 2000-04-07

PRIOR FILING DATE: 2000-08-03

NUMBER OF SEQ ID NOS: 7059

SOFTWARE: Patentin ver. 3.0

SEQ ID NO 5581

LENGTH: 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REFERENCE: 249-125 CURRENT APPLICATION NUMBER: US/09/738,626 CURRENT FILING DATE: 2000-12-19 PRIOR APPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5581, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:

i TYPE: PRT
i ORGANISM: Corynebacterium glutamicum
US-09-738-626-5581

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , TYPE: PRT
, ORGANISM: Saccharomyces cerevisiae
US-10-732-620-119
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ANDO, SEIKO
HAYASHI, MIKIRO
OCHIAI, KEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52.6%;
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      VLRP--SRVHNSEE 13
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64 VLRPILLRIHNSEQ 77
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Best Local Similarity 64.3
Matches 9; Conservative
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ng, Young-Soon
TION: PHENOTYPIC SCREEN OF CHIMERIC PROTEINS
: 12279-007001
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PRIOR FILING DATE: 2001-12-07
PRIOR FILING DATE: 2002-04-26
PRIOR FILING DATE: 2002-04-26
PRIOR APPLICATION NUMBER: US 60/400,904
PRIOR PRILICATION NUMBER: US 60/401,089
PRIOR PRILICATION NUMBER: US 60/401,089
PRIOR FILING DATE: 2002-08-02
PRIOR FILING DATE: 2002-08-05
                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 266
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 223
LENGTH: 238
                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/314,669 CURRENT FILING DATE: 2002-12-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: plasmid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Matches 9; Conservative
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                                                                                                                  TITLE OF INVENTI
FILE REFERENCE:
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                                                                                                                                                                                                                                Length 210;
                                                                                                                                                                                                                                Score 40; DB 4; Length 210
Pred. No. 1.1e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ITLE OF INVENTION: PHENOTYPIC SCREEN OF CHIMERIC PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 52.6%; Score 40; DB 4; Best Local Similarity 64.3%; Pred. No. 1.3e+02; Matches 9; Conservative 2; Mismatches 1
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 222
LENGTH: 238
NUMBER OF SEQ ID NOS: 261
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 221
LENGTH: 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/314,669 CURRENT FILING DATE: 2002-12-09
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APPLICATION NUMBER: US 60/400,904
FILING DATE: 2002-08-02
APPLICATION NUMBER: US 60/401,089
FILING DATE: 2002-08-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ), OTHER INFORMATION: plasmid sequence US-10-314-669-222
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. Sequence 223. Application US/10314669
. Publication No. US20030194727A1
. GENERAL INFORMATION:
                                                                                                                                                                ; OTHER INFORMATION: plasmid sequence US-10-669-861-221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 222, Application US/10314669
                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                Query Match 52.6%;
Best Local Similarity 64.3%;
Matches 9; Conservative
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Lee, Seong-il
                                                                                                                                              FEATURE:
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Length 238;
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                             1.3e+02;
Score 40; DB 4;
Pred. No. 1.3e+02
                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 12279-007001
CURRENT APPLICATION NUMBER: US/10/314,669
CURRENT FILING DATE: 2002-12-09
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         URRENT FILING DATE: 2002-12-09
RIOR APPLICATION NUMBER: US 60/338,441
RIOR FILING DATE: 2001-12-07
RIOR APPLICATION NUMBER: US 60/376,053
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PRIOR APPLICATION NUMBER: US 60/401,089
PRIOR FILING DATE: 2002-08-05
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US-10-314-669-224
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o. US20030194727A1
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Sequence 72739, Application US/10425114

Sequence 72739, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liou, Yihua

APPLICANT: Lou, Yihua

APPLICANT: Tabaek, Jack E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B

CURRENT APPLICATION NUMBER: US/10/425,114
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                                                                                                                                                                                              Length 238;
                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                           Score 40; DB 4; 1
Pred. No. 1.3e+02;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lee, Yangsoon
APPLICANT: Kim, Jin-Soo
TITLE OF INVENTION: DIFFERENTIATION PROTEINS
FILE REFERENCE: 12279-0077002
CURRENT APPLICATION NUMBER: US/10/669,861
CURRENT FILING DATE: 2003-09-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 10/314,669
PRIOR FILING DATE: 2002-12-09
PRIOR FILING DATE: 2001-12-07
PRIOR FILING DATE: 2001-01-07
PRIOR FILING DATE: 2002-04-26
PRIOR PILING DATE: 2002-04-26
PRIOR PLING DATE: 2002-04-26
PRIOR FILING DATE: 2002-08-02
PRIOR FILING DATE: 2002-08-05
PRIOR FILING DATE: 2002-08-05
PRIOR FILING DATE: 2002-08-05
NUMBER OF SEQ ID NOS: 261
SOFTWARE: FASLESQ for Windows Version 4.0
SSOFTWARE: 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 224, Application US/10669861 Publication No. US20040209277A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: plasmid sequence
                                                                                               ; FEATURE:
; OTHER INFORMATION: plasmid sequence
US-10-669-861-223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                 Query Match 52.6%;
Best Local Similarity 64.3%;
Matches 9; Conservative
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212 VLRPILLRIHNSEQ 225
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212 VLRPILLRIHNSEQ 225
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SEQ ID NO 223
                          LENGTH: 238
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52.6%; Score 40; DB 4; Length 238;
Best Local Similarity 64.3%; Pred. No. 1.38+02;
Matches 9; Conservative 2; Mismatches 1; Indels
     Pred. No. 1.3e+02;
2; Mismatches 1; Indels
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Fublication No. US20040209277A1
GENERAL INPORMATION:
APPLICANT: Lee, Yangsoon
TILE OF INVENTION:
FILE REPERENCE: 12279-007002
CURRENT APPLICATION NUMBER: US.10/669,861
CURRENT FILING DATE: 2003-09-24
PRIOR APPLICATION NUMBER: US.60/314,669
PRIOR APPLICATION NUMBER: US.60/314,669
PRIOR APPLICATION NUMBER: US.60/316,669
PRIOR PILING DATE: 2002-12-09
PRIOR FILING DATE: 2002-09-26
PRIOR PLIING DATE: 2002-09-26
PRIOR APPLICATION NUMBER: US.60/400,904
PRIOR FILING DATE: 2002-04-26
PRIOR PILING DATE: 2002-04-26
PRIOR PILING DATE: 2002-08-05
PRIOR FILING DATE: 2002-08-05
PRIOR FILING DATE: 2002-08-05
PRIOR FILING DATE: 2002-08-05
PRIOR FILING DATE: 2002-08-05
NUMBER OF SEQ ID NOS: 261
NUMBER OF SEQ ID NOS: 261
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APPLICANT: Lee, Yangsoon
APPLICANT: Lee, Yangsoon
TITLE OF INVENTION: DIFFERENTIATION PROTEINS
FILE REFERENCE: 12279-007002
CURRENT FILING DATE: 2003-09-24
PRIOR APPLICATION NUMBER: US 10/314,669
PRIOR PILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: US 60/338,441
PRIOR APPLICATION NUMBER: US 60/338,441
PRIOR FILING DATE: 2002-04-26
PRIOR PILING DATE: 2002-04-26
PRIOR PILING DATE: 2002-04-26
PRIOR PILING DATE: 2002-08-05
PRIOR PILING DATE: 2002-08-05
PRIOR APPLICATION NUMBER: US 60/401,089
PRIOR FILING DATE: 2002-08-05
NUMBER OF SEQ ID NOS: 261
SOFTHARE: FASTEER FOR Windows Version 4.0
                                                                                                                                                                                                                                                        Sequence 222, Application US/10669861
Publication No. US20040209277A1
GENERAL INFORMATION:
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US-10-669-861-222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
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212 VLRPILLRIHNSEQ 225
                                                                                                               |||| |:|||| |:||||:
212 VLRPILLRIHNSEQ 225
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                                                                               2 VLRP--SRVHNSEE 13
     Best Local Similarity 64.3
Matches 9, Conservative
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US-10-669-861-222
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TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DROSOPHILA GENES.
FILE REFERENCE: CLOODY, 143
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 2005-04-04
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                                                                                                                                                                                                                                                                      Length 836;
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                                                                                                                                                                                                                                                                  Score 40; DB 4;
Pred. No. 5.1e+02
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Fast ED NOS: 43008
SOFTWARE: Fast ED for Windows Version 4.0
SEQ ID NO 40320
PRIOR APPLICATION NUMBER: PCT/US01/29288
PRIOR FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: US 60/233,564
PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 308
SOFTWARE: Patentin version 3.1
SEQ ID NO 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR PILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR PILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-29
PRIOR FILING DATE: 1999-11-2
PRIOR FILING DATE: 1999-11-2
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR PILING DATE: 1999-11-2
PRIOR PILING DATE: 1999-11-2
PRIOR FILING DATE: 1999-11-2
PRIOR FILING DATE: 2000-01-12
PRIOR FILING DATE: 2000-01-12
PRIOR PILING DATE: 2000-03-24
PRIOR PILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-23
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 40320, Application US/11097143 Publication No. US20050208558A1 GENERAL INFORMATION:
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                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-149-310-106
                                                                                                                                                                                                                                                                      52.6%;
                                                                                                                                                                                                                                                                                                                                                                                          |||| |:||||:
571 VLRPILLRIHNSEQ 584
                                                                                                                                                                                                                                                                                                                                                             2 VLRP--SRVHNSEE 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Venter, J. Craig
                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 PSRVHNSEENT 15
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84 PDRIHESDRNT 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                LENGTH: 836
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Jeidant: Li, Ping
Ji, Ping
Ji, Ping
Ji, Ping
Ji, Ping
Ji, Ping
Ji, Ping
Ji, Ping Nucleic Acid Molecules and Other Molecules As
JIILE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules As
JIILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
Ji, CURRENT REPRINCE: 38-21(53221)B
JI, CURRENT FILING DAIR: 2003-6-14
JI, NUMBER OF SEQ ID NOS: 204966
Ji, SEQ ID NO 157183
JESQTH: 671
JEVENT
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US-10149-310-106

Sequence 106, Application US/10149310

Publication No. US20040077039A1

GENERAL INPORMATION:
APPLICANT: Holtzman, Douglas
APPLICANT: Maxon, Mary
APPLICANT: Sherman, Amir
TITLE OF INVENTION: Modulation of Secondary Metabolite Production by
TITLE OF INVENTION: 2inc Binuclear Cluster Proteins
FILE REFERENCE: 14184-019US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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64.3%; Pred. No. 4e+02;
tive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                    Length 313;
                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , OTHER INFORMATION: Clone ID: PAT_MRT4530_S677C.i.pep
US-10-437-963-157183
                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: LIB3587-232-A9_FLI.pep
US-10-425-114-72739
                                                                                                                                                                                                                                Score 40; DB 4; I
Pred. No. 1.7e+02;
4; Mismatches 1;
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OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 157183, Application US/10437963 Publication No. US20040123343A1
      NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 72739
                                                                                                                                                                                                                                  Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: La ROBA, Thomas J. APPLICANT: Kovalic, David K. APPLICANT: Zhou, Yihua APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 VLRPSRVHNSEENT 15
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Best Local Similarity 64.3
Matches 9; Conservative
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241 VMLRPLQIHNS 251
                                                                                                                                                                                                                                                                                                                           1 IVLRPSRVHNS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Publication No. US200
GENERAL INFORMATION:
                                                                                                   TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-437-963-157183
                                                                                 LENGTH: 313
                                                                                                                                                     FEATURE:
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LOCATION: (119)...(128)

OTHER INFORMATION: Zinc finger C3HC4 type (RING finger), proteins. domain

OTHER INFORMATION: identified by eMATRIX, accession number BL00518, p-value=2.800e-1

OTHER INFORMATION: raw score of 12.23

FEATURE:

NAME/KEY: DOMAIN

LOCATION: (104)...(144)
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OTHER INFORMATION: Zinc finger, C3HC4 type (RING finger) domain identified by
OTHER INFORMATION: PFam, accession name zf-C3HC4, E-value=6.2e-13, PFam score of 46.
Page 18

TITLE OF INVENTION: Bice Nucleic Acid Molecules and Other Molecules Associated With; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement; FILE REFERENCE: 38-21(53221)B

CURRENT PAPLICAN UNDER: US/10/437,963

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 103361

LENGTH: 417

TYPE: nr.
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## Sequence 58855, Application US/10450763

## Publication No. US20050196754A1

## CENTERAL INFORMATION:

## APPLICATION NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

## PILE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

## PILE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

## CURRENT APPLICATION NUMBER: US/10/450,763

## CURRENT FILING DATE: 2003-06-11

## PRIOR PELICATION NUMBER: OF/540,217

## PRIOR PELICATION NUMBER: OS/640,167

## PRIOR PELICATION NUMBER: OS/649,167

## PRIOR PELING DATE: 2000-03-31

## PRIOR PILING DATE: 2000-03-31

## PRIOR PILING DATE: 2000-03-31

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Clone ID: PAT_MRT4530_100799C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51.3%; Score 39; DB 4; I 63.6%; Pred. No. 3.5e+02;

    Mismatches

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US-09-796-753-116
Sequence 116, Application US/09796753
Publication No. US20030027998A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 63.6
Matches 7; Conservative
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Matches 8; Conservative
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33 LAPSRTHNTSE 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Oryza Bativa
FEATURE:
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-437-963-103361
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APPLICANT: La Royalit, David K.
APPLICANT: Shou, Yihua
APPLICANT: Shou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21 [53222] B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 255664
LENGTH: 124
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                                                                                                                                                                                                       APPLICANT: VAN LEYEN, KLAUS
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR EVALUATION AND MODULATION
TITLE OF INVENTION: OF FERTILITY
FILE REFERENCE: UVMO: 031US
CURRENT APPLICATION NUMBER: US/10/898,141
CURRENT APPLICATION NUMBER: 60/489,871
PRIOR PILING DATE: 2004-07-24
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PACENTIN Ver. 2.1
SEQ ID NO 17
LENGTH: 13
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40.0%; Pred. No. 93;
ive 5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51.3%; Score 39; DB 5; Length 13; 88.9%; Pred. No. 7.8; tive 0; Mismatches 1; Indels
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US-10-425-115-253664
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OTHER INFORMATION: unsure at all Xaa locations
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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
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Matches 6, Conservative
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Matches 8; Conserv
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ORGANISM: Porcarius
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US-10-437-963-103361
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US-10-425-115-253664
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APPLICANT: Chou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Buckharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 172291
LENGTH: 946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwa Title
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/206428
SEQ ID NOS: 369326
SEQ ID NO 296047
LENGTH: 60
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Pred. No. 8.7e+02;
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63;
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US-10-437-963-172291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: MRT4577_33072C.1.pep
US-10-425-115-296047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (1)..(60)
OTHER INFORMATION: unsure at all Xaa locations
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Pred. No. 63;
5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 296047, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
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Best Local Similarity 42.9%;
Matches 6; Conservative 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51.3%;
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Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Oryza sativa ·
FEATURE:
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74 ILRPADSHNSE 84
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ORGANISM: Zea mays
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NAME/KEY: unsure
LOCATION: (1)..((
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McCarthy, Sean A.
/ENTION: SECRETED PROTEINS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 39; DB 3; 1
Pred. No. 4.3e+02;
1; Mismatches 4,
                                                       CURRENT APPLICATION NUMBER: US/09/796,753
CURRENT FILING DATE: 2001-03-01
PRIOR PLILING DATE: 2001-03-01
PRIOR FILING DATE: 1998-10-30
PRIOR PLILOR DATE: 1998-12-30
PRIOR PLILOR DATE: 1999-02-46
PRIOR PLILOR DATE: 1999-02-46
PRIOR PLILOR DATE: 1999-02-46
PRIOR PLILOR DATE: 1999-02-46
PRIOR PLILOR DATE: 1999-03-01
                                                                                                                                                                                                                                                                                                                                 FILING DATE: 1999-03-01
APPLICATION NUMBER: 09/312,359
FILING DATE: 1999-05-14
FILING DATE: 1999-06-18
FILING DATE: 1999-06-18
APPLICATION NUMBER: 09/342,687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 09/409,634
FILING DATE: 1999-09-30
APPLICATION NUMBER: 09/471,179
FILING DATE: 1999-12-23
APPLICATION NUMBER: 09/474,071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 1999-12-29
APPLICATION NUMBER: 09/474,072
FILING DATE: 1999-12-29
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APPLICATION NUMBER: 09/572,002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 09/597,993
FILING DATE: 2000-06-19
APPLICATION NUMBER: 09/599,596
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FILING DATE: 2000-06-29
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FILING DATE: 2000-06-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09/516,745
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Best Local Similarity 58.3%;
Matches 7; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000-05-14
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PLICATION NUMBER: 09/
LING DATE: 1999-06-30
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PRIOR APPLICATION NUMBER: 0
PRIOR FILING DATE: 2000-09-
PRIOR FILING DATE: 2000-09-
NUMBER: 0F SEQ ID NOS: 162
SEQ ID NO 116
LENGTH: 497
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ORGANISM: Mus musculus
US-09-796-753-116
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RESULT 53

4 RPSRVHNSEENT 15

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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 8.3

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 8.3

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 7.6

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 7.6

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 7.9

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 7.9

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 7.9

OTHER INFORMATION: EXPRESSED IN BT414, SIGNAL = 7.9

OTHER INFORMATION: EXPRESSED IN BT414, SIGNAL = 9.4

OTHER INFORMATION: EXPRESSED IN FIFTAL LIVER, SIGNAL = 8.6

OTHER INFORMATION: EXPRESSED IN FIRTAL LIVER, SIGNAL = 8.6

OTHER INFORMATION: EXPRESSED IN FIRTAL LIVER, SIGNAL = 8.6

OTHER INFORMATION: EXPRESSED IN FIRTAL LIVER, SIGNAL = 8.6

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OTHER INFORMATION: EXPRESSED IN FIRTAL LIVER, SIGNAL = 8.6

OTHER INFORMATION: EXPRESSED IN FIRTAL LIVER, SIGNAL = 8.6

OTHER INFORMATION: SWISSPROT HIT: 035136, EVALUE 8.00e-12
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Pred. No. 2.1e+02;
8; Mismatches 2; Indel8
                            FRILING APPLICATION NUMBER: 08 09/632,366
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-08-38
PRIOR PRILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR APPLICATION NUMBER: PCT/USO1/00667
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR PILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 50.0%;
Best Local Similarity 28.6%;
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-864-761-35808
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Betent No. US20020048763A1

GENERAL INFORMATION:
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-K-1
CURRENT APPLICATION NUMBER: US/09/864,761
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US-10-108-260A-2889
is Sequence 2889, Application US/10108260A
; Sequence 2889, Application No. US20040005560A1
; Publication No. US20040005560A1
; GENERAL INFORMATION:
is APPLICANT: HELIX RESEARCH INSTITUTE
it ITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
FILE REFERENCE: H.-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEG ID NOS: 5458
; SOFTWARE: PetentIn Ver. 2.1
; SEQ ID NO 2889
. LENGTH: 148
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Pred. No. 1.7e+02;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 38; DB 4; Length 122;
Pred. No. 1.4e+02;
1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , OTHER INFORMATION: Clone ID: PAT_MRT3847_52112C.1.pep
US-10-424-599-232656
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Best Local Similarity 57.1%;
Matches 8; Conservative
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Best Local Similarity 50.0
Matches 6; Conservative
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47 MVLSPARIHESQ 58
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ORGANISM: Glycine max
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US-09-864-761-35808
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APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Mucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERRICE: 38-21(53221)B
CURRENT APPLICATION WUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 204794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 32297, Application US/10767701

Publication No. US20040172684A1

GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128

SEQ ID NO 32297
LENGTH: 235
                                                                                                                                                                                                                         Length 232;
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US-10-767-701-32297
                                                                                                                                                                                                                              50.0%; Score 38; DB 3; I
80.0%; Pred. No. 2.8e+02;
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Pred. No. 2.8e+02;
3; Mismatches 4
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: PastSEQ for Windows Version 4.0
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LENGTH: 232
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-12569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 204794, Application US/10437963 Publication No. US20040123343A1
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
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Best Local Similarity 46.2%;
Matches 6; Conservative
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Best Local Similarity 80.v.
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ORGANISM: Sorghum bicolor
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ORGANISM: Oryza sativa
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US-10-767-701-32297
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APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Tamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANTON: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
CURRENT APPLICATION NUMBER: 00/209/815,242
CURRENT FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PRILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-22
                                                                           APPLICANT: ITEMATON, OLIMIES.
APPLICANT: TAMEMOLO, ROBERT T.
APPLICANT: Yamemoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REPERENCE: ELITAN.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/203, PRIOR APPLICATION NUMBER: 60/203, PRIOR PRILICATION NUMBER: 60/207,727
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PRIOR FILING DATE: 2000-10-24
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PRIOR APPLICATION NUMBER: 60/253, 625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253, 635
PRIOR FILING DATE: 2000-11-27
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Pred. No. 2.8e+02;
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Patent No. US20020061569Al
GENERAL INFORMATION
APPLICANT: Haselbeck, Robert
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; ORGANISM: Staphylococcus aureus
US-09-815-242-5560
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            Zyskind, Judith W.
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Best Local Similarity 80.0
Matches 8; Conservative
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                                 wall, Daniel
Trawick, Johr
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RESULT 60
US-10-767-701-35712
; Sequence 35712, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Plante and Uses Thereof For Plant Improvement
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; CURRENT FILING DATE: 2004-01-29
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LENGTH: 303
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50.0%; Score 38; DB 4; Length 303;
Best Local Similarity 57.1%; Pred. No. 3.7e+02;
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ORGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: SORBI-28MAY03-C72553_1.pep
US-10-767-701-35712
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38, Appl 5, Appli 3, Appli 115, App 27299, A 328, App 5689, Ap

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	Sequence 147, App Sequence 37, Appl Sequence 3855, Ap Sequence 29141, A Sequence 2594, Ap	Sequence 29140, A Sequence 17, Appl Sequence 142, App Sequence 142, App	Sequence 23133, App Sequence 313, App Sequence 231, App	Sequence 1648, Ap Sequence 141, App Sequence 260, App	Sequence 28130, A Sequence 28129, A Sequence 152, App	Sequence 28128, A Sequence 2850, Ap	Sequence 258, App Sequence 266, App Sequence 280, App	Sequence 10366, A Sequence 228, App	Sequence 903, App Sequence 392, App Sequence 499, App	o)							٠		SSMENT, PREVENTION, AND						•		
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Sequence 24673, Ap. Sequence 27208, A Sequence 24673, A Sequence 9861, Ap. Sequence 9860, A Sequence 9860, A	27207, 21549, 2038, 6338, 1752,	Sequence 27675, A Sequence 9410, Ap Sequence 7007, Ap Sequence 118, App	Sequence 27674, A Sequence 5412, Ap Sequence 24672, A Sequence 9409, Ap	Sequence 4976, Ap Sequence 270, App	Sequence 6225, Ap Sequence 1628, Ap Sequence 11432, A	Sequence 3715, Ap Sequence 18959, A Sequence 18958, A	Sequence 14664, A Sequence 425, App	Sequence 19533, A Sequence 5368, Ap Sequence 19532, A	Sequence 309, App Sequence 30094, A	Sequence 2, Appli Sequence 1349, Ap	Sequence 192, App Sequence 28872, A	Sequence 11244, Ap Sequence 1755, Ap Sequence 1909, Ap	Sequence 10922, A Sequence 7754, Ap	Sequence 29032, A Sequence 12, Appl	Sequence 219, App					Sequence 333/, Ap Sequence 14663, A			Sequence 2032, Ap Sequence 28294, A	Sequence 28589, A Sequence 2, Appli		Sequence 264, App	Sequence 394, App Sequence 28293, A
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APPLICANT: Alexandrov, Nickolai et al.

TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 21150
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APPLICANT: Alexandrov, Nickolai et al.

TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides

TITLE OF INVENTION: Therby

FILE REFERENCE: 2750-1522PUS2

CURRENT APPLICATION NUMBER: US/11/096,568A

CURRENT FILING DATE: 2005-04-01

NUMBER OF SEQ ID NOS: 34471

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 7;
16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 40; DB 7;
Pred. No. 14;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
i LOCATION: (1)..(377)
cother information: Ceres Seq. ID no. 12401931
US-11-096-5688-21150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ID no. 12401933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 40;
Pred. No.
                                                                                                                             Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                        Sequence 21152, Application US/11096568A publication No. US20060048240A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-11-096-568A-21150
; Sequence 21150, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (1) ... (331)
COTHER INFORMATION: Ceres Seq. US-11-096-568A-21152
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Best Local Similarity 54.5%;
Matches 6; Conservative '
                                                                                                                          53.9%;
35.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 52.6%;
Best Local Similarity 54.5%;
Matches 6; Conservative
                                                                                                                                                                                                                                          1 IVLRPSRVHNSEEN 14
                                                                                                                                                                    Conservative
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259 VMLRPLQIHNS 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Zea mays subsp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 IVLRPSRVHNS 11
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                                       TYPE: PRT
CORGANISM: Homo Sapiens
US-11-186-284-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
                                                                                                                                            Best Local Similarity
Matches 5; Conserv
SEQ ID NO 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 377
                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Veiby, Petter Ole
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
TITLE OF INVENTION: AND OVARIAN CANCER
FILE REFERENCE: MRI-039
CURRENT APPLICATION NUMBER: US/11/080,991
CURRENT PILING DATE: 2005-03-11
PRIOR FILING DATE: 2002-06-21
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 54
LENGTH: 2928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPOSITIONS, KITS, AND IDENTIFICATION, ASSESSMENT, PREVENTION, AND
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                                                                                                                               Gaps
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                                                                                   Length 760;
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                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: MILIAM ALLEGATOR APPLICANT: Guillemette, Tracy L.
APPLICANT: Guillemette, Tracy L.
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Hibodeau, Stephen N.
APPLICANT: Hibodeau, Stephen N.
APPLICANT: Hibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: METHODS FOR IDENTIFICATION
TITLE OF INVENTION: METHODS FOR IDENTIFICATION
FILE REFERENCE: MPMO1-029P2RNM
CURRENT APPLICATION NUMBER: US/11/186,284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 41; DB 7
Pred. No. 98;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR PELICATION NUMBER: US/10/301,822
PRIOR FILING DATE: 2002-11-21
PRIOR FILING DATE: 2002-112-10
PRIOR FILING DATE: 2001-12-10
PRIOR FILING DATE: 2001-12-10
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Millennium Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 49, Application US/11186284
Publication No. US20050266493A1
                                                                                                                                                                                                                                                                                                                         Sequence 54, Application US/11080991
Publication No. US20050266437A1
GENERAL INFORMATION:
                                                                                     100.0%; Sc
100.0%; Pr
tive 0;
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35.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 IVLRPSRVHNSEENT 15
                                                                                                                                                                                                     24 IVLRPSRVHNSEENT 38
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Best Local Similarity 35.7-
Best Local Si Conservative
5, Conservative
                                                                                     Query Match
Best Local Similarity 100.
Matches 15; Conservative
                        , ORGANISM: Homo Sapiens
US-11-186-284-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-11-080-991-54
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      TYPE: PRT
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Sequence 28365, Application US/11096568A

Publication No. US20060048240A1

GENERAL INFORMATION:
APPLICANT Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
SEQ ID NO 28365
LENGTH: 507
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; APPLICANT: Abad, Mark S. et al.; TITLE OF INVENTION: Genes and Uses for Plant Improvement; FILE REFERENCE: 38-21(53450) B EP; CURRENT APPLICATION NUMBER: US/11/087,099; CURRENT FILING DATE: 2005-03-22; NUMBER OF SEQ ID NOS: 12464; SQ ID NO 11054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 507;
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24;
                                                                                                                                                                                                                                                                                     Length 949;
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            TYPE: PRT
ORGANISM: Arabidopsis thaliana
ORGANISM: Arabidopsis thaliana
PERTURE:
NAME/KEY: misc_feature
COTHER INFORMATION: (1)...(949)
COTHER INFORMATION: Ceres Seq. ID no. 15221079
FEATURE:
NAME/KEY: misc_feature
COCATION: (1)...(1)
COCATION: (1)...(1)
COCATION: (1)...(1)
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Pred. No. 75;
                                                                                                                                                                                                                                                                                       Score 39; DB 7
Pred. No. 66;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 38; DB 7
Pred. No. 24;
0; Mismatches
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LOCATION: (1). (507)
CTHER INFORMATION: Ceres Seq. ID no. 2715595
US-11-096-568A-28365
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54.5%;
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80.0%;
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Best Local Similarity 35.7%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   : |:|::||:
79 VFLKPAKVHDDDED 92
                                                                                                                                                                                                                                                                                                                                                                           1 IVLRPSRVHNSEEN 14
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Best Local Similarity 80.0.
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US-11-087-099-11054
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Best Local Similarity
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US-11-096-568A-28365
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SEQ ID NO 32094
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Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE REPERENCE: 2750-1592P028
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT PILING DATE: 2005-04-01
SEQ ID NO 32095
LIENGTH: 917
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Publication No. US20060048240A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION WUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 40; DB 7; Length 532;
Pred. No. 24;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                    Sequence 7794, Application US/11087099; Publication No. US20060041961A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement; FILE REFERENCE: 38-21(53450)B EP; CURRENT APPLICATION NUMBER: US/11/087,099; CURRENT FILING DATE: 2005-03-22; SEQ ID NOS: 12464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature

LOCATION: (1)...(917)

CTHER INFORMATION: Ceres Seq. ID no. 15221080

US-11-096-5688-32095
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                                                                                                                                                                                                                                                                                                                                                                                                                                            52.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : |:|::||: 47 VFLKPAKVHDDDED 60
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56 LKPRQVHRPESNT 68
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 52.6
Best Local Similarity 53.9
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 35.7
Matches 5, Conservative
305 VMLRPLQIHNS 315
                                                                                                                                                                                                                                                                                                                                                                         , ORGANISM: Daucus carota
US-11-087-099-7794
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US-11-096-568A-32094
                                                                                                     US-11-087-099-7794
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APPLICANT: BAUDU, Philippe
TITLE OF INVENTION: CANINE HERPESVIRUS BASED RECOMBINANT LIVE VACCINE, I
TITLE OF INVENTION: PARTICULAR AGAINST CANINE DISTEMPER, RABIES OR THE
TITLE OF INVENTION: PARAINFLUENZA 2 VIRUS
TITLE OF INVENTION: PARAINFLUENZA 2 VIRUS
THE REPERENCE: 454313-2200.1
CURRENT APPLICATION NUMBER: 2004-09-07
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TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Pibrosis Methods of Detection and Uses Thereof
FILE REFERENCE: CL001519.ORD
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                                                                                                                                                                                                                                                              Length 2479;
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            APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(5345)B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 2391
LENGTH: 2479
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Pred. No. 4.2e+0
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Pred. No. 91;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 2004-09-07
PRIOR PLILING DATE: 2000-06-19
PRIOR PLILING DATE: 2000-06-19
PRIOR PLILING DATE: 1998-12-16
PRIOR PLILING DATE: 1998-12-16
PRIOR PLILING DATE: 1998-06-27
PRIOR PLILING DATE: 1996-06-27
PRIOR PLILING DATE: 1996-06-27
PRIOR PLILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATCHILING DATE: 1997-06-13
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APPLICANT: Michele Cargill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jean-Christophe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-935-494-3
; Sequence 3, Application US/10935494
; Publication No. US20060024329A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                              48.7%;
milarity 61.5%;
Conservative 1
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                                                                                                                                                                                                    ORGANISM: Neurospora crassa
US-11-087-099-2391
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245 VLRPPRSLNSSDN 257
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Best Local Similarity
Matches 7; Conserv
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Sequence 28165, Application US/11096568A

Publication No. US20060048240A1

GENERAL INFORMATION:

SEQUENCE ALIVERMINION: Sequence-Determined DNA Fragments and Corresponding Polypeptides

TITLE OF INVENTION: Therby

TITLE OF INVENTION: Therby

TITLE REFERENCE: 2750-1592PUS.

CURRENT APPLICATION NUMBER: US/11/096,568A

CURRENT FILING DATE: 2005-04-01

SEQ ID NOS: 34471

SEQ ID NOS: 34471

SEQ ID NOS: 34471
                                                                                                                                                                      Sequence 28364, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Thecby
TITLE OF INVENTION: 1952PUSZ
CURRENT AFPERGNCE: 2750-1592PUSZ
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
ENGTH: 632
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54.5%; Pred: No. 1.1e+02;
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LOCATION: (1). (732)
CTHER INFORMATION: Ceres Seq. ID no. 2715593
US-11-096-568A-28363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: misc_feature
; LOCATION: (1). (622)
; OTHER INFORMATION: Ceres Seq. ID no. 2715594
US-11-096-568A-28364
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Pred. No. 95;
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Publication No. US20060041961A1
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Best Local Similarity 54.5
Matches 6; Conservative
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248 LQPSHLHNSRQ 258
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148 LQPSHLHNSRQ 158
  6; Conservative
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                                           3 LRPSRVHNSEE 13
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23 LQPSHLHNSRQ 33
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Matches 6; Conserva
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US-11-087-099-2391
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APPLICANT: Retter, APPLICANT: APPLICANT: Stolk, John A. APPLICANT: Bay, Carig H. APPLICANT: Carig H. APPLICANT: Carig H. APPLICANT: Carig H. APPLICANT: Carig H. APPLICANT: Carig H. APPLICANT: Carig H. APPLICANT: Carig H. APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: Manag. Aijun
TITLE OF INVENTION: PROSPATE-SPECIFIC POLYPEPTIDES AND FUSION TITLE OF INVENTION: PROSPATE-SPECIFIC POLYPEPTIDES HERROF FILENCE APPLICANTON WINDER: US) 1/23, 786
CUURRENT PELING DATE: 2010.143/31.786
CUURRENT PELING DATE: 2010.65.09
PRIOR PILING DATE: 2000.65.19
PRIOR PILING DATE: 2000.65.19
PRIOR PILING DATE: 1099-11.12
PRIOR PILING DATE: 1099-11.12
PRIOR APPLICANTON WINDER: US 09/139, 313
PRIOR PILING DATE: 1999-10.15
PRIOR PILING DATE: 1999-10.15
PRIOR PAPLICANTON WINDER: US 09/159, 812
PRIOR PILING DATE: 1999-10.15
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PRIOR PAPLICANTON WINDER: US 09/159, 812
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                                                                                                                                                                      DB 7; Length 205;
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Pred. No. 1.1e+02;
4; Mismatches 3
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Pred. No. 62;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 590, Application US/11234786
Publication No. US20060024301A1
GENERAL INFORMATION:
APPLICANT: Vi, Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Reades, Michael D.
APPLICANT: Renger, Gary R.
APPLICANT: Relea, Michael D.
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Best Local Similarity 41.7.
Best Local Si Conservative
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Best Local Similarity 63.6
Matches 7; Conservative
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                                                 ORGANISM: Zea mays
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publication No. US20060024329A1

GENERAL INPORMATION:
APPLICANT: AUDONNET, Jean-Christophe
APPLICANT: BAUDU, Philippe
TITLE OF INVENTION: CANINE HERPESVIRUS BASED RECOMBINANT LIVE VACCINE, IN
TITLE OF INVENTION: PARTICULAR AGAINST CANINE DISTEMPER, RABIES OR THE
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TITLE OF INVENTION: PARTICULAR AGAINST CANINE DISTEMPER, RABIES OR THE
CURRENT FILING DATE: 2004-09-07
PRIOR APPLICATION NUMBER: US/09/596,479
PRIOR PILING DATE: 1998-12-16
PRIOR FILING DATE: 1998-12-16
PRIOR FILING DATE: 1999-06-27
PRIOR FILING DATE: 1999-06-27
PRIOR PILING DATE: 1996-06-27
PRIOR PILING DATE: 1999-06-27
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US-11-087-099-835
i Sequence 835, Application US/11087099
i Publication No. US20060041961A1
i GENERAL INFORMATION:
i APPLICANT: Abad, Mark S. et al.
i TITLE OF INVENTION: Genes and Uses for Plant Improvement
i FILE REFERENCE: 38-21(53450)B EP
i CURRENT APPLICATION NUMBER: US/11/087,099
i CURRENT FILING DATE: 2005-03-22
i NUMBER OF SEQ ID NOS: 12464
i SEQ ID NO 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47.4%; Score 36; DB 7; 1 54.5%; Pred. No. 1.9e+02; iive 1; Mismatches 4;
PRIOR FILING DATE: 2004-05-07
PRIOR APPLICATION NUMBER: US 60/582,609
PRIOR FILING DATE: 2004-06-25
PRIOR APPLICATION NUMBER: US 60/599,554
PRIOR FILING DATE: 2004-08-09
NUMBER OF SEQ ID NOS: 34460
SEQ ID NO 473
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Best Local Similarity 54.5
Best Local 6; Conservative
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Best Local Similarity 50.0
Matches 7; Conservative
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503 PLRIHEKEEET 513
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                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-124-367A-473
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US-10-935-494-31
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                                                                                                                                                                               Length 555;
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 829, Application US/11087099; Publication No. US20060041961A1.
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement FILE REFERENCE: 38-21(53450) B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1383, Application US/11087099
Publication No. US20060041961A1
GENERAL INFORMATION:
APPLICAT: Abad, Mark S. et al.
TITLE CO INVENTION: Genes and Uses for Plant Improvement FILE REFERENCE: 38-21(53450) B. EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT PILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Bacillus subtilis str. 168
                                                             NAME/KEY: misc_feature; LOCATION: (538) ... IOCATION: (538) ... OTHER INFORMATION: Xaa is any aa, unknown or other US-11-096-568A-11818
LOCATION: (325)..(325)
OTHER INFORMATION: Xaa is any aa, unknown or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.8e+02;
                                                                                                                                                                             Score 35; DB 7; Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44.7%; Score 34; DB 7; 50.0%; Pred. No. 81; tive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 35;
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                                                                                                                                                                               46.1%;
61.5%;
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                                                                                                                                                                                                                                                                                                                    439 IVLRGCRVNGSDE 451
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                                                                                                                                                                                  Query Match
Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT CRGANISM: Brassica rapa US-11-087-099-829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 5
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Best Local Similarity
Matches 8; Conserv
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US-11-096-568A-5328
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                                                                                                   US-11-096-568A-11819
Sequence 11819, Application US/11096568A
Sequence 11819, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 11819
LENGTH: 542
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APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 11818
LENGTH: 555
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LOCATION: (324)...(324)
OTHER INFORMATION: Xaa is any aa, unknown or other
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LOCATION: (312)..(312)
OTHER INFORMATION: Xaa is any aa, unknown or other
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LOCATION: (311)..(311)
OTHER INFORMATION: Xaa is any aa, unknown or other
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61.5%; Pred. No. 1.8e+02;
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LOCATION: (1). (555)
OTHER INFORMATION: Ceres Seq. ID no. 15220615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (1). 7(542)
OTHER INFORMATION: Ceres Seq. ID no. 15220616
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                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Triticum aestivum
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  320 RSNRIHRQKQNT 331
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Matches 8; Conserv
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US-11-067-231-153

US-11-067-231-153

Sequence 153, Application US/11067231

Publication No. US20050272063A1

GENERAL INFORMATION:

APPLICANT: Nakamura, Yusuke

APPLICANT: Ratagiri, Toyomasa

APPLICANT: Ratagiri, Toyomasa

APPLICANT: Fukukawa, Chikako

ITILE CO INVENTION: METHOD FOR TREATING SYNOVIAL SARCOMA

FILE REFERENCE: 1254-0272PUS1

CURRENT APPLICATION NUMBER: US/11/067,231

CURRENT FILING DATE: 2002-08-30

PRIOR PILING DATE: 2002-08-30

PRIOR PILING DATE: 2003-07-11

PRIOR PILING DATE: 2003-07-11

PRIOR PILING DATE: 2003-08-21

PRIOR PILING DATE: 2004-02-24

PRIOR PILING DATE: 2004-02-24

PRIOR FILING DATE: 2004-02-24

PRIOR FILING DATE: 2004-02-24

PRIOR FILING DATE: 2004-02-24

PRIOR FILING DATE: 2004-02-24

SROPTWARR: PARELICATION NUMBER: US 60/598,834

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
44.7%; Score 34; DB 7; Length 486;
Best Local Similarity 53.8%; Pred. No. 2.38+02;
Matches 7; Conservative 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                 Length 377;
                                                                                                                                                                                                                                                                                                                                                 Score 34; DB 7; Length 37;
Pred. No. 1.8e+02;
5; Mismatches 2; Indels
              PRIOR APPLICATION NUMBER: US 60/568,845
PRIOR FILING DATE: 2004-05-07
PRIOR FILING DATE: 2004-11-09
NUMBER OF SEQ ID NOS: 21112
SOFTWARE: FBSESEQ for Windows Version 4.0
SEQ ID NO 210
LENGTH: 377
TYPE: PRI
YORGANISM: Homo sapiens
US-11-124-368A-210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Corynebacterium efficiens YS-314
US-11-087-099-4550
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Best Local Similarity 41.7%;
Matches 5; Conservative
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GENERAL INFORMATION:

APPLICANT: Alexandrov, Nickolai et al.

TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
SURENT FILING DATE: 2005-04-01
SEQ ID NOS: 34471
SEQ ID NOS: 338
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APPLICANT: Michele Cargill
APPLICANT: James J. Devlin
APPLICANT: James J. Devlin
APPLICANT: James J. Devlin
APPLICANT: James J. Devlin
APPLICANT: James J. Devlin
APPLICANT: James J. Devlin
TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
FILE REFERENCE: CLOOIS 24
CURRENT APPLICATION NUMBER: US 60/568,845
PRIOR APPLICATION NUMBER: US 60/568,845
PRIOR PILING DATE: 2004-05-07
PRIOR PILING DATE: 2004-11-09
NUMBER OF SEQ ID NOS: 21112
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 202
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US-11-124-368A-210
US-11-124-368A-210
Sequence 210, Application US/11124368A
Publication No. US20050287559A1
GENERAL INFORMATION:
APPLICANT: Michele Cargill
APPLICANT: James J. Devlin
APPLICANT: May Luke
TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
FILE REFERENCE: CL001524
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41.7%; Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 363;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 44.7%; Score 34; DB 7; I
Best Local Similarity 46.2%; Pred. No. 1.7e+02;
Matches 6; Conservative 3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: misc_feature
; LOCATION: (1)..(363)
; OTHER INDEMATION: Ceres Seq. ID no. 14308169
US-11-096-568A-5328
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95 VLIRLSRLHNOQ 106
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41 LRPSMIKNKEKRS 53
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Matches 5; Conservative
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ORGANISM: Homo sapiens
US-11-124-368A-209
                                                                                                                                                                                                                                                                                                         ORGANISM: Glycine max
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168 LFRPQRPHSAQEH 180
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Best Local Similarity 38...
Best Local Si Conservative
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Matches 7; Conservative
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CORGANISM: Homo sapiens
US-11-054-281-91
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US-11-087-099-3671
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Publication No. US20060013813A1

GENERAL INFORMATION:

TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

FILE REFERENCE: 21402-2440IP

CURRENT APPLICATION NUMBER: US/11/054,281

CURRENT APPLICATION NUMBER: 60/261,014

PRIOR FILING DATE: 2001-01-11

PRIOR APPLICATION NUMBER: 60/261,018

PRIOR APPLICATION NUMBER: 60/261,018

PRIOR APPLICATION NUMBER: 60/261,018

PRIOR PELLING DATE: 2001-01-11

PRIOR APPLICATION NUMBER: 60/318,410

PRIOR FILING DATE: 2001-09-10
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TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same FILE REPERENCE: 21402-240CIP
CURRENT APPLICATION UNDBER: US/11/054,281
CURRENT FILING DATE: 2005-02-08
PRIOR PAPLICATION NUMBER: 60/261,014
PRIOR FILING DATE: 2001-01-11
PRIOR PILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/261,026
PRIOR FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/261,026
PRIOR FILING DATE: 2001-01-11
PRIOR PILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/261,029
PRIOR FILING DATE: 2001-01-11
PRIOR PILING DATE: 2001-01-11
PRIOR FILING DATE: 2001-08-17
PRIOR FILING DATE: 2002-01-11
NUMBER OF SEQ ID NOS: 324
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Pred. No. 2.8e+02;
5; Mismatches 3; Indels
                                                                                                                                                                                             Score 34; DB 7; Length 581;
Pred. No. 2.8e+02;
5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 22, Application US/11054281; Publication No. US20060013813A1; GENERAL INFORMATION:
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Best Local Similarity 38.5%;
Matches 5; Conservative
                                                                                                                                                                                                      Query Match
Best Local Similarity 38.5%;
Matches 5; Conservative
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168 LFRPQRPHSAQEH 180
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168 LFRPQRPHSAQEH 180
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                                       TYPE: PRT
CORGANISM: Homo sapiens
US-11-067-231-153
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ORGANISM: Homo sapiens
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LENGTH: 581
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: STAPPHICACCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
TITLE OF INVENTION: STAPPHICACCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT APPLICATION NUMBER: 60/164,258
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 3328
INSTANTING NO 3328
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70.0%; Pred. No. 2.9e+02;
ive 0; Mismatches 3; Indels
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Pred. No. 2.8e+02;
5; Mismatches 3; Indels
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TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REPERENCE: 38-21(5)3450) B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
SNG ID NOS: 12464
LENGTH: 593
PRIOR APPLICATION NUMBER: 60/261,013
PRIOR FILING DATE: 2001-01-11
PRIOR PLILING DATE: 2001-01-11
PRIOR PLILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/261,029
PRIOR FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/313,170
PRIOR FILING DATE: 2001-08-17
PRIOR FILING DATE: 2001-08-17
PRIOR FILING DATE: 2002-01-11
NUMBER OF SEQ ID NOS: 324
SOFTWARE: PATENTIN VOIS: 324
SOFTWARE: PATENTIN VOIL: 2.1
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38.5%;
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1 IVLRPSRVHNSEENT 15
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SEQ ID NO 157
LENGTH: 757
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Best Local Similarity 70.0
Matches 7; Conservative
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256 ARVHVSEEGT 265
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US-10-821-234-1592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-10-055-877-157
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IIILE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
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                                                                                                       Score 34; DB 7; Length 593; Pred. No. 2.9e+02;
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Sequence 9040, Application US/11087099

PUBLICALION NO. US20060041961A1

GENERAL INFORMATION:

APPLICANT: Abad, Mark S. et 'al.

TITLE OF INVENTION: Genes and Uses for Plant Improvement

FILE REFERENCE: 38-21 (53450) B EP

CURRENT APPLICATION NUMBER: US/11/087,099

CURRENT FILING DATE: 2005-03-22

NUMBER OF SEQ ID NOS: 12464

SEQ ID NO 9040

LENGTH: 594
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44.7%; Score 34; DB 7; 1
Best Local Similarity 53.3%; Pred. No. 2.9e+02;
Matches 8; Conservative 2; Mismatches 1.
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; ORGANISM: Schizosaccharomyces pombe
US-11-087-099-9040
, ORGANISM: Schizosaccharomyces pombe US-11-087-099-3671
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Taupier Jr., Raymond
Pena, Carol
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Shimkets, Richard
Gusev, Vladimir
                                                                                                          Query Match
Best Local Similarity 53.3%;
Matches 8; Conservative
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53 LRPDNEFAEVHNSED 67
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53 LRPDNEFAEVHNSED 67
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US-10-055-877-157
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APPLICANT:
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Sequence 1592, Application US/10821234

Sequence 1592, Application US/10821234

Publication No. US20050255114A1

GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Andarmani, Susan
APPLICANT: Andarmani, Susan
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APPLICANT: Andarmani, Susan
APPLICANT: APPLICATION NUMBER: US 60/462,047

PRIOR FILING DATE: 2003-04-07
NUMBER: OF SEQ ID NOS: 1704
SEQ ID NO 1592
LENGTH: 782
LENGTH: 782
LENGTH: 782
LENGTH: 782
LENGTH: 782
CURRENT PAPPLICATION NUMBER: US/10/055,877

CURRENT PILING DATE: 2002-01-22

PRIOR APPLICATION NUMBER: 60/262,892

PRIOR PILING DATE: 2001-01-19

PRIOR PILING DATE: 2001-01-23

PRIOR PILING DATE: 2001-01-24

PRIOR PILING DATE: 2001-01-24

PRIOR PLICATION NUMBER: 60/264,117

PRIOR PLICATION NUMBER: 60/264,117

PRIOR PLICATION NUMBER: 60/264,117

PRIOR PLICATION NUMBER: 60/264,139

PRIOR PLICATION NUMBER: 60/264,478

PRIOR PLICATION NUMBER: 60/264,478

PRIOR PLING DATE: 2001-01-26

PRIOR PLING DATE: 2001-01-26

PRIOR PLING DATE: 2001-01-26

PRIOR PLING DATE: 2001-01-26

PRIOR PLING DATE: 2001-01-36

PRIOR PLING DATE: 2001-01-36

PRIOR PLING DATE: 2001-01-36

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-03-02

PRIOR PLING DATE: 2001-03-04

PRIOR PLING DATE: 2001-03-14

PRIOR PLING DATE: 2001-03-14

PRIOR PLING DATE: 2001-03-14

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PRIOR PLING DATE: 2001-03-14

PRIOR PLING DATE: 2001-03-14
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Best Local Similarity 33.3%; Pred. No. 3.8e+02;
Matches 5; Conservative 7; Mismatches 3; Indels
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Pred. No. 3.9e+02;
1; Mismatches 2; Indels
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70.08;
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276 LVMRKNKINHLNENT 290
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Query Match
Best Local Similarity 56.22
Best Local 9; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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) ORGANISM: Human HLA-DRB

US-10-884-730-115
                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
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                                                                      APPLICANT: Venetta, Thomas M.
APPLICANT: Venetta, Thomas M.
APPLICANT: Blaesius, Rainer H.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TITLE OF INVENTION: DETECTION OF OVARIAN DISEASE FILE REFERENCE: 46143/294851
CURRENT APPLICATION NUMBER: US/11/177,506
CURRENT APPLICATION NUMBER: 60/586,856
PRIOR FILING DATE: 2004-07-09-
PRIOR FILING DATE: 2004-07-09-
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 38
LENTH: 782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Liou, Simon
TITLE OF INVENTION: Human BMP2 Inducible Kinases
FILE REFERENCE: 004974, 01015
CURRENT APPLICATION NUMBER: US/10/509,422
CURRENT FILING DATE: 2004-09-24
PRIOR FILING DATE: 2003-03-20
PRIOR PLICATION NUMBER: US 60/367,512
PRIOR PLICATION NUMBER: US 60/367,512
PRIOR PLICATION NUMBER: US 60/406,936
PRIOR PLICATION NUMBER: US 60/406,936
PRIOR PILING DATE: 2002-03-27
PRIOR FILING DATE: 2002-03-27
PRIOR FILING DATE: 2002-03-27
SPRIOR PILING DATE: 2003-03-05
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FREESEQ for Windows Vergion 4.0
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Pred. No. 3.9e+02;
1; Mismatches 2;
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Pred. No.
Sequence 38, Application US/11177506
Publication No. US20060029956A1
GENERAL INFORMATION:
APPLICANT: Beyer, Wayne F.
APPLICANT: Venetta, Thomas M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/11179624
Publication No. US20060040372A1
GENERAL INFORMATION:
APPLICANT: Sakaguchi, Nobuo
APPLICANT: Kuwahara, Kazuhiko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-509-422-5; Sequence 5, Application US/10509422; Publication No. US20050244825A1; GENERAL INFORMATION:
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Best Local Similarity 85.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44.7%;
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Best Local Similarity 70.0
Matches 7; Conservative
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256 ARVHVSEEGT 265
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ORGANISM: Homo sapiens
US-10-509-422-5
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ORGANISM: Homo sapiens
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Sequence 115, Application US/10884730
; Sequence 115, Application US/10884730
; Publication No. 282050250161A1
; GENERAL INFORMATION:
; APPLICANT: Suciu-Foca, Nicole
; APPLICANT: Chang, Chih-Cohao
; APPLICANT: Chang, Chih-Cohao
; TITLE OF INVENTION: Refection
; TITLE OF INVENTION: Rejection
; FILE REFERENCE: 0575/58332-B
; CURRENT APPLICATION NUMBER: US/10/746,311
; PRIOR APPLICATION NUMBER: PCT/US00/16594
; PRIOR APPLICATION NUMBER: PCT/US00/16594
; PRIOR PILING DATE: 2000-06-15
; NUMBER OF SEQ ID NOS: 382
; SOFTWARE: Patentin version 3.1
; FENCENTIAL OF SECTION OF SEC
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Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
ATITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
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FILE REFERENCE: 050208-0018
CURRENT APPLICATION NUMBER: US/11/179,624
CURRENT FILING DATE: 1055-07-13
PRIOR APPLICATION NUMBER: PCT/JP99/04634
PRIOR FILING DATE: 1999-08-27
PRIOR FILING DATE: 1099-08-24
PRIOR FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 9
SEQ ID NOS: 9
SEQ ID NOS: 9
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Pred. No.
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Sequence 327, Application US/11096568A

Sequence 327, Application US/11096568A

Publication No. US20060048240A1

GENERAL INFORMATION:
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
CURRENT APPLICATION NUMBER: US/11/096,568A

CURRENT APPLICATION NUMBER: US/11/096,568A

SEQ ID NO 327
LENGTH: 231

LENGTH: 231
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TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides FILTE REPERENCE: 2750-1929 PUGS.
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 329
LENGTH: 231
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               Query Match
Best Local Similarity 33.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 5; Mismatches 5; Indels
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43.4%; Score 33; DB 7; I
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 1;
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! LOCATION: (1) ... (231)

! OTHER INFEMATION: Ceres Seq. ID no. 16625618

US-11-096-568A-329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: (1)._(231)
; OTHER INFORMATION: Ceres Seq. ID no. 15179511
US-11-096-568A-327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 329, Application US/11096568A Publication No. US20060048240A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Zea maye subsp. mays
FEATURE:
NAME/KEY: misc_feature
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47 IITKPQKVHSTTRAT 61
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Best Local Similarity 85...
Best Local 6; Conservative
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APPLICANT: Alexandrov, Nickolai et al.
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 328
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; Sequence 5689, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION: Genes and Uses for Plant Improvement
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; TILE REPRENCE: 38-21 (53450) B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 5689
                                                                                                                                                                                                                                                                                Query Match
43.4%; Score 33; DB 7; Length 173;
Best Local Similarity 53.8%; Pred. No. 1.18+02;
Matches 7; Conservative 2; Mismatches 4; Indels
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85.7%; Pred. No. 1.2e+02;
tive 0; Mismatches 1; Indels
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: LOCATION: (1)..(184)

: OTHER INFORMATION: unsure at all Xaa locations

US-11-099-5689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
| LOCATION: (1).:(180)
| OTHER INFORMATION: Ceres Seq. ID no. 15179512
US-11-096-5688-328
                                                                                                                                                                    ; NAME/KEY: misc_feature
; LOCATION: (1)...(173)
; OTHER INFORMATION: Ceres Seq. ID no. 13610690
US-11-096-568A-27299
CURRENT APPLICATION NUMBER: US/11/096,568A CURRENT FILING DATE: 2005-04-01 NUMBER OF SEQ ID NOS: 34471 SEQ ID NO 27299 LENGTH: 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-11-096-568A-328

Sequence 328, Application US/11096568A

Publication No. US20060048240A1

GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Zea mays subsp. mays
                                                                                                                  TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                     10 LRPSLVHDFLQQT 22
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Best Local Similarity 85.7
                                                                                                                                                                                                                                                                                                                                                                            3 LRPSRVHNSEENT 15
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FEATURE:
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Sequence 19351, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
SEQ ID NO 19351
LENGTH: 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
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                                                                                                                                                                                                          Score 33; DB 7; Length 287;
Pred. No. 2e+02;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 7; Length 295;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  no. 12372809
FILE REFERENCE: 38-21(53450)B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 287
LENGTH: 287
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 19350, Application US/11096568A Publication No. US20060048240A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: (1). (295)
OTHER INFORMATION: Ceres Seq. ID
                                                                                                                                                  , ORGANISM: Arabidopsis thaliana US-11-087-099-287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Zea mays subsp. mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Zea mays subsp. mays
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Best Local Similarity 46.2%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                           255 VEMRKRRVHREEE 267
                                                                                                                                                                                                                                                                                                    1 IVLRPSRVHNSEE 13
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Best Local Similarity
Matches 6; Conserv
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LENGTH: 295
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APPLICANT: Chang, Chih.-Chao
APPLICANT: Chang, Chih.-Chao
APPLICANT: Cortesini, Raffaello
TITLE OF INVENTION: Generation of Antigen-Specific T Suppressor Cells For Treatment of TITLE OF INVENTION: Rejection
FILE REFERENCE: 0575/58332-B
CURRENT APPLICATION NUMBER: US/09/746,311
PRIOR APPLICATION NUMBER: US/09/746,311
PRIOR PILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: PCT/US00/16594
PRIOR FILING DATE: 2000-6-15
NUMBER OF SEQ ID NOS: 382
SOFTWARE: Parentin version 3.1
SEQ ID NO114
LENGTH: 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                              APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STARHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 1999-11-09
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1894
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence: synthetic; ; OTHER INFORMATION: amino acid sequence US-10-793-626-1894
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TITLE OF INVENTION: Genes and Uses for Plant Improvement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 33; DB 6; 1
Pred. No. 1.6e+02;
4; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 33; DB 6;
Pred. No. 1.8e+02;
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                          Sequence 1894, Application US/10793626
Publication No. US200S0255478A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 114, Application US/10884730 Publication No. US/20050250161A1 GENERAL INFORMATION:
APPLICANT: Suciu. Foca, Nicole APPLICANT: Liu, Zhuoro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 287, Application US/11087099
Publication No. US20060041961A1
GENERAL INFORMATION:
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85.7%;
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213 ILFEPKKIDNTEE 225
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Best Local Similarity 85.7
Matches 6; Conservative
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Matches 5; Conservative
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ORGANISM: Human HLA-DRB
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                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
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RESULT 51
US-11-096-568A-12602
Sequence 12602
048240A1
SERENTION: OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides FITTLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
STILE REPERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT PILING DATE: 2005-04-01
SEQ ID NOS: 34471
SEQ ID NO 12602
LENGTH: 339
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Pred. No. 2.7e+02;
6; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: MASIGNANI VEGA
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 33; DB 7; 1
Pred. No. 2.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
| LOCATION: (1): 1339)
| OTHER INDEMATION: Ceres Seq. ID no. 14302455
| US-11-096-568A-12602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
FRIOR APPLICATION NUMBER: GB-0103424.8
FRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 5522
LENGTH: 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5522, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SpA
APPLICANT: FONTANA Maxia Rita
APPLICANT: PIZZA Maxiagrazia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-11-069-642-92; Sequence 92, Application US/11069642; Publication No. US20050260626A1; GENERAL INFORMATION: APPLICANT: LORENS, JAMES B.; APPLICANT: PRAY, TODD R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 62.5%;
Matches 5; Conservative
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35.7%;
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Best Local Similarity 35.7<sup>1</sup>
Matches 5; Conservative
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alexandrow, Nickolai et al.
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 19149
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Pred. No. 2.2e+02;
4; Mismatches 4; Indels
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85.7%; Pred. No. 2.2e+02;
iive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                             APPLICANT: FORSTER, RICHARD L.
APPLICANT: FORSTER, RICHARD L.
APPLICANT: CONNETT, WARIE B.
APPLICANT: GRICOR, MURRAY ROBERT
APPLICANT: HIGGINS, COLLEEN M.
APPLICANT: HIGGINS, COLLEEN M.
APPLICANT: MACHISIN, ANDREAS
APPLICANT: MACHISIN, ANDREAS
TITLE OF INVENTION: CELL CYCLE GENES AND RELATED METHODS
TITLE OF INVENTION: CELL CYCLE GENES AND RELATED METHODS
CURRENT APPLICATION NUMBER: US/11/024,959
CURRENT APPLICATION NUMBER: 2004-12-30
PRIOR FILING DATE: 2003-12-30
85.7%; Pred. No. 2e+02;
tive 0; Mismatches 1; Indels
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; OTHER INFORMATION: Ceres Seq. ID no. 12372808
US-11-096-568A-19349
                                                                                                                                                                                                                  ; Sequence 267, Application US/11024959
; Publication No. US20060010516A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 782
SOFTWARE: Patentin version 3.3
SEQ ID NO 267
LENGTH: 313
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Best Local Similarity 38.5%;
Matches 5; Conservative
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41 VALKKTRLHEDEE 53
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Best Local Similarity 85.7
Matches 6; Conservative
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Eucalyptus sp.
US-11-024-959-267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: misc_feature
                                                                                                          112 RPSREHN 118
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US-11-024-959-267
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8 VHNSEEN 14
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US-11-069-642-47

Sequence 47, Application US/11069642

Publication No. US2005260626A1

GENERAL INFORMATION:
APPLICANT: LORENS. JAMES B.
APPLICANT: RINSELLA, TODD R.
APPLICANT: BENET, MARK B.
TITLE OF INVENTION: INHIBITING PROTEIN-PROTEIN INTERACTION
TITLE OF INVENTION: INHIBITING PROTEIN-PROTEIN INTERACTION
TITLE OF INVENTION: INHIBITING PROTEIN-PROTEIN INTERACTION
TITLE OF INVENTION: LORENS B.
CURRENT APPLICATION NUMBER: US/11/069,642

CURRENT FILING DATE: 2005-02-28

PRIOR FILING DATE: 2003-02-28

PRIOR FILING DATE: 2003-04-23

PRIOR FILING DATE: 2003-04-23

PRIOR FILING DATE: 2003-04-23

PRIOR FILING DATE: 2000-03-06

PRIOR FILING DATE: 2000-03-06

PRIOR FILING DATE: 2000-03-06

PRIOR FILING DATE: 2000-03-06

NUMBER OF SEQ ID NOS: 168

SOUTH NO ATSION NUMBER: 06/187,130
APPLICANT: KINSELLA, TODD M.
APPLICANT: BENNETT, MARK K.
TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES FOR TITLE OF INVENTION: INHIBITING PROTEIN-PROTEIN INTERACTION FILE REFERENCE: RIGL-022CIP3
CURRENT ENFLICATION NUMBER: US/11/069,642
CURRENT APPLICATION NUMBER: US/22,758
PRIOR FILING DATE: 2005-02-28
PRIOR FILING DATE: 2002-08-30
PRIOR FILING DATE: 2003-04-23
PRIOR PAPLICATION NUMBER: 10/422,536
PRIOR PLING DATE: 2001-03-06
PRIOR PLING DATE: 2001-03-06
PRIOR FILING DATE: 2001-03-06
PRIOR FILING DATE: 2001-03-06
PRIOR FILING DATE: 2000-03-06
NUMBER OF SEQ ID NOS: 168
SOFTWARE: Patentin version 3.2
LENGTH: 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: DnaB intein cyclization scaffold with GFP US-11-069-642-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43.4%; Score 33; DB 7; Length 437; 85.7%; Pred. No. 3.1e+02; tive 1; Mismatches 0; Indels
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Pred. No. 3.1e+02;
1; Mismatches 0; Indels
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; ORGANISM: Synechocystis PCC6803
US-11-069-642-47
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Best Local Similarity 85.7%;
Matches 6; Conservative 1
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ORGANISM: Artificial sequence
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Best Local Similarity 85.7
Matches 6; Conservative
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50 VHNSEED 56

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| Sequence 49, Application US/11056642
| Sequence 49, Application US/11056642
| Publication No. USGNOSO6066A1
| GREEAL INFORMATION
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// ORGANISM: Synechocystis PCC6803
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Matches 6; Conservative
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                                                                                                                                                                                                                        Sequence 53, Application US/11069642
; Sequence 53, Application US/11069642
; Publication No. US20050260626A1
; GENERAL INFORMATION:
APPLICANT: LORENS, JAMES B.
APPLICANT: PRAY, TODD R.
APPLICANT: RINSELLA, TODD M.
APPLICANT: RINSELLA, TODD M.
TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES FOR TITLE OF INVENTION: INVIHIBITING PROTEIN PROTEIN INTERACTION FILE REFERENCE: RIGL-022CIP3
CURRENT APPLICATION NUMBER: US/11/069,642
; CURRENT FLING DATE: 2005-02-28
; PRIOR FILING DATE: 2005-04-23
; PRIOR FILING DATE: 2003-04-23
; PRIOR FILING DATE: 2003-04-23
; PRIOR FILING DATE: 2003-04-23
; PRIOR FILING DATE: 2003-04-36
; PRIOR FILING DATE: 2003-04-36
; PRIOR FILING DATE: 2003-03-06
; RIOR FILING DATE: 2001-03-06
; RIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PARENTIN VEXBION 3.2
; SEQ ID NO 53
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US-11-069-642-55
US-11-069-642-55
Sequence 55, Application US/11069642
Publication No. US20050260626A1
GENERAL INFORMATION:
APPLICANT: LORENS, JAMES B.
APPLICANT: RINSELLA, TODD R.
APPLICANT: RINSELLA, TODD M.
APPLICANT: BENNETT, MARK K.
TITLE OF INVENTION: INHIBITING PROTEIN INTERACTION
FILE REFERENCE: RIGL-022CIP3
FILE REFERENCE: RIGL-022CIP3
CURRENT APPLICATION NUMBER: US/11/069,642
CURRENT APPLICATION NUMBER: 10/232,758
PRIOR FILING DATE: 2005-02-28
PRIOR PELING DATE: 2003-04-23
PRIOR PELING DATE: 2003-04-23
PRIOR APPLICATION NUMBER: 09/800,770
PRIOR FILING DATE: 2001-03-06
PRIOR FILING DATE: 2001-03-06
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Pred. No. 3.1e+02;
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; ORGANISM: Synechocystis PCC6803
US-11-069-642-53
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; ORGANISM: Synechocystis PCC6803
US-11-069-642-55
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Matches 6; Conservative
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US-11-069-642-57

Sequence 57, Application US/11069642

Publication No. US2005060626A1

GENERAL INFORMATION:
APPLICANT: LORENS, JAMES B.
APPLICANT: RINSELLA, TODD M.
APPLICANT: RINSELLA, TODD M.
APPLICANT: RINSELLA, TODD M.
APPLICANT: RINSELLA, TODD M.
APPLICANT: RINSELLA, TODD M.
APPLICANT: RINSELLA, TODD M.
APPLICANT: RINSELLA, TODD M.
APPLICANT: ARK KI.
TITLE OF INVENTION: INHIBITING PROTEIN INTERACTION
TITLE OF INVENTION: INHIBITING PROTEIN INTERACTION
FILE REFERENCE: RICL-022C18
CURRENT FILING DATE: 2005-02-28
FRIOR APPLICATION NUMBER: 10/422,536
FRIOR PILING DATE: 2003-04-23
FRIOR FILING DATE: 2003-04-23
FRIOR FILING DATE: 2003-04-23
FRIOR FILING DATE: 2003-04-23
FRIOR FILING DATE: 2003-06
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| Sequence 59, Application US/11069642
| Publication No. US20050260626A1
| GENERAL INFORMATION:
| APPLICANT: PRAY, TODD R.
| APPLICANT: KINSELLA, TODD M.
| APPLICANT: KINSELLA, TODD M.
| APPLICANT: BENNETT, MARK K.
| TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES FOR TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES FOR TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES FOR TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES FOR FILE OF INVENTION NUMBER: US/11/069,642
| CURRENT FILING DATE: 2005-02-28
| PRIOR FILING DATE: 2002-04-23
| PRIOR FILING DATE: 2003-04-23
| PRIOR FILING DATE: 2001-03-06
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Pred. No. 3.1e+02;
1; Mismatches 0; Indels
43.4%; Score 33; DB 7; Length 438; 85.7%; Pred. No. 3.1e+02; tive 1; Mismatches 0; Indels
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43.4%; Score 33; DB 7; Length 438;
Best Local Similarity 85.7%; Pred. No. 3.18+02;
Matches 6; Conservative 1; Mismatches 0; Indels
; SEQ ID NO 59
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Synechocystis PCC6803
US-11-069-642-59
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Immune libration, LIDIATE acceptation, processes, and infilar administration, the paper acceptance, antiinflammatory; cns-gen.; immune disorder; neurological disease; autoimmune disease; immune papersesive, graft versus host disease; transplant rejection; endoctoxic shock; osteoarthritis; antiathritic; osteopathic; musculoskeletal disease; allergy; antiallergic; asthma; antiatenthmatic; inflammation; respiratory disease; atheroscalerosis; antiateriosclerotic; antithyroid; endocrine disease; metabolic disorder; hashimotos disease; antiinflammatory; gastrointestinal-gen; gastrointestinal-gen; gastrointestinal disease; rheumatoid arthritis; antirheumatory; hepatotropic; autoprotective; autoimmune hepatitis; antiinflammatory; hepatotropic;
                                                                                                                                                                                                                                                                                                            a procein having a molecular weight of 180 kD in a dimeric form as determined by SDS-PAGE, where each subunit of the dimeric form has a molecular weight of 97 kD as determined by SDS-PAGE, and where the enzyme cleaves precursor alpha2-antiplasmin at the Pro12-Asn13 bond. The enzyme inhibitors of the enzyme and methods for detecting such inhibitors are useful for treating conditions involving fibrin, e.g. inflammatory conditions such as all forms of arthritis, organ fibrosis, undesirable scarring, cancer or its metastases; or atherothrombotic disease such as accordary thrombosis, stroke, pulmonary embolism, all other forms of arterial and venous thromboses. This peptide is an internal sequence of the alpha2-antiplasmin cleaving enzyme corresponding to amino acids
                                                                                                                                                                                                                                                                                             invention relates to an alpha2-antiplasmin cleaving enzyme comprising
                                                                                                                                             alpha-2-antiplasmin cleaving enzyme, useful for treating conditions slving fibrin, e.g. inflammatory conditions such all forms of
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                                                                                                                                                                     involving fibrin, e.g. inflammatory conditions such all forn
arthritis, organ fibrosis, undesirable scarring, cancer, or
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                                                               Christiansen VJ;
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                                                                                                                                                                                                                                                     Claim 2; SEQ ID NO 6; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AEB94227 standard; protein; 723 AA.
                                                               Lee KN, Jackson KW,
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(JACK/) JACKSON K W.
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Matches 13; Conservative
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Gaps

The invention relates to a method of down-regulating an immune response, which comprises administering to a subject a fibroblast activation protein (FAR) alpha dimer enzyme in an amount effective to down-regulate an immune response. Also included are the following: a composition

Down-regulating an immune response comprises administering to a subject in need a fibroblast activation protein (FAP) alpha dimer enzyme in an amount effective to down-regulate an immune response.

Claim 134; SEQ ID NO 70; 177pp; English.

Jesson MI

Miller GT,

Jones B,

Mclean PA,

WPI; 2005-564220/57.

(POIN-) POINT THERAPEUTICS INC 09-JAN-2004; 2004US-0535577P. 10-JAN-2005; 2005WO-US000709.

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comprising a FAP alpha dimer enzyme in a pharmaceutically acceptable carrier, where the composition is serile and lacks an adjuvant; a composition of serile and lacks an adjuvant; a composition as the land a control and a control and a control and a control and a control and a control and a control and a control and a composition comprising an amino acid aubstitution of A657D; and a comprising an PAP alpha dimer enzyme lacking amino acids 269-448 and comprising an PAP alpha dimer enzyme lacking amino acids 269-448 and comprising an anti-inflammatory agent, immunosuppressant, or the second agent is an anti-inflammatory agent, immunosuppressant, or anti-infective agent such as antibacterial, antiviral, antifungal, anti-control anti-inflammatory agent. Immunosuppressant, or anti-infective agent such as antibacterial, antiviral, antifungal, anti-control anti-inflammatory agent. The FAP alpha dimer enzyme is a truncation trype FAP alpha dimer enzyme. The FAP alpha dimer enzyme is a fusion or chimmeric procein. The FAP alpha dimer enzyme is a fusion or chimmeric procein. The FAP alpha dimer enzyme is a fusion or chimmeric procein. The FAP alpha dimer enzyme is a heterodimer of a PAP alpha monomer and a DPPIV/CDS monomer. The FAP alpha dimer enzyme comprises an amino acid substitution is present in the beta-propeller domain, the catalytic condition, abnormal immune response is an especially an IL-I mediated condition, abnormal immune response is an elected from inflammation.

Condition, toxic shock syndrome, allergy, asthma, atherosclerosis, condition, and subsequent to an infection, such as an RSV infection. The response is subsequent to an infection, such as an RSV infection. The response is subsequent to an infection, such as an RSV infection. The response is subsequent to an infection, such as an RSV infection. The uncommune disease is selected from continumune disease. Statistance of autoimmune disease is selected from continumune disease. In a subsequent to an infection, such as an RSV infection of the papers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      myasthenia gravis, glomerulonephritis, autoimmue hepatitis and multiple sclerosis. The subject does not have cancer or a predisposition to cancer. The present sequence represents the amino acid sequence of human soluble fibroblast activation protein (FAP) alpha dimer (corresponding to AEB94159 minus N-terminal amino acids 1-37).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 62; DB 9; Length 723; 100.0%; Pred. No. 0.47; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Crohn's disease, Guillain-Barre's syndrome, psoriasis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             450 ILEENKELENALK 462
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Best Local Similarity luv...
Best Local 3; Conservative
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systemic lupus erythematosus; dermatological; dermatological disease; uveitis; ophthalmological; autoimmune hemolytic anemia; antianemic; hematological disease; rheumatic fever; antipyretic; Crohns disease; psoriasis; antipyretic; graves disease; antityroid;

infection; respiratory-gen.; virucide;

respiratory syncytial virus infection CD26 dipeptidyl peptidase IV; DPPIV

MO2005071073-A1.

04-AUG-2005

Homo sapiens

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The invention relates to a method of down-regulating an immune response, which comprises administering to a subject a fibroblast activation protein (FAP) alpha dimer enzyme in an amount effective to down-regulate an immune response. Also included are the following: a composition comprising a FAP alpha dimer enzyme in a pharmaceutically acceptable carrier, where the composition is sterile and lacks an adjuvant; a composition comprising a FAP alpha dimer enzyme in a pharmaceutically acceptable carrier, and a non-adjuvant second agent; a composition comprising a mon-adjuvant second agent; a nation acide 269-48 from mouse FAP.

CC Anti-infective agent such as antibacterial, antitiumgl, antitipated antitipate and anti-inferent agent; immunosuppressant, or anti-infective agent such as antibacterial, antitiungal, antitipated appression or chimeric protein. The FAP alpha dimer enzyme is a fusion or chimeric protein. The FAP alpha dimer enzyme is a fusion or chimeric protein. The FAP alpha dimer enzyme is a fusion or chimeric protein. The FAP alpha dimer enzyme is a fusion or chimeric protein. The FAP alpha dimer enzyme is a fusion or chimeric protein. The FAP alpha dimer enzyme is a fusion or chimeric contribution relative to wild type FAP alpha dimer. The FAP alpha dimer enzyme is a fusion or chimeric contribution relative to wild type FAP alpha dimer. The FAP alpha dimer enzyme is a fusion or chimeric contribution relative to wild type FAP alpha dimer. The minnon relative to wild type FAP alpha dimer. The minnon condition, or an N-linked glycosylation site and alters disated condition, abnormal immune response is an especially an ILT mediated accordance of subsequent to an infection, such as an RSV infection. The response is selected from cautoimmune d The alpha dimer; guillain barre solvation; processed to the annual content of the annual Down-regulating an immune response comprises administering to a subject in need a fibroblast activation protein (FAP) alpha dimer enzyme in an amount effective to down-regulate an immune response. immune inhibition; fibroblast activation protein alpha dimer; Human soluble (FAP) alpha dimer SEQ ID NO:61. Jesson MI; Claim 134; SEQ ID NO 61; 177pp; English. Miller GT, POIN-) POINT THERAPEUTICS INC 09-JAN-2004; 2004US-0535577P. 10-JAN-2005; 2005WO-US000709. Jones B, WPI; 2005-564220/57. WO2005071073-A1 Homo sapiens. 04-AUG-2005 Mclean PA, 

immune inhibition, fibroblast activation protein alpha dimer;

Wh Pap alpha dimer; guillain barre syndrome; antiinflammatory; cns-gen.;

Wh Pap alpha dimer; guillain barre syndrome; antiinflammatory; cns-gen.;

Mimunosuppressive; graft versus host disease; transplant rejection;

Wh motoxic shock; osteoarthritis; antiarthritic; osteopathic;

Minflammation; respiratory disease; atherosclerossis; antiarteriosclerotic;

Wh antiinflammation; respiratoric disease; inflammatory bowel disease;

Wheumatoid arthritis; antiinflammatory; pastrointestinal disease;

Wheumatoid arthritis; antiinflammatory; hepatociopic;

Wheumatoid arthritis; antiinflammatory; hepatociopic;

Wheumatoid arthritis; antiinflammatory; hepatociopic;

Wheumatoid arthritis; antiinflammatory; hepatociopic;

Wheumatoid arthritis; antiinflammatory; hepatociopic;

Whematological disease; rheumatic fever; antipyretic; cnemia; antianemic;

Whematological disease; rheumatic fever; antipyretic; Crohns disease;

Whematological disease; rheumatic fever; antipyretic; Crohns disease;

Whematological disease; rheumatic fever; antipyretic; Crohns disease;

Whematological disease; rheumatic fever; antipyretic; rohns disease;

Whematological disease; rheumatic fever; antipyretic; Crohns disease;

Whematological disease; rheumatic fever; antipyretic; repairatory syncytial virus infection; respiratory-gen.; virucide; myasthenia gravis, glomerulonephritis, autoimmune hepatitis and multiple sclerosis. The subject does not have cancer or a predisposition to cancer. The present sequence represents the amino acid sequence of human soluble fibroblast activation protein (FAP) alpha dimer (corresponding to AEB94159 minus N-terminal amino acids 1-26). Down-regulating an immune response comprises administering to a subject in need a fibroblast activation protein (FAP) alpha dimer enzyme in an amount effective to down-regulate an immune response. Gарв ö Human soluble fibroblast activation protein (FAP) alpha dimer. 100.0%; Score 62; DB 9; Length 734; 100.0%; Pred. No. 0.47; 0; Indels Jesson MI; 0; Mismatches /note= "Encoded by taa" Claim 73; SEQ ID NO 4; 177pp; English Location/Qualifiers AEB94161 standard; protein; 750 AA. Miller GT, (POIN-) POINT THERAPEUTICS INC. 09-JAN-2004; 2004US-0535577P. 10-JAN-2005; 2005WO-US000709 461 ILEENKELENALK 473 (first entry) 1 ILEENKELENALK 13 Best Local Similarity 100. Matches 13; Conservative Jones B, WPI; 2005-564220/57. N-PSDB; AEB94160. Misc-difference Sequence 734 AA; WO2005071073-A1. Homo sapiens. 06-OCT-2005 04-AUG-2005. Mclean PA, AEB94161; Query Match RESULT 4 AEB94161 88888888 ઠે 셤

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an immune response. Also included are the following a composition comprishing a FAP alpha dimer enzyme in a pharmaceutically acceptable carrier, where the composition is sterile and lacks an adjuvant; a composition comprishing a FAP alpha dimer enzyme is a pharmaceutically acceptable carrier, and a non-adjuvant second agent; a composition comprishing an amino acid substitution comprishing an amino acid substitution comprishing an amino acid substitution comprishing and a composition comprished and comprished configured comprished and comprished comprished comprished and comprished comprished comprished comprished comprished comprished comprish
                                   ich comprises administering to a subject a fibroblast activation otein (FAP) alpha dimer enzyme in an amount effective to down-regulate immune response. Also included are the following: a composition
invention relates to a method of down-regulating an immune response,
                                         which
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100.0%; Score 62; DB 9; Length 750; 100.0%; Pred. No. 0.48; 0; Indels Mismatches ; 0 1 ILEENKELENALK 13 Local Similarity 100. 1es 13; Conservative Query Match Best Loca Matches 셤 ò

Sequence 750 AA;

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Gaps

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AAW31963 standard; protein; 759 AA. RESULT 5 AAW31963

Fibroblast activation protein-alpha; FAP-alpha; human; type II integral membrane proteins; epithelial cancer. Human fibroblast activation protein-alpha (FAP-alpha) 21-JAN-1998 (first entry) Homo sapiens. AAW31963; THE HELL LETTERS ON THE STATE OF THE STATE O

1. .759 /label= FAP-alpha /note= "Fibroblast activation protein alpha" Location/Qualifiers Modified-site Protein

49.51 700te= "Agn is N-glycosylated" 191. 209 7/label= fap-1 7/note= "Putative functional element; not defined further in specification"

Region

114. .216
/note= "Ann is N-glycosylated"
220. .240
/label= fap-2
/note= "Putative functional element; not defined further in specification" 510. .521 /labol= fap-3 /note= "putative functional element; not defined further in specification" Dimeric fibroblast activation protein alpha - capable of degrading extracellular matrix protein, useful to treat epithelial cancers. 525. .668 /note= "alternative sequence found in AAW27438" 637. .639 /note= "Asn is N-glycosylated" 678. .680 /note= "Asn is N-glycosylated" Rettig W, Old LJ; (LUDW-) LUDWIG INST CANCER RES. (BOEH ) BOEHRINGER INGELHEIM INT GMBH. Example 5; Fig 1; 40pp; English. 97WO-US004215. 96US-00619280. Zimmerman R, Park JE, WPI; 1997-480164/44. N-PSDB; AAT89286. Modified-site Modified-site Modified-site 12-MAR-1997; WO9734927-A1 25-SEP-1997. Region Region Region 

This sequence represents the dimeric fibroblast activation protein alpha (FAP-alpha). The FAP-alpha molecule is capable of degrading extracellular matrix proteins and exhibits structural features typical of type II integral membrane proteins, including a large COOH-terminal extracellular domain, a hydrophobic transmembrane segment and a short cytoplasmic tail.

CG domain, a hydrophobic transmembrane segment and a short cytoplasmic tail. The putative extracellular domain is described as containing five contential N-glycosylation sites, eleven conserved catalytic domains three segments corresponding to highly conserved catalytic domains cancers including breast, lung, skin, pancreas and colorectal carcinomas contain abundant FAP-alpha reactive stronal fibroblasts which accompany tumour blood vessels. The induction of FAP-alpha fibroblasts at times and carcinogenesis is consistent with its putative role in normal fibroblast carcinogenesis la consistent with its putative role in normal fibroblast (S)-valy1-pyrrolidine-Z(R)-boronic acid, may be used to treat various epithelial cancers, e.g. breast, lung, skin, pancreas or colon cancer. Note: This sequence differs from the amino acid sequence of FAP-alpha counting the amino acid sequence of FAP-alpha contains and colon cancer.

100.0%; Score 62; DB 2; Length 759; 100.0%; Pred. No. 0.49; ive 0; Mismatches 0; Indels 1 ILEENKELENALK 13 13; Conservative Best Local Similarity Query Match Matches

Sequence 759 AA;

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Gaps

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AAW27438 standard; protein; 760 AA.

487 ILEENKELENALK 499

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AAW27438 ID AAW2 XX RESULT 6

AAW27438

Protein

Region

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The present invention describes a method for assessing whether a patient is afflicted with breast cancer. The method comprises comparing the level of expression of a marker (gene/polypeptide see ACCS0076 to ACCS034 and ABR47386 to ABR47632) in a patient sample and the normal level of expression of the marker in a control non-breast cancer sample, where a significant increase in the level of expression of the marker in the patient asmple and the normal level is an indication that the patient is afflicted with breast cancer. The breast cancer associated sequences from the present invention have cytostatic activities and can be used in gene therapy. The method is useful for diagnosing and treating breast cancer. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Breast cancer diagnosis or treatment by comparing the level of expression of a marker in a patient sample with that in the control non-breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     growth; differentiation; blood endothelial cell; BEC;
lymphatic endothelial cell; LEC; hereditary lymphoedema; VEGFR-3;
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Wang Y, Xu Y, Zhao X, Meyer
L, Meric F, Sahin A, Mills
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100.0%; Pred. No. 0.49;
tive 0; Mismatches 0; Indels
                                          Breast cancer associated protein sequence SEQ ID NO:136.
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                                                                                        cancer; cytostatic; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 136; 128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gannavarapu M, Glatt K, 1, Monahan JE, Myer V, Wang Hortobagyi GN, Pusztai L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADN95552 standard; protein; 760 AA.
                                                                                                                                                                                                                                                                                                                   21-JUN-2001, 2001US-0299887P.
27-JUN-2001, 2001US-0301572P.
18-JUL-2001, 2001US-0306501P.
25-SPC-2001, 2001US-0352602P.
05-MAR-2002, 2002US-0362585P.
14-MAY-2002; 2002US-0380391P.
                                                                                                                                                                                                                                                                           21-JUN-2002; 2002WO-US019669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MILL-) MILLENIUM PHARM INC.
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12-JUN-2003 (first entry)
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Les 13; Conservative
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                                                                                                                                                                                  WO2003004989-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer sample.
                                                                                        Human; breast
                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                16-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lillie J, Mertens M,
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ADN95552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents a dimeric fibroblast activation protein alpha (FAP-alpha) which is capable of degrading extracellular matrix proteins. The APP-alpha molecule exhibits structural features typical of type II integral membrane proteins, including a large COMH-terminal extracellular domain, a hydrophobic transmembrane segment and a short cytoplasmic tail. Most common types of epithelial cancers including breast, lung, skin, ancreas and colorectal carcinomas contain abundant FAP-alpha reactive stromal fibroblasts which accompany tumour blood vessels. The induction of FAP-alpha fibroblasts at times and sites of tissue remodalling during fetal development, tissue repair and carcinogenesis is consistent with its putative role in normal fibroblast physiology. FAP alpha inhibitors, particularly a collagen derivative or (S)-valy-pyrrolidine-2(R)-boronic carcin, may be used to treat various epithelial cancers, e.g. breast, lung, skin, pancreas or colon cancer. Note: This sequence differs from the carcinome acid sequence of FAP-alpha found in AAW31963 between residues 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dimeric fibroblast activation protein alpha - capable of degrading extracellular matrix protein, useful to treat epithelial cancers.
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                                                                                                                                                                                                                                                                                                                                                                          /note= "alternative sequence found in AAW31963"
                                                                                                                                                                                                                                                        1. .760 | Jabels FAP-alpha | /labels FAP-alpha | /notes | Fibroblast activation protein alpha | 625. .670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 62; DB 2; Length 760;
Pred. No. 0.49;
Mismatches 0; Indels
                                                                                             Human fibroblast activation protein-alpha (FAP-alpha).
                                                                                                                                       Fibroblast activation protein-alpha, FAP-alpha, human, type II integral membrane proteins, epithelial cancer.
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(BOEH ) BOEHRINGER INGELHEIM INT GMBH.
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Best Local Similarity 100.0%;
Matches 13; Conservative 0
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                                               (first entry)
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                                                  21-JAN-1998
                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                composition comprising an agent that differentially modulates blood or composition comprising an agent that differentially modulates blood or lymphatic endothelial cells. Treating hereditary lymphoedema comprises identifying a human subject with lymphoedema and with a mutation in at least one allele of a gene encoding a LEC protein, where the mutation in at correlates with lymphoedema in human subjects, and with the proviso that composition comprising a lymphatic growth agent selected from VEGF-C or VEGF-D polypeptides and polynucleotides. The invention may be useful for the development of compounds with an antiangiogenic, cytostatic, vasotropic or antiinflammatory activity or for gene therapy. The method is useful in modulating the growth or differentiation of blood endothelial cells or lymphatic endothelial cells, in treating hereditary lymphatic producer or in monitoring the efficacy or toxicity of a drug on endothelial cells. In modulating modulation of blood endothelial cells or lymphatic vessel endothelial cell disorder or toxicity of a drug on endothelial cells. The agent is useful in manufacturing a medicament for the disorder or in monitoring the efficacy or toxicity of a drug on endothelial cell growth or differentiation. The lymphatic yessel endothelial cell growth or differentiation. The cell or lymphatic vessel endothelial cell growth or differentiation. The lymphatic growth agent may also be used in manufacturing a medicament for the treatment of hereditary lymphoedema resulting from a mutation. The lymphatic gene or of other diseases and cancer metastasis via the lymphatic expressed protein which is related to the method of the invention. Note: This sequence does not appear in the specification but was obtained by the indexer using the source data given in table 14 of the specification.
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                                                                                                                                                                                                                                                                                                                                                         This invention relates to a method of differentially modulating the growth or differentiation of blood endothelial cells (BEC) or lymphatic endothelial cells (LEC) comprises contacting endothelial cells with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
 lymphatic growth agent; VEGF-C; VEGF-D; antiangiogenic; cytostatic;
                 vasotropic; antiinflammatory; gene therapy; endothelial cell diso
inflammatory disease; cancer metastasis; lymphatic system; human.
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                                                                                                                                                                                                                                                      Petrova T, Saharinen P, Saharinen J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 62; DB 7; Length 760; 100.0%; Pred. No. 0.49;
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                                                                                                                                                                                                            (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                               07-MAR-2002; 2002US-0363019P.
                                                                                                                                                   07-MAR-2003; 2003WO-US006900.
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Best Local Similarity luv...
Best Local 3; Conservative
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                                                                                                                                                                                                                                                       Alitalo K, Makinen T,
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                                                                                        WO2003080640-A1.
                                                            Homo sapiens
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                                                                                                                     02-OCT-2003
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soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Barly detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
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/label= Signal_peptide
10. .15
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                                                                                                                                                                                                                                                                                                                                                                                                 (PROT-) PROTEIN DESIGN LABS INC.
                                                                                                                                                                                                                                                                                                                                 26-NOV-2002; 2002US-0429739P.
                                                                                                                                                                                                                                                                 26-NOV-2003; 2003WO-US038193.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ginsburg WM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-441208/41.
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                                                                                                                                      WO2004048938-A2
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                                                                         Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sarcoma
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New Tumor-associated Antigenic Target polypeptides useful for diagnosing, preventing or treating cell proliferative disorders such as cancer or
                                                                                                                                                                                   138. .443
Inote= "Cytochrome c family heme-binding site signature"
170. .475
                                                                                                                                                                                                                                                                                               "Prolyl endopeptidase family serine active site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ashkenazi A, Cairns B, Dowd P, Frantz G, French D, Gonzalez L;
Polakis P, Smith V, Wolf B, Wu TD, Zhang Z;
                                                                                                                                          note= "Prolyl oligopeptidase family homology"
                                                                                                                                                                                                                                                                                                                                 note= "Glycosaminoglycan attachment site"
       "Dipeptidyl peptidase IV"
                                                                                                                                                                                                                                                                                                                                                                           738. 743
/note= "N-myristoylation site"
                                                                                              note= "N-myristoylation site"
                                                                                                               note= "N-myristoylation site"
14. .317
                                                                                                                                                                                                                         "N-myristoylation site"
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                                         "N-myristoylation site"
                                                                   9. 102
note= "N-glycosylation site"
59. 164
                        "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                    "N-glycosylation site"
                                                           "N-glycosylation site"
                                                                                                                                note= "N-glycosylation site"
                                                                                                                                                                             19. .422
note= "Amidation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-JUL-2003; 2003US-0484959P.
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                                                                                                                                                                                                          . . . 475
/note= "W
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/note= "P-
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/note= "N
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            .52
/note= ""
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                                                  . 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tumor.
Region
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The present sequence is that of novel tumor-associated antigenic target polypeptide TAT430. TAT polypeptides have been identified ADW14770-ADW14776 whose expression is upregulated in particular tumor tissues. Tissue expression profiling using GeneExpress indicated that TAT430 is upregulated in breast, pancreatic, colon, adrenal, bladder, kidney, liver, lung, lymphoid, ovarian, prostate and stomach tumor stroma as

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W. FAP alpha dimer; guillain barre syndrome; antiinflammatory; cne-gen.;

W. FAP alpha dimer; guillain barre syndrome; antiinflammatory; cne-gen.;

W. immune disorder; neurological disease; autoimmune disease;

W. immuneuppressive; graft versus host disease; transplant rejection;

W. maculookeletal disease; antiarthritic; osteopathic;

W. milammation; respiratory disease; atherosclerossis, antiarteriosclerotic;

W. inflammation; respiratory disease; atherosclerossis, antiarteriosclerotic;

W. antiinflammatory; gastrointestinal gen.; gastrointestinal disease;

W. mutinflammatory; gastrointestinal gen.; gastrointestinal disease;

W. antiinflammatory; antirheumatic; multiple sclerosis; neuroprotective;

W. autoimmune hepatitis; antiinflammatory; hepatotropic;

W. systemic lupus erythematosus; dermatological; dermatological disease;

W. hematological disease; theumatic fever; antipyretic; crohne disease;

W. hematological disease; theumatic fever; antipyretic; crohne disease;

W. psoriasis; antipsoriatic; graves disease; antithyroid;
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compared to the corresponding healthy tissues. Upregulation in ovarian tumor tissue was confirmed by quantitative analysis of TAT mRNA expression, and upregulation in breast, pancreatic, colon, adremal and bladder tumors was confirmed by gene expression profiling in silico (GEPIS) analysis. The TAT polypeptide may comprise the full-length polypeptide, or may lack the associated signal peptide, or may comprise an extracellular domain with or without its associated signal peptide, or may be any of these fused to a heterologous polypeptide such as an epitope tag, or the Pc region of an immunoglobulin. TAT polypeptides of the invention, and their encoding nucleic acids, provide targets for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Down-regulating an immune response comprises administering to a subject
in need a fibroblast activation protein (FAP) alpha dimer enzyme in an
amount effective to down-regulate an immune response.
                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    respiratory syncytial virus infection; respiratory-gen.; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human wild type fibroblast activation protein (FAP) alpha dimer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immune inhibition; fibroblast activation protein alpha dimer;
                                                                                                                                                                                                                                                                                                  100.0%; Score 62; DB 9; Length 760; 100.0%; Pred. No. 0.49;
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                                                                                                                                                                                                                     diagnosis and therapy of cancer.
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Best Local Similarity 100.
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2005-564220/57.
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                                                                                                                                                                                                                                                                 Sequence 760 AA;
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The invention relates to a method of down-regulating an immune response, which comprises administering to a subject a fibroblast activation protein (PAP) alpha dimer enzyme in an amount effective to down-regulate an immune response. Also included are the following: a composition comprising a FAP alpha dimer enzyme in a pharmaceutically acceptable carrier, and a non-adjuvant second agent; a composition comprising a FAP alpha dimer enzyme in a pharmaceutically composition comprising a FAP alpha dimer enzyme in a pharmaceutically composition comprising a FAP alpha dimer enzyme is a maino acid substitution comprising a FAP alpha dimer enzyme lacking amino acids 269-448 fam mouse FAP.

The accondagent is an anti-inflammatory agent, immunosuppressant, or the second agent is an anti-inflammatory agent, immunosuppressant, or anti-infective agent such as antibaccerial, antiviral, antifungal, anti-proceed agents and anti-inflammatory agent, immunosuppressant, or anti-infective agent such as antibaccerial, antiviral, antifungal, anti-proceed adminer enzyme is a function or anti-infective agent such as antibaccerial, antiviral, antifungal, anti-proceed adminer enzyme is a function or chimeric procein. The PAP alpha dimer enzyme is a function or anti-infective agent such as antibaccerial, antiviral, antifungal, anti-composition comparises and antipaccerial agent. The amino acid cubstitution relative to wild type FAP alpha dimer. The amino acid cubstitution relative to wild type FAP alpha dimer. The amino acid commation or an N-linked glycosylation site and alters disament or as upperable or condition, abnormal immune response selected from inflammatic forence condition, abnormal immune response selected from inflammatic response is subsequent to an infection, such as an RV infection, cubstitution such as an RV inflammatory condition, and dualian-Barre's syndrome. The abnormal immune cresponse is subsequent to an infection, such as an RV indicated condition, disease, sepsis, graft, versus host barbormal immune expressed is s Disclosure, SEQ ID NO 2, 177pp, English. 

Sequence 760 AA;

Gaps ö 100.0%; Score 62; DB 9; Length 760; 100.0%; Pred. No. 0.49; ive 0; Mismatches 0; Indels Conservative Local Similarity 13; Query Match Matches

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AEB94163 standard; protein; 761 AA. 

RESULT 12

AEB94163;

06-OCT-2005 (first entry)

Mouse wild type fibroblast activation protein (FAP) alpha dimer.

immune inhibition, fibroblast activation protein alpha dimer;
PAP alpha dimer; guillain barre syndrome; antiinflammatory; cns-gen.;
immune disorder; neurological disease; autoimmune disease;
immunosuppressive; graft versus host disease; transplant rejection;
endotoxic shock; osteoarthritis; antiarthritic; osteopathic;
musculoskeletal disease; allergy; antiallergic; asthma; antiasthmatic;
inflammation; respiratory disease; atheroselerosis; antiateriosclerotic;
cardiovascular disease; metabolic disorder; hashimotos disease; antithyroid; endocrine disease; inflammatory bowel disease; antiinflammatory; gastrointestinal-gen.; gastrointestinal disease; rheumatoid arthritis; antirheumatic; multiple sclerosis; neuroprotective; autoimmune hepatitis; antiinflammatory; hepatorropic; systemic lupus erythematosus; dermatological; dermatological disease; uveitis; ophthalmological; autoimmune hemolytic anemia; antianemic;

The mectod further compities an anti-inflammatory agent, immunosuppressant, or anti-infective agent such as antibacterial, antiviral, antifungal, anti-infective agent such as antibacterial, antiviral, antifungal, anti-infective agent such as antibacterial, antiviral, antifungal, anti-infective agent such as antibacterial, antiviral, antifungal, anti-infective agent such as antibacterial, antifungal, anti-infective rayme is a truncation when the FAP alpha dimer enzyme is a truncation. The mutant. The FAP alpha dimer enzyme of a repression or chimeric protein. The CC substitution relative to wild type FAP alpha dimer. The amino acid substitution relative to wild type FAP alpha dimer. The amino acid compatin, or an N-linked glycosylation site and alters disulfide bond formation. The immune response is an especially an IL-I mediated condition, abhormal immune response selected from inflammation, cantommune disease, sepsis, agaft versus host disease, transplant rejection, toxic shock syndrome, allergy, asthma, atherosclerosis, catcoimmune disease is selected from or such as an RSV infection. The response is subsequent to an infection, such as an RSV infection. The cutoimmune disease is selected from or such as an RSV infection. The cutoimmune disease is selected from or an englas, cancer or thy infection. The cutoimmune disease, Guillain-Barre's syndrome, psoriasis, Graves' disease, Crohn's disease, Guillain-Barre's syndrome, psoriasis, Graves' disease, mysathenia gravis, glomerulonephritis, autoimmune hepatitis and multiple conterosis. The invention relates to a method of down-regulating an immune response, which comprises administering to a subject a fibroblast activation proteain (FAR) alpha dimer enzyme in an amount effective to down-regulate an immune response. Also included are the following: a composition comprising a FAP alpha dimer enzyme in a pharmaceutically acceptable carrier, where the composition is sterile and lacks an adjuvant; a composition comprising a FAP alpha dimer enzyme in a pharmaceutically acceptable carrier, and a non-adjuvant second agent; a composition comprising a FAP alpha dimer enzyme an amino acid substitution of A657D; and a composition comprising a FAP alpha dimer enzyme lacks an amino acid substitution of A657D; and a composition comprising a FAP alpha dimer enzyme lacking amino acids 269-448 and comprising a FAP alpha dimer enzyme lacking the method further comprises administering to the subject a second agent. cancer. The present sequence represents the amino acid sequence of mouse wild type fibroblast activation protein (FAP) alpha dimer. Down-regulating an immune response comprises administering to a subject in need a fibroblast activation protein (FAP) alpha dimer enzyme in an amount effective to down-regulate an immune response. hematological disease; rheumatic fever; antipyretic; Crohns disease; psoriasis; antipsoriatic; graves disease; antithyroid; respiratory syncytial virus infection; respiratory-gen.; virucide; Jesson MI; Disclosure; SEQ ID NO 6; 177pp; English Mclean PA, Jones B, Miller GT, (POIN-) POINT THERAPEUTICS INC. 09-JAN-2004; 2004US-0535577P. 10-JAN-2005; 2005WO-US000709 WPI: 2005-564220/57. N-PSDB; AEB94162 WO2005071073-A1. 04-AUG-2005. Mus musculus. 

9; Length 761; ; Score 55; DB 9; Pred. No. 6; 3; Mismatches 88.7%; 76.9%; Local Similarity 76.9 les 10; Conservative Query Match Matches

Sequence 761 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention describes a recombinant DNA construct comprising a polymucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at the sequence. The recombination of patent of polymucleotide of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, increased resistance to plant disease, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one caress condition or for modifying seed oil or protein yield and/or content. This is the amino acid sequence of a plant full length insert or polypeput that can be used in the recombinant DNA construct of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for
                                                                                                                                                        plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; yest colorance; palactoromannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield; protein content.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cao Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Таравка ЈЕ,
                                                                                                                                  Plant full length insert polypeptide seqid 52777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Screen SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 52777; 15pp; English.
                                                     ADX90113 standard; protein; 562 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhou Y, Kovalic DK,
                                                                                                                                                                                                                                                                                                                                                                                     06-MAY-1999; 99US-00304517.
05-NOV-2001; 2001US-00985678.
                                                                                                                                                                                                                                                                                                                                                              28-APR-2003; 2003US-00425114
                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    KOVALIC D K.
SCREEN S E.
TABASKA J E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-180133/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  improving yield.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 562 AA;
                                                                                                                                                                                                                                                                                                           US2004034888-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                LIU J.
ZHOU Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAO
                                                                                                                                                                                                                                                                                 Unidentified
                                                                                                         21-APR-2005
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                                                                                 ADX90113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (KOVA/)
(SCRE/)
(TABA/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                            ZHOU/)
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                              RESULT 13
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Score 49; DB 8; Length 562; Pred. No. 37;

> 79.0%; 69.2%;

> Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a Helicobacter pylori cytoplasmic protein
                                                                                                                                                                                                                                                                                                                                                                                                                    Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis; envelope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Helicobacter pylori nucleic acid sequences and related polypeptide(s) useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter.
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                                                                                                                                                                                                                                                                                                                                                                   H. pylori cytoplasmic protein hplp13922orf30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mellgaerd BL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 61; Page 1349; 1481pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW20427 standard; protein; 296 AA.
                                                                                                                                                                                                 AAW20957 standard; protein; 223 AA.
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96US-00630405,
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208 ILTESKEIEBALK 220
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1 ILEENKELENALK 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Berglindh OT,
                                Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-052306/05.
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les 9; Conserv
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01-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9640893-A1
                                                                                                                                                                                                                                                                                                                    21-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-DEC-1996
                                                                                                                                                                                                                                                            AAW20957;
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                                                                                                                                               RESULT 14
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ID AAW
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Helicobacter pylori; two-hybrid system; protein-protein interaction;
bait polypeptide; gastric ulcer; antibacterial.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Helicobacter pylori bait polypeptide #41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB52523 standard; protein; 346 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      represent an illegible residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-APR-2000; 2000WO-IB000603.
                                                                                                                                               28-DEC-2001; 2001WO-EP015428.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69.4%;
69.2%;
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                                                                                                                                                                               02-JAN-2001; 2001US-0259302P
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157 ILTESKEIBEALK 169
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                                                                                                                                                                                                              (HYBR-) HYBRIGENICS.
(INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                Rain J,
                                                                                                                                                                                                                                                                                              WPI; 2002-674910/72.
N-PSDB; ABX65874.
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                                              Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 345 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200066722-A1.
                                                                             WO200266501-A2
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                                                                                                                                                                                                                                                               Legrain P,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence encodes a Helicobacter pylori cytoplasmic protein that may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in B. coli hosts
                                                                                                                                 bacteria; inhibitor;
                                                                                                                Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor duodenal ulcer disease; chronic gastritis; diagnosis; envelope; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Helicobacter pylori nucleic acid sequences and related polypeptide(s) useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter.
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                                                                                 H. pylori cytoplasmic protein 34089087.aa.
                                                                                                                                                                                                                                                   /note= "encoded by TGS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mellgaerd BL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 61; Page 605; 1481pp; English
                                                                                                                                                                                                                Location/Qualifiers
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69.2%;
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96US-00630405
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                                                 (first entry)
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                                                                                                                                                                                   Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-052306/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                     Key
Misc-difference
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                                                 14-JUL-1997
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                 AAW20427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smith D,
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8×4×5×8

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Gaps

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2; Indels

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The invention describes a complex of protein-protein interactions in Helicobacter pylori selected from 421 complexes given in the specification. The complex of protein-protein interactions are useful for screening for agents which modulate the interaction of proteins. Modulating compounds which binds to a targeted bacterial protein may be used for treating or preventing ulcers in a human or animal. This is the amino acid sequence of a selected interacting domain (SID), identified via protein-protein interactions. Note: Where the patent number printed at the top of the pages in the specification has obscured areas of protein sequence, the indexer has replaced the residue with an X to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New complexes of protein-protein interactions in Helicobacter pylori, useful for identifying modulating compounds for treating or preventing ulcers in mammals.
Protein-protein interaction; ulcer; selected interacting domain; SID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Labigne A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       De Reuse H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 6; Page 200; 642pp; English.
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Length 706; 1; Indels

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The invention relates to multiprotein complexes from eukaryotes. Proteins of the invention and DNA sequences encoding them are given in records ABR52568-ABR53003 and ACC6610-ACC6194 respectively. The complexes are obtainable by using a protein as a bait and isolating the set of proteins which is attached thereto from cells. Such protein complexes may comprise up to 30 distinct proteins. Protein complexes of the invention are useful for diagnosing a disease or disorder, or as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of a disease or disorder. Note: The sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the European Patent Office. The complete document is available on CD-ROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to the isolation of histone deacetylase polypeptides and the genes encoding them. The compositions of the present invention are useful for the diagnosis and treatment of disorders associated with the aberrant expression or activity of the histone deacetylases, such as breast, bladder, colon, lung, rectal, endometrial, overtan and prostate cancer, Paget's disease, melanoma and adenocarcinomas. This sequence represents the histone deacetylase SC_HDAl protein used for sequence comparison with the novel proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytostatic; histone deacetylase; diagnosis; breast; bladder; colon; lung; rectal; endometrial; ovarian; prostate; cancer; Paget's disease; melanoma; adenocarcinoma; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated human histone deacetylase polypeptide, useful for and treating disorders with aberrant expression or activity of histone deacetylases, such as breast, colon, lung and prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gottardie M;
                                                                                                                                                                                                                                                                                                                                                         Score 43; DB 6;
Pred. No. 4e+02;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 43; DB 7;
Pred. No. 4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yeast histone deacetylase SC_HDA1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jackson DG, Lorenzi MV, Attar RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 14B; 206pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADB96560 standard; protein; 706 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BRIM ) BRISTOL-MYERS SQUIBB CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69.4%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-JUN-2002; 2002WO-US019560.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-JUN-2001; 2001US-0298296P.
                                                                                                                                                                                                                                                                                                                                                           69.4%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 LEENKEEENSL 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 LEENKELENAL 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-167442/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ä
                                                                                                                                                                                                                                                                                                                Sequence 706 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADB96560;
                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 19
ADB96560
                8,83333333333333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                         The present sequence is a bait polypeptide used in a Helicobacter pyloritwo-hybrid screen to identify protein protein interactions. The method is used to identify a recombinant cell clone expressing a prey polypeptide which is capable of interacting with the bait polypeptide. The two hybrid system is useful for screening compounds for antibacterial activity. It may be used in the treatment of gastric ulcers. The polynucleotides are useful as amplification primers or specific detection probes. The mono- or polyclonal antibodies. The polynucleotides is immunogens to produce antibodies, vectors, host cells or modulating agents can be used to produce a pharmaceutical composition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                          two-hybrid system for identifying compounds useful in the treatment of gastric ulcers comprises producing a collection of recombinant cell lones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated protein complexes useful for diagnosing a disease or disorder, or as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of disease or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kuester BD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 43; DB 3; Length 346;
Pred. No. 1.9e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Multiprotein complex; eukaryote; drug target; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kruse UD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bauer A, Gavin A, Grandi P, Krause R, K.
Marzioch M, Schultz JD, Superti-Furga GD;
                                                                                                                                                                                                                                                                          Example 5; Page 131-132; 267pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABR53675 standard; protein; 706 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein sequence #SEQ ID 2215
                                                                Rain J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69.4%;
69.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-MAY-2001; 2001EP-00111774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-DEC-2001; 2001EP-00130253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157 ILTESKEIEEALK 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 69.2.
Best Local Similarity 69.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ILEENKELENALK 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae
                   (HYBR-) HYBRIGENICS SA
                                                                Legrain P, Selig L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-250078/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CELL-) CELLZOME AG
                                                                                                         WPI; 2000-687535/67.
N-PSDB; AAC97269.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ACC61717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 346 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-JUN-2003
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ABR53675;

RESULT 18 ABR53675 ID ABR XX

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diagnosing the cancer.

Length 706;

ADL70610 standard; peptide; 17 AA.

RESULT 21

20-MAY-2004

ADL70610;

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The invention relates to novel protein complexes comprising a first and a second protein, or its derivative, fragment, homologue or variant. The proteins are selected from given protein complexes, which are not defined in the specification. The variants are encoded by nucleic acids that hybridize to the nucleic acids encoding the proteins under low stringency conditions. The protein complexes are useful as targets for an active separt a pharmaceutical. These protein complexes are particularly useful as drugs targets for the treatment or preventing of a disease or disorder. The complexes and methods above are useful in diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject. These are also useful in screening for a drug for treatment or prevention of a disease or disorder. The molecule that modulates the amount, activity or protein components of the complex is useful for the manufacture of a medicament of for the treatment or prevention of a disease or disorder. The sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               targets in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 corresponds to a protein of the invention. (Note: the sequence data for this patent did not form part of the printed specification but was obtained from the EPO in electronic format).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New proteins and protein complexes from eukaryotes, useful as targets drug screening, of in diagnosing or screening for the presence of a disease or disorder, or a predisposition for developing a disease or
 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Superti-Furga G, Kuester B, Schultz J;
P, Krause R, Kruse U, Merino A, Bauch A;
C, Rick J;
 ö
 IndelB
                                                                                                                                                                                                                                                                       Disease treating protein complex-derived protein #1333.
 1;
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 2665; 13pp; English.
                                                                                                                                                                                                                                                                                                             protein complex; drug target; diagnosis.
                                                                                                                                                              ADK64084 standard; protein; 706 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-DEC-2002; 2002EP-00102902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-DEC-2001; 2001EP-00130253
                                                                                                                                                                                                                                      (first entry)
 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gavin A, Supe
M, Grandi P,
Leutwein C,
                                   2 LEENKELENAL 12
                                                                     22 LEENKEEENSL 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disorder in a subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CELL-) CELLZOME AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2003-638460/61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ADK64085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 706 AA;
                                                                                                                                                                                                                                                                                                                                                 Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                     EP1338608-A2.
                                                                                                                                                                                                                                      06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bauer A, Ga
Marzioch M,
                                                                                                                                                                                                                                                                                                                                                                                                                         27-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Michon A,
                                                                                                                                                                                                     ADK64084;
 Matches
                                                                                                                              RESULT 20
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The present sequence is that of an epitope of human thrombospondin-1

(TSP) ADL70639. The epitope is found in TSP and also in a TSP fragment

(TSP) ADL70639. The epitope is found in TSP and also in a TSP fragment

(TSP) Dal Jound in plasma, and their use in clinical assays for

or 20-35 kDa) found in plasma, and their use in clinical assays for

carcer and for generation of antibodies and other binding agents. A

carcer abliding molecule, e.g. an antibody, to obtain anvolves:

(I) using an epitope shared by TSP and the TSP fragment or portion as

target for a binding molecule, e.g. an antibody, to obtain a quantitation

of TSP plus TSP fragment or portion; (2) using an epitope present in TSP

cot TSP plus TSP fragment or portion; (2) using an epitope present in TSP

cot (3) using the difference between (1) and (2) as a quantitation of the

amount of TSP fragment or portion; (2) using an epitope present in TSP

cot (3) using the difference between (1) and (2) as a quantitation of the

amount of TSP fragment or portion; (2) using an epitope present in TSP

cot (3) using the difference between (1) and (2) as a quantitation of the

amount of TSP fragment or portion; (2) using an equalitation of the

cot amount of TSP fragment or portion; (3) using the condition or getted from cancer, renal failure, renal disease,

disease or condition selected from cancer, renal failure, renal disease,

cot dermatchis, myocardial infarction, liver disease, splenectomy,

diabetes mellitus, myocardial infarction, ilver disease, splenectomy,

demacomyositis, rheumatodia arthritis, vasculitis syndrome, Henoch-

condition, a condition associated with consumption of

condition, a condition associated with consumption of

condition, a condition associated with consumption of

platelet activation, a condition associated with intravascular

condition associated with condition, a condition associated with production and/or release of thrombosycopanic derman in travascular coagulation, an emperatment and and/or a condition associated with pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypersensitivity, scleroderma, conditions associated with plugging of vessels, a condition associated with a cryofibringen, a condition associated with a cryofibringen, a condition casociated with an antication and a condition associated with an antication antibody. The cancer is selected from adenoma, adenocarcinoma, carcinoma, lymphoma, leukaemia, solid cancer, liquid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer, metastatic cancer, pre-metastatic cancer, non-metastatic cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New purified thrombospondin fragment extracted from a body fluid, useful for diagnosing cancer e.g. adenoma, adenocarcinoma, carcinoma, lymphoma or leukemia or as calibrators, indicators, immunogens and analytes.
                                                                                                                                      Human thrombospondin-1 epitope, useful for cancer diagnosis.
                                                                                                                                                                                             Human; thrombospondin-1; epitope; cancer; diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 10; SEQ ID NO 9; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-AUG-2002; 2002US-0405494P.
21-APR-2003; 2003US-00419462.
                                                                                                                                                                                                                                                                                                                                                                                                  20-AUG-2003; 2003WO-US026023.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (WILL/) WILLIAMS K J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-226901/21.
                                                                                                                                                                                                                                                                                             WO2004018995-A2.
                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                 04-MAR-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Williams KJ;
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Gaps

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69.4%; Score 43; DB 7; Length 706; 81.8%; Pred. No. 4e+02; ive 1; Mismatches 1; Indels

Conservative

Best Local Similarity Matches 9; Conserv

Query Match

2 LEENKELENAL 12

8

LEENKEEENSL

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The present sequence is that of an epitope of human thrombospondin-1 (TSP) ADL70619. The epitope is found in TSP and also in a TSP fragment present in plasma. The invention relates to TSP fragments (80-110, 40-60 or 20-35 kDa) found in plasma, and their use in clinical assays for cancer and for generation of antibodies and other binding agents. A method that distinguishes TSP from a TSP fragment or portion involves: (1) using an epitope shared by TSP and the TSP fragment or portion as a target for a binding molecule, e.g. an antibody, to obtain a quantitation of the but not in the fragment or portion; (2) using an epitope present in TSP but not in the fragment or portion; (2) using an epitope or present in TSP to mount of TSP fragment or portion to obtain a quantitation of the and (3) using the difference between (1) and (2) as a quantitation of the step (1). Detection or quantification of the TSP fragment or portion. The present epitope can be used in step (1). Detection or quantification of the TSP fragment or portion is performed in order to detect the presence, or monitor the course, of a disperse or condition selected from cancer, renal failure, renal disease, atopic dermatitis, vaccultis, actue vascullitis, renal allograft, asthma, condition and the course of the disbetes mellitus, myocardial infarction, liver disease, splenectomy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                           the respiratory system, circulatory system, musculoskeletal system, muscle, bone, a joint, tendon or ligament, digestive system, liver or biliary system, pancreas, head, neck, endocrine system, reproductive system (male or female), genitourinary system, kidney, urinary tract, sensory system, nervous system, lymphoid organ, blood, a gland, mammary sland, prostette gland, endometrial tissue, mesodermal tissue, ectodermal tissue, endodermal tissue, a poorly-differentiated cancer, a well-differentiated cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New purified thrombospondin fragment extracted from a body fluid, useful for diagnosing cancer e.g. adenoma, adenocarcinoma, carcinoma, lymphoma or leukemia or as calibrators, indicators, immunogens and analytes.
cancer with vascular invasion, internal cancer, skin cancer, cancer of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human thrombospondin-1 epitope, useful for cancer diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 42; DB 8; Length 17;
Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; thrombospondin-1; epitope; cancer; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 10; SEQ ID NO 10; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADL70611 standard; peptide; 18 AA.
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21-APR-2003; 2003US-00419462.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67.7%;
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3 VTEENKELANELR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 61.5
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17 AA;
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cuernacionyositis, polystuceritis nonosas, systemic lupus erythematosus, Kawasaki syndrome, non-specific vasculitis, juvenile rhematoid arthritis, vasculitis syndrome, Henoch-Schoenlain purpura, thrombocytopenic purpura, an inflammatory condition, a condition associated with clotting, a condition associated with containing a condition associated with consumption of platelet activation, a condition associated with consumption of condition associated with consumption of platelets heparin-induced thrombocytopenia, disseminated intravascular coagulation, intravascular coagulation, accondition associated with endothelial activation, a condition associated with conduction and/or release of thrombospondin and/or a thrombospondin condition associated with endothelial activation, an antibiotic with production and/or release of thrombospondin and/or a thrombospondin condition associated with a cryoglobulin, and associated with plugging of vessels, a condition associated with a cryoglobulin, and a condition associated with a cryoglobulin, and a condition associated with a cryoglobulin, and a condition associated with a cryoglobulin, and a condition associated with a cryoglobulin, and a condition associated with a cryoglobulin, and a condition associated with a cryoglobulin, and a condition associated with a cryoglobulin, and a condition associated with a cryoglobulin, and a condition associated with a cryoglobulin, and a condition associated with a cryoglobulin, and a condition associated with a cryoglobulin, and a condition associated with a cryoglobulin, and a condition associated with a cryoglobulin, and a condition associated with a cryoglobulin, and a condition associated with a cryoglobulin, and a condition associated with a cryoglobulin, and a condition associated with a cryoglobulin, and a condition associated with a cryoglobulin, and a condition associated with a cryoglobulin, and a cancer, non-metastatic cancer, a cancer, per-metastatic cancer, non-metastatic cancer of the respiratory system, tendon or ligament,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
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polyarteritis nodosa, systemic lupus erythematosus,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
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Pred. No. 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAO04456 standard; protein; 52 AA.
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18-MAY-2000; 2000US-00577409.
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4 VTEENKELANELR 16
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N-PSDB; AAI84387.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18 AA;
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The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polyneptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity, inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is that of the procollagen homology domain of human thrombospondin-1 (TSP) ADL70639. It includes the N-terminal portion of the collagen V binding region; the remainder of this region lies in the type 1 repeat domain ADL70644. The invention relates to TSP fragments (80)
Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
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for diagnosing cancer e.g. adenoma, adenocarcinoma, carcinoma, lymphoma
or leukemia or as calibrators, indicators, immunogens and analytes.

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    /note= "Collagen V binding region (N-terminal portion)"

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                                                          Claim 20; SEQ ID NO 18348; 1399pp + Sequence Listing; English.
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21-APR-2003; 2003US-00419462.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 61.5%;
8; Conservative
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Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                        Sequence 52 AA;
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the TSP fragment or portion is performed in order to detect the presence, or monitor the course, of a disease or condition selected from cancer, renal failure, renal disease, atopic dermatiis, vascultis, acute vasculitis, renal allograff, asthma, diabetes mellitus, cute cute vasculitis, renal allograff, asthma, diabetes mellitus, myocardial infarction, liver disease, splenectomy, dermatomyositis, myocardial cinfarction, liver disease, splenectomy, dermatomyositis, myocardial condosa, systemic lupus erythematosus, lupus erythematosus, Kawasaki condosa, systemic lupus erythematosus, lupus erythematosus, Kawasaki condosa, non-specific vasculitis, juvenile rheumatoid arthritis, corrematoid arthritis, corrematoid arthritis, associated with clotting, a condition associated with platelet condition associated with platelet corrivation, a condition associated with intravascular platelet corrivation, a condition associated with consumption of platelets, heparin associated with endothelial activation, a condition associated with conduction and/or release of thrombospondin and/or a thrombospondin conduction and/or release of thrombospondin and/or a thrombospondin correction, an aspartame reaction, acondition, a condition, acondition, aconditions aconditions aconditions aconditions.
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clinical assays for cancer and for generation of antibodies and other binding agents. A method that distinguishes TSP from a TSP fragment or portion involves: (1) using an epitope shared by TSP and the TSP fragment or portion as a target for a binding molecule, e.g. an antibody, to obtain a quantitation of TSP plus TSP fragment or portion; (2) using an epitope present in TSP plus TSP fragment or portion; (2) using an epitope present in TSP plus TSP fragment or portion; (2) using an quantitation of TSP only; and (3) using the difference between (1) and (2) as a quantitation of the amount of TSP fragment or portion. Suitable epitopes are provided ADL70602-ADL70638, Detection or quantification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypersensity vity, scleroderma, conditions associated with hypersensity vity, scleroderma, conditions associated with a cryofibrinogen, a condition associated with a cryofibrinogen, a condition associated with an anticardiolipin antibody. The cancer is selected from adenoma, actinoma, prophoma, leukaemia, solid cancer, liquid cancer, metastatic cancer, pre-metastatic cancer, scancer, increased with vascular invasion, internal cancer, skin cancer of the respiratory system, circulatory system, musculoskeletal system, muscle, bone, a joint, tendon or ligament, digestive system, liver or billiary system, pancreas, head, neck, endocrine system, reproductive system (male or female), genitourinary system, kidney, urinary tract, sensory system, nervous system, lymphoid organ, blood, a gland, mammary gland, prostate gland, endometrial tissue, mesodermal issue,
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tissue, endodermal tissue, a teratoma, a poorly-differentiated cancer, a
well-differentiated cancer or a moderately differentiated cancer.
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Pred. No. 70;
2; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67.78;
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21 VTEENKELANELR 33
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 98 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADQ39359
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Sequence 432 AA;
                                           WO2004058052-A2
Homo sapiens
                                                                                      15-JUL-2004
                                                                                                                                                                                                                                                                                                                               Cargill M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU02916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU02916
ID AAU0
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AC AAU0
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DT 12-S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual's nucleic acids, where the presence of the SNP is correlated with an altered risk for myocardial infarction in the individual the invention curther comprises: an isolated nucleic acid molecule comprising at least a configuous nucleotides where one of the nucleotides is an SNP given in the specification or its complement and encoding any one of the amino acid sequences given in the specification; an antibody that specification or its complement and encoding any one of the amino comprising an amino acid sequence given in the specification; an antibody that specification and which is between about 16 and 1000 nucleotides in length; a kit for detecting an SNP in a nucleic acid comprising the specification and which is between about 16 and 1000 nucleotides in length; a kit for detecting an SNP in a nucleic acid comprising the nucleic acid molecule; a method of detecting a variant polypeptide; and a nucleic acid molecule; a method of detecting a variant polypeptide; and enthod for identifying an agent useful in treating or preventing myocardial infarction may be used in gene therapy. The method is useful in identifying myocardial infarction and for preparing a preparing and presented and an encompanies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              associated gene containing one or more SNP's of the invention. Note: This sequence was not shown in the specification. The sequence has come from an electronic sequence listing downloaded from the WIPO website.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human myocardial infarction-associated gene derived protein, SEQ ID 1020.
                                                                                                                                                                                                                                                                                                                        Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in the individual's nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Myocardial infarction; detection; single nucleotide polymorphism; SNP; cardiant; gene therapy; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       composition for treating or preventing myocardial infarction. This sequence represents the protein of a human myocardial infarction-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67.7%; Score 42; DB 8; Length 432; 61.5%; Pred. No. 3.4e+02; ive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 10; SEQ ID NO 1022; 145pp; English.
                                                                                                                                                                                                                        Cargill M, Devlin JJ, Iakoubova O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADQ39357 standard; protein; 432 AA.
                                                                                      10-MAR-2003; 2003US-0453135P.
30-APR-2003; 2003US-0466412P.
23-SEP-2003; 2003US-0504955P.
                                                                  20-DEC-2002; 2002US-0434778P
                      22-DEC-2003; 2003WO-US040978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 VTEENKELANELR 313
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                                                                                                                                                                           (APPL-) APPLERA CORP.
                                                                                                                                                                                                                                                                 WPI; 2004-533949/51
                                                                                                                                                                                                                                                                                        N-PSDB; AD038531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 432 AA;
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The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleocide polymorphism (SNP) in any one of the nucleocide sequences given in the specification in the individual's altered risk for myocardial infarction in the individual. The individual's conclete acids, where the presence of the SNP is correlated with an correlated risk for myocardial infarction in the individual. The invention further comprises an isolated nucleic acid molecule comprising at least contiguous nucleotides where one of the nucleotides is an SNP given in the specification an its complement and encoding any one of the amino acid sequence given in the specification; an antibody comprising an amino acid sequence given in the specification; an antibody comprising an amino acid sequence given in the specification; an antibody comprising an amino acid sequence given in the specification; an amplified polymucleotide contist an SNP in a nucleic acid molecule, and an enzyme; a method of detecting an SNP in a nucleic acid molecule; a method of detecting a variant polypeptide; and contist and an enzyme; an enthod of detecting an SNP in a nucleic acid molecule; a method of detecting a variant polypeptide; and a nucleic acid and infarction. The novel detecting a variant polypeptide; and an enzyme; an enthod of set on gene therapy. The composition for treating or preventing myocardial infarction. This composition for treating or preventing myocardial infarction. This composition is not an enth of a the invention and composition on the protein of a human myocardial infarction. This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in the individual's nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gape
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Pred. No. 3.4e+02;
2; Mismatches 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 10; SEQ ID NO 1020; 145pp; English
                                                                                                                                                                                                                                                                                                                                                                                     Iakoubova 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU02916 standard; protein; 459 AA.
                                                                                                                        10-MAR-2003; 2003US-0453135P.
30-APR-2003; 2003US-0466412P.
23-SEP-2003; 2003US-0504955P.
22-DEC-2003; 2003WO-US040978.
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61.58;
                                                                                        20-DEC-2002; 2002US-0434778P
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301 VTEENKELANELR 313
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Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          Devlin JJ,
                                                                                                                                                                                                                                                                                                     (APPL-) APPLERA CORP
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N-PSDB; ADQ38529.
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Barroso I, Baughn MR, Becha SD, Borowsky ML;
Elliott VS, Emerling BM, Forsythe IJ, Gietzen KJ;
Graul RC, Griffin JA, Gururajan R, Hafalia AJA, Ison CH;
Khan FA, Lee S, Li JX, Reddy R, Richardson TW;
Swarnakar A, Tang YT, Warren BA, Xu Y, Yao MG, Yue H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polypeptide associated with cell growth, differentiation and death, useful for preparing a composition for diagnosing or treating a disease e.g., cardiovascular or neurological disorders or cancer.
                                        Human, cell growth, differentiation and death, CGDD, cardiant; cancer;
cytostatic, neuroprotective; gene therapy; diagnosis; cardiovascular;
Human CGDD protein 7727886CD1 SEQ ID 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 67; Page 215-216; 267pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                             2001US-0322182P.
2001US-0340747P.
2001US-0342761P.
                                                                                                                                                                                                                                                                                                                                          2001US-0313071P.
2001US-0314678P.
                                                                                                                                                                                                                                                                                                                                                                                    2001US-0316692P.
2001US-0317913P.
                                                                                                                                                                                                                                                          08-AUG-2002; 2002WO-US025465
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61.5%;
                                                                                                                                                                                                                                                                                                                        2001US-0313070P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2002US-0369129P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Conservative
                                                                                neurological disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-268197/26.
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Best Local Similarity
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                                                                                                                                                                       WO2003014322-A2.
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Kable AE, Kh
Sprague WW,
                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                       31.-AUG-2001;
07-SEP-2001;
                                                                                                                                                                                                                                                                                                    08-AUG-2001;
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                                                                                                                                                                                                               20-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Duggan BM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yue H;
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ID AAB4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence represents an angiotenain converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor IC, cellular tumour antigen P53, and vasoactive intestinal colypeptide receptor 2. The polypeptides and their associated nucleic colds are useful for identification of variant sequences and detection of candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various disorders including cardiovascular diseases such as arteriosclerosis, myocardial infarction and coronary arterial thrombosis, renal diseases when as hypertrophy, immune disorders such as immune complex nephritis, multiple sclerosis, cancer, sarcoidosis, nonarcoidocic pulmonary granulomatous diseases such as as asbestosis and vascular pathologies involving an endothelial
                                   Angiotensin converting enzyme splice variant; ACBV; interleukin 6; granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen P53; cyclin-dependent kinase inhibitor IC; vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; myocardial infarction; coronary arterial thrombosis; renal disease; diabetic nephropathy; muscular disease; immune disorder; sarcoidosis; multiple sclerosis; immune complex nephritis; deep vein thrombosis; nonarcoidotic pulmonary granulomatous disease; endothelial abnormality; vascular disorder; asbestosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
  Angiotensin converting enzyme (ACEV) splice variant protein #16.
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Pred. No. 3.66+02;
Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Khosravi R, Bernstein J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67.7%;
61.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          99IL-00132978
99IL-00133455
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Best Local Similarity 61.5
Best Local 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-336004/35.
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                                                                                                                                                                                                                                                                                                                             WO200136632-A2
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10-DEC-1999;
                                                                                                                                                                                                                                                                                    domo sapiens.
                                                                                                                                                                                                                                                                                                                                                                       25-MAY-2001
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     growth,
                                                                                                                                                  cancer.
This invention describes a novel polypeptide associated with cell growt differentiation and death (CGDD) which has cardiant, cytostatic and neuroprotective activity. The polypeptides of the invention are useful
                                                                               for preparing a composition for disgnosting, or treating a disease or condition associated with decreased expression or overexpression of functional CGDD e.g., cardiovascular or neurological disorders or can The polymuclectides of the invention can be used for gene therapy. ABG74675-ABG74701 represent the human CGDD polypeptides encoded by
                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                           Score 42; DB 6; Length 465; Pred. No. 3.7e+02; 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human cancer associated protein sequence SEQ ID NO:1047.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB43602 standard; protein; 466 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB43602;
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(first entry)

10-MAY-2003

XXXEX

RESULT 28 ABG74686

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Human; cancer associated gene; cancer antigen; detection; cancer; diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antishematic; antitheumatic; antiarthritic; antiviral; dermitinflammatory; antithyroid; antiallergic; antibacterial; cardiant; dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; haematopoletic call disorder; autoimmune disorder; all disorder; autoimmune disorder; haemostatic; call disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening.
                                                                                                                                                                                                                                                                                                                                                                     Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; Page 1636-1638; 2352pp; English.
                                                                                                                                                                                                                              08-MAR-2000; 2000WO-US005882.
                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                       99US-0124270P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the present invention
                                                                                                                                                                                                                                                                                                        Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                                                                  WPI; 2000-587533/55
                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAC77811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 466 AA;
                                                                                                                                                                             WO200055350-A1
                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                         12-MAR-1999;
                                                                                                                                                                                                      21-SEP-2000
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Claim 9; SEQ ID NO 3; 71pp; English

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AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB4429. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antiathritic; antidiabetic; antibacterial; antithritic; antidiabetic; antibacterial; antithritic; antidiabetic; antibacterial; antithritic; cardiant; firombolytic; cagulant; neuroprotective; cardiant; firombolytic; cagulant; cootropic; vasotropic; antiporiatic and antianglogenic. The polynucleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Polynucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoietic cells, autoimmune disorders, allergic reactions, graft versus host disease and organ rejection, modulate haemostatic or thrombolytic activity, modulate consists and antagonists may be also be used in drug screens. AAC78449 to AAC7845 and AAB44240 represent sequences used in the exemplification of
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Gaps ö Score 42; DB 3; Length 466; pred. No. 3.7e+02; 2; Mismatches 3; Indels 67.7%; 61.5%; Local Similarity 61.5 les 8; Conservative Query Match Best Loc Matches

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1 ILEENKELENALK 13

ADY49758 standard; protein; 534 AA. ADY49758; RESULT 30 ADY49758 ΩI XXXX

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Isolated mammalian nucleic acid molecule encoding cancer associated antigen T21, useful for detecting or monitoring, or treating gastric or
                       tumor marker; cancer; cytostatic; neoplasm; gastrointestinal tumor; gastrointestinal disease; prostate tumor; andrology; genitourinary disease; T21.
           Human cancer associated antigen T21 SEQ ID NO 3.
                                                                                                                            (UYNO-) UNIV NOTTINGHAM TRENT
                                                                                                       29-AUG-2003; 2003GB-00020305.
02-APR-2004; 2004GB-00007586.
                                                                                           27-AUG-2004; 2004WO-GB003650
                                                                                                                                                            N-PSDB; ADY49756, ADY49757.
19-MAY-2005 (first entry)
                                                                                                                                        Miles A;
                                                                                                                                                     WPI; 2005-214542/22
                                                                                                                                                                                       prostate cancer.
                                                                                                                                        Li G,
                                                                 WO2005021588-A1.
                                                    Ното варіеля
                                                                              10-MAR-2005.
                                                                                                                                         Rees RC,
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The invention describes an isolated mammalian nucleic acid molecule (I) cancoding cancer associated antigen T21, comprising fully defined 2781 cancoding cancer associated antigen T21, comprising fully defined 2781 cancoding cancer associated antigen T21, comprising fully defined 2781 capable (SEQ ID No. 1) or 1605 (SEQ ID No. 2) nucleotic acid molecule (II) capable acid molecule which is at least 90% homologous to a nucleic acid molecule (III) comprising in a normal state; an cancerous tissue compared to that tissue when in a normal state; an cancerous tissue compared to that tissue when in a normal state; an cancerous tissue compared to that tissue when in a normal state; an cancerous tissue compared to that tissue when in a normal state; an cancerous tissue comparising to a sequence of (II), but not (IV) comprising (IV) (II) or (III); a fragment or derivative (VII) or (IVI) but not (IVI); an isolated polypeptide (VI) comprising an amino acid sequence acid residues 39-77 of SEQ ID No. 3; an isolated nucleic acid molecule (VII) or (VIII); a monoclonal antibody (IX) organism (VII); a monoclonal antibody (IX) organism (VII); but not to the protein bound by MAD 3H12; use of an uncleic acid probe (IV), but not to the protein bound by MAD 3H12; use of an uncleic acid probe (IV) which is capable of specifically hybridizing (II), (III) or (VIII); but not to the protein bound by MAD 3H12; use of IV, (III), (III), (III), (VIII) or (VIII), but not to the protein bound by MAD 3H12; use comprising (I), (III), (VIII) or (VIII), ( protective or therapeutic immunity. This is the amino acid sequence of human cancer associated antigen T21.

Sequence 534 AA;

Query Match

DB 9; Length 534; 67.7%; Score 42;

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Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies.
                                                                                      granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen, PS3; cyclin-dependent kinase inhibitor IC; vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; myocardial infarction; coronary arterial thrombosis; renal disease; diabetic nephropathy; muscular disease; immune disorder; sarcoidosis; multiple sclerosis; immune complex nephritis; deep vein thrombosis;
                                                                                                                                                                                              nonarcoidotic pulmonary granulomatous disease; endothelial abnormality; vascular disorder; asbestosis
                                                                       converting enzyme splice variant; ACEV; interleukin 6;
                                        Angiotensin converting enzyme (ACEV) splice variant protein #15.
                                                                                                                                                                                                                                                                                                                                              17-NOV-2000; 2000WO-IL000766.
             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          David A,
                                                                                                                                                                                                                                                                                                                                                                                                                           (COMP-) COMPUGEN LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-336004/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAS06015.
                                                                                                                                                                                                                                                                                  WO200136632-A2.
                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                               17-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                             10-DEC-1999;
                                                                                                                                                                                                                                                                                                               25-MAY-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Levine Z,
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual determinated soft tissue sample from an individual determining the expression of a gene in both samples and comparing the expression of a gene in both soft tissue samples where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The mucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated protein of the invention. The current sequence is not shown within the
                                                                                                                                                                                                                                                                                     soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Early detection of soft tissue sarcoma comprises determining expression
                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          specification per se but was submitted in CD format by the inventor.
                ö
                                                                                                                                                                                                                                                    Human soft tissue sarcoma-upregulated protein - SEQ ID 4109.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 42; DB 8; Length 535
Pred. No. 4.3e+02;
Mismatches 2; Indels
Pred. No. 4.3e+02;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; SEQ ID NO 4109; 210pp; English.
                                                                                                                                                         ADQ21289 standard; protein; 535 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zlotnik A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PROT-) PROTEIN DESIGN LABS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.7%;
Local Similarity 61.5%;
les 8; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                              26-NOV-2002; 2002US-0429739P.
                                                                                                                                                                                                                                                                                                                                                                                                              26-NOV-2003; 2003WO-US038193.
 53.8%;
                                                                                                                                                                                                                       26-AUG-2004 (first entry)
                                               1 ILEENKELENALK 13
                                                               ::||||:|| :|
70 LVEENKQLEEGMK 82
                7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ginsburg WM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-441208/41.
 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 535 AA;
                                                                                                                                                                                                                                                                                                                                                   WO2004048938-A2.
                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                10-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                        ADQ21289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aziz N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loc
Matches
                 Matches
                                                                            a
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Bernstein J;

Khosravi R,

Azar I,

99IL-00132978.

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                                                                                                                                                                                                 polypeptide receptor 2. The polypeptides and their associated nucleic acids are useful for identification of variant sequences and detection of candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various disorders including cardiovascular diseases such as arteriosclerosis,
                                               The sequence represents an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of ganulocyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor 1C, cellular tumour antigen P53, and vasoactive intestinal
                                                                                                                                                                                                                                                                                                                                                             myocardial infarction and coronary arterial thrombosis, renal diseases such as diabetic nephropathy, muscular diseases such as hypertrophy, immune disorders such as immune complex nephritis, multiple sclerosis, cancer, sarcoidosis, nonarcoidotic pulmonary granulomatous diseases such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer, sarcoidosis, nonarcoidotic pulmonary granulomatous dise
as asbestosis and vascular pathologies involving an endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 42; DB 4;
Pred. No. 4.4e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        abnormality such as deep vein thrombosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADN02474 Btandard; protein; 548 AA.
Claim 4; Fig 15; 519pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 VTEENKELANELR 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 61.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ILEENKELENALK 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 546 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADN02474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 33
ADN02474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , 유
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AAU02915 standard; protein; 546 AA.

RESULT 32

AAU02915

AAU02915

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1 ILEENKELENALK 13

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The sequence represents an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor 1C, cellular tumnour antigen PS3, and vasoactive intestinal colypeptide receptor 2. The polypeptides and their associated nucleic caids are useful for identification of variant sequences and detection of candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various can disorders including cardiovascular diseases such as arteriosclerosis, myocardial infarction and coronary arterial thrombosis, renal diseases such as diabetic nephropathy, muscular diseases such as hypertrophy, immune disorders such as immune complex nephritis, multiple sclerosis, cancer, sarcoidosis, nonarcoidotic pulmonary granulomatous diseases such as assestosis and vascular pathologies involving an endothelial
                                                                                                                                                                                                                                                                                                                               Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; destruction; pathogen tolerance; herbicide tolerance; extreme esmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 42; DB 4; Length 555
Pred. No. 4.4e+02;
2; Mismatches 3; Indels
                                                                                                                                                                                                           Levine Z, David A, Azar I, Khosravi R, Bernstein J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plant full length insert polypeptide segid 64494.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADY08679 standard; protein; 625 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Fig 14; 519pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67.7%;
61.5%;
                                          17-NOV-2000; 2000WO-IL000766.
                                                                                        99IL-00132978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : ||||| | |:
301 VTEENKELANELR 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-APR-2005 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ILEENKELENALK 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                   (COMP-) COMPUGEN LTD
                                                                                                                                                                                                                                                                WPI; 2001-336004/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 8; Conserv
                                                                                                                                                                                                                                                                                    N-PSDB; AAS06014.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 555 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US2004034888-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein content
                                                                                          17-NOV-1999;
10-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-FEB-2004.
25-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADY08679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADY08679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      XBXBXBXBXBXBXBXXBXXBXXBXXBXXBX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to a novel recombinant adenovirus vector mediated anti-neoplastic composition is prepared through cloning the cDNA sequence from the human peripheral blood cell by specific primer and reverse transcription-polymerase chain reaction (RT-PCR) method for coding TSF polypeptide, construction in human embryonic kidney cell 293 by AdRasy system, and packaging and expressing the recombinant adenovirus vector of TSF. It can suppress the growth and transfer of cancer. The present sequence represents the TSF polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Angiotensin converting enzyme splice variant; ACEV; interleukin 6; granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C; vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; myocardial infarction; coronary arterial thrombosis; renal disease; diabetic nephropathy; muscular disease; immune disorder; sarcoidosis; multiple sclerosis; immune complicitis; deep vein thrombosis; nonarcoidotic pulmonary granulomatous disease; endothelial abnormality; vascular disorder; asbestosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tumor suppressing polypeptide TSF and gene therapy vector composition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Angiotensin converting enzyme (ACEV) splice variant protein #14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                        adenovirus vector; anti-neoplastic; TSF polypeptide; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67.7%; Score 42; DB 7; Length 548; 61.5%; Pred. No. 4.4e+02; ive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  (TAID-) TAIDA LIFE SCI TECH RES CENT HEMATOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; SEQ ID NO 1; 13pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU02914 standard; protein; 555 AA.
                                                                                                                                                                                                                                                                                                                  21-AUG-2002; 2002CN-00129408
                                                                                                                                                                                                                                                                                                                                                                  21-AUG-2002; 2002CN-00129408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : |||||| |:
301 VTEENKELANELR 313
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                         17-JUN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ILEENKELENALK 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-469302/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; ADN02475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 548 AA;
                                                                           TSF polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ното варіеля
                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-SEP-2001
                                                                                                                                                                                                                   CN1401387-A.
                                                                                                                                                                                                                                                                     12-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU02914;
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Query Match

RESULT 34 AAU02914

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Han Z,

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**Gaps** 

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Length 555;

Azar I, Khosravi R, Bernstein J;

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Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies.
                                                                                                                                                                                                                                                                                                                                          Claim 4; Fig 13; 519pp; English.
                                                                                                  17-NOV-2000; 2000WO-IL000766.
                                                                                                                                99IL-00132978.
99IL-00133455.
                                                                                                                                                                            (COMP-) COMPUGEN LTD
                                                                                                                                                                                                          David A,
                                                                                                                                                                                                                                      WPI; 2001-336004/35
                                                                                                                                                                                                                                                     N-PSDB; AAS06013.
                                         WO200136632-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
             Homo sapiens.
                                                                                                                                 17-NOV-1999;
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                                                                                                                                              10-DEC-1999;
                                                                       25-MAY-2001
                                                                                                                                                                                                          Levine Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB00042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB00042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠ
                                                                                                                                                                                                                                                                                                                                        The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at t. E. pseqdata.uspto.gov/sequence.html?DocID:2004014888. The polynucleotide of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme campoints, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing glaactomannan, increased resistance to plant disease, for producing glaactomannan, increased resistance to plant disease, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This is the amino acid sequence of a plant full length insert polypeptide that can be used in the recombinant DNA construct of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                    New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Angiotensin converting enzyme splice variant; ACEV; interleukin 6; granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen P53; cyclin-dependent kinase inhibitor IC; vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; myocardial infarction; coronary arterial thrombosis; renal disease; diabetic nephropathy; numscular disease; immune disorder; sarcoidosis; numltiple sclerosis; immune complex nephritis; deep vein thrombosis; nonarcoidotic pulmonary granulomatous disease; endothelial abnormality; vascular disorder; asbestosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Angiotensin converting enzyme (ACEV) splice variant protein #13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67.7%; Score 42; DB 8; Length 625;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                              Screen SE, Tabaska JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 5e+0
2; Mismatches
                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 64494; 15pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU02913 standard; protein; 731 AA.
                                                                                                                                                                                Zhou Y, Kovalic DK,
   28-APR-2003; 2003US-00425114
                              06-MAY-1999; 99US-00304517.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :||| |||| :|
432 VLEEKAELENRMK 444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ILEENKELENALK 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                     KOVALIC D K.
SCREEN S E.
TABASKA J E.
                                                                                                                                                                                                             WPI; 2004-180133/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                      improving yield.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 625 AA;
                                                                                                                                                  CAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU02913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                    (TABA/)
(CAOY/)
                                                                                                                        SCRE/)
                                                                                                         KOVA/)
                                                                                                                                                                                Liu J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
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The sequence represents an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor 1c, cellular tumour antigen P53, and vasoactive intestinal colypeptides and their associated nucleic acids are useful for identification of variant sequences and detection of candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various disorders including cardiovascular diseases such as arteriosclerosis, myocardial infarction and coronary arterial thrombosis, renal diseases such as diabetic nephropathy, muscular diseases such as hypertrophy, cumune disorders such as immune complex nephritis, multiple sclerosis, cancer, sarcoidosis, nonarcoidotic pulmonary granulomatous diseases such as asbestosis and vascular pathologies involving an endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TSP-1; TSP-2; COMP; cartilage oligomeric matrix protein; thrombospondin; angiogenesis; tumour; treatment; cancer; arthritis; psoriasis; diabetic retinopathy; corneal graft rejection; glaucoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67.7%; Score 42; DB 4; Length 731; 61.5%; Pred. No. 6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361. .416
/label= Type 1 repeat region
417. .473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   abnormality such as deep vein thrombosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB00042 standard; protein; 1152 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human thrombospondon-1 (TSP-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 VTEENKELANELR 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ILEENKELENALK 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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New nucleic acids are described which encode a protein comprising the second and third type 1 repeats of human TSP (thrombospondin)-1, but not the TGF (transforming growth factor)-beta activation region of human TSP-1. The nucleic acid of TSP (thrombospondin)-1 containing the second and third type-1 repeats and the COMP (cartilage oligomeric matrix protein) assembly sequence (COMP/TSP-1) was produced by PCR (polymerase chain creation). Expression of COMP/TSP-1 caused inhibition of the growth of tumours in mice models. Thus the nucleic acids and proteins may be useful for treating angiogenesis related diseases such as cancer (by reducing the rate of growth and size of tumours), arthritis, psoriasis, diabetic retinopathy, corneal graft rejection, and glaucoma. They may also be used for treating human immunodeficiency virus (HIV) infection. Anti-angiogenic therapy has little toxicity, does not require the therapputic angiogenic therapp has little toxicity, does not require the therapputic tumour growth independently of growth of tumour cell heterogeneity, and cons induce drug resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thrombospondin-1; TSP-1; cytostatic; angiogenesis; vasotropic; vulnerary; neovascularisation; cell proliferation inhibitor; cancer; solid tumour; haemangioma; acoustic neuromas; neurofibroma; trachoma; acoustic neuromas; are neurofibroma; trachoma; pyogenic granulomas; rheumatoid arthritis; ocular angiogenic disease; retinopathy; psoriasis; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; rebeosis; angiofibroma; obler-webber syndrome; myocardial angiogenesis; haemophilac joints; plaque neovascularisation; telangiectasia; wound granulation; apoptosis.
                                                                                                                                                                                                                                 Nucleic acids encoding chimeric proteins such as cartilage oligomeric matrix protein (COMP)/thrombospondins (TSP)-1 and 2, useful for inhibiting angiogenesis and treating diseases such as cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67.7%; Score 42; DB 3; Length 1152; 61.5%; Pred. No. 9.7e+02; ive 2; Mismatches 3; Indels
/label= Type 1 repeat region 474. .530 /label= Type 1 repeat region
                                                                                                                                                        (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU74771 standard; protein; 1152 AA.
                                                                                                                                                                                                                                                                                      Disclosure; Fig 1; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human thrombospondin-1 (TSP-1).
                                                                                                     01-FEB-2000; 2000WO-US002482
                                                                                                                              99US-0118053P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 61.5%;
les 8; Conservative
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283 VTEENKELANELR 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ILEENKELENALK 13
                                                                                                                                                                                                          WPI; 2000-514823/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1152 AA;
                                                   WO200044908-A2
                                                                                                                              01-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-APR-2002
                                                                            03-AUG-2000
                                                                                                                                                                                   Lawler JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU74771;
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                Region
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Homo sapiens

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The invention describes a composition comprising cDNA encoding fragments of human thrombospondin-1 (TSP -1), a type 1 repeat polypeptide and potent inhibitor of tumour growth and angiogenesis. The composition is useful for killing cancerous cells (preferably tumour); for reducting volume or inhibiting growth of a tumour (inhibiting neovascularisation in the tumour); for decreasing proliferation of tumour cells; in the treatment of diseases and conditions associated with angiogenic activity or misregulated growth and angiogenesis-mediated diseases such as cancer, solid tumour, tumour metastasis, benign tumour, (e.g. heemangioms, neurofibroms, trachoms, and pyogenic granuloms), rheumatoid arthritis, psoriasis, ocular angiogenic diseases (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               698. 325
/label= Type_3_repeat_domain
/note= "This region contains 7 type 3 repeats, from
residues 698-733, residues 734-756, residues 757-792,
residues 793-815, residues 816-853, residues 854-889 and
residues 890-925"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Composition useful for treatment of cancer comprises cDNA encoding amino acids of human thrombospondin-1 or its conservative variant and a
                                                                                                                                            361..530
/label= Type_1 repeat_domain
/note= "This region contains 3 type 1 repeats, from
residues 361-416, residues 417-473 and residues 474-530"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ĕ
                                                                                                                                                                                                                                                                                                                                                'note= "Necessary and sufficient for activation ransforming growth factor beta (TGF beta)"
                                                                                                                                                                                                                                                                                                                                                                                                      118. .423
/label= TGF-beta_and_fibronectin_binding_domain
/ncte= "Transforming growth factor"
                                                                                              /label= Procollagen homology domain
/note= "Required in Inhibition of anglogenesis"
                            63. .360
|abel= Procollagen_homology_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       164. .370
| Jabel = Heparin_binding_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70. .601
| label= Calcium binding_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heparin_binding_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            label= Heparin_binding_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29. 434
|abel= Cell_binding_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell_binding_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
location/Qualifiers
                                                                                                                                                                                                                                                                                                                            label= RFK motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 7; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-MAY-2000; 2000US-0207994P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAY-2001; 2001WO-US017250.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .491
/label= cr
                                                                            309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-106273/14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   carrier.
       Key
Region
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06-MAR-2001; 2001US-0273573P.
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                               Abdelouahed M;
                                                                             gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                           06-JUN-2001
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                                                                                                                                                                                                                                                                                                                                             AAB74450;
                                                                                                                                                                                                                                                                                                              RESULT 40
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        corneal graft rejection, neovascular glaucoma, retrolental fibroplasias, rebeosis), Osler-Webber syndrome, myocardial angiogenesis, telangiectasia, plaque neovascularisation, haemophiliac joints, angiofibroma or wound granulation. The composition induces apoptosis and inhibits neovascularisation in the tumour cells. This amino acid sequence represents human thrombospondin-1 (TSP-1), on which the recombinant proteins of the invention are based
  diabetic retinopathy, retinopathy of prematurity, macular degeneration,
                                                                                                      Gaps
                                                                                                                                                                                                                                         TSP-1; carrier protein; chimeric; multimerization domain; spacer; therapeutic; gene therapy; human; thrombospondin-1.
                                                                                                     ö
                                                                                     Length 1152;
                                                                                                     Indels
                                                                                                                                                                                                                                                                                         263. .360 .
/note= "Procollagen homology region"
                                                                                      Score 42; DB 5; Le:
Pred. No. 9.7e+02;
2; Mismatches 3;
                                                                                                                                                                                                                           Human thrombospondin-1 (TSP-1) protein sequence.
                                                                                                                                                                                                                                                                                                                                                                             "type 2 repeat"
                                                                                                                                                                                                                                                                                                                                                                                    330. .673 /
/note= "type 2 repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "type 3 repeat"
                                                                                                                                                                                                                                                                                                                                                                                                    674. .697
/note= "type 2 repeat"
698. .733
/note= "type 3 repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    757. .792
/note= "type 3 repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "type 3 repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "type 3 repeat"
                                                                                                                                                                                                                                                                                                                               "type 1 repeat"
                                                                                                                                                                                                                                                                                                                                               "type 1 repeat"
                                                                                                                                                                                                                                                                                                                                                             'note= "type 2 repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                           "type 3 repeat'
                                                                                                                                                                                                                                                                                                                note= "type 1 repeat"
                                                                                                                                                                             ABB82285 standard; protein; 1152 AA.
                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "type 3
                                                                                       67.7%;
61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-MAR-2002; 2002WO-US006882
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "tvr
| 916.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (1)
/note= "tvm"
474.
                                                                                                                                                                                                                                                                                                                                                                 ....629
/note= "tv-
                                                                                                                               : |||||| | |:
283 VTEENKELANELR 295
                                                                                                                                                                                                                                                                                                                                                                                                                                   734. .756
/note= "ty
                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                        .416
                                                                                                                                                                                                                                                                                                                                                      531. .571
                                                                                                                     1 ILEENKELENALK 13
                                                                                                       8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= '858. .86
                                                                                                                                                                                                                                                                                                                                               'note=
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                                                                                     Query Match
Best Local Similarity
                                                                       Sequence 1152 AA;
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                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                            08-JAN-2003
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                                                                                                                                                                              New carrier chimeric protein having a multimerization domain and a spacer
to which at least one drug is attached, useful as therapeutic agent or in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, variant thrombospondin 1; variant thrombospondin 4; SNP; polymorphism; vascular disease; coronary artery disease; forensics; myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Pred. No. 9.7e+02;
2; Mismatches 3; IndelB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (WHED ) WHITEHEAD INST BIOMEDICAL RES.
(MILL-) MILLENNIUM PHARM INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB74450 standard; protein; 1170 AA
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                                                                                                                                                                                                                                                                                                           Example 1; Fig 2; 32pp; English
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26-JUL-2000; 2000US-0220947P.
16-AUG-2000; 2000US-0225724P.
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61.5%;
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283 VTEENKELANELR 295
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Best Local Similarity 61...
8; Conservative
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(ABDE/) ABDELOUAHED M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-226749/23.
N-PSDB; AAF95238.
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Sequence 1170 AA;
        Sequence 1170 AA;
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                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                             30-OCT-2002
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                                                                                                                                                                                       AAE25030;
                                                                                                                                                                                                                                                             Human:
                                                                                                                                         RESULT 42
                                                                                                                                                     AAE2503
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                                                                                      The present invention provides a method of diagnosing a vascular disease in an individual, involving determining the sequence at various polymorphic sites within the human thrombospondin 1 and thrombospondin 4 genes. The sequences at a number of polymorphic sites are also provided in the specification. In particular, the method can be used in the diagnosis of atherosclerosis, myocardial infarction, coronary heart diseases, vertoke, peripheral vascular diseases, venous thromboembolism and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also useful in forensics, paternity testing, genetic analysis and phenotype correlations to diseases. The present sequence is the human variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         shear stress-response protein; vascular disease; arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides the protein and coding sequences of a number of human shear stress response proteins. These are useful in the diagnosis, treatment and screening of vacular diseases caused by arteriosclerosis, including heart failure, post-PTCA restenosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sakurada K;
                                                                                                                                                                                                                                                                                      Gaps
       Nucleic acids comprising single nucleotide polymorphisms, useful in applications such as forensics, paternity testing, medicine, genetic analysis and phenotype correlations to diseases such as diabetes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA sequences, proteins encoded by them and antibodies against useful in diagnosis and treatment of vascular disease caused by
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                                                                                                                                                                                                                                                           Score 42; DB 4; Length 1170;
Pred. No. 9.8e+02;
2; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human shear stress-response protein SEQ ID NO: 100.
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Sugano S;
                                                                                                                                                                                                                                                                                      2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                              AAB90800 standard; protein; 1170 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yoshisue H, Obayashi
skine S, Nakamura Y,
                                                                     Claim 20; Fig 1; 242pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-OCT-2000; 2000WO-JP006840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99JP-00280976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (KYOW ) KYOWA HAKKO KOGYO KK (NOJI/) NOJIMA H.
                                                                                                                                                                                                                                                             67.7%;
61.5%;
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Query Match
Best Local Similarity 61.55,
Best Local Similarity 61.55,
Best Local Similarity 61.55,
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301 VTEENKELANELR 313
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                                                                                                                                                                                                                  thrombospondin 1 protein
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                                                                                                                                                                                                                                       Sequence 1170 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       arteriosclerosis
                                               atherosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200125427-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypertension
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                                                                                                                                                                                                                                                                                                                                                                                                                      AAB90800;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Diagnosing and monitoring a cardiovascular disease in a patient, by assessing the level of thrombospondin protein and/or gene expression in a
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                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       anticoagulant therapy; atherosclerosis; coronary artery disease; MI; myocardial infarction; venous thromboembolism; pulmonary embolism; peripheral vascular disease; congestive heart failure; gene therapy; stroke; TSP-1; single nucleotide polymorphism; SNP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cardiovascular disease; CVD; diagnosis; thrombospondin; TSP;
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                     Length 1170;
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Pred. No. 9.8e+02;
2; Mismatches 3; Indels
                                                                           3; Indels
                                                . 9.8e+02;
                          DB 4;
                                                                           Mismatches
                          Score 42;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human thrombospondin (TSP)-1 protein.
                                                                                                                                                                                                                                                                                                            AAE25030 standard; protein; 1170 AA.
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22-DEC-2000; 2000US-0257417P.
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                     67.7%;
llarity 61.5%;
Conservative
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301 VTEENKELANELR 313
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Best Local Similarity 61..
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8; Conserve
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The invention relates to an Erg (a member of the Ets family of transcription factors) modulator for use in medicine, where the modulator is not tumour necrosis factor-alpha (TNF-alpha) or interleukin-1 (IL-1).

Also included are a method of screening for a drug or drug candidate, involving determining whether or not a group being screened modulates the effect of Erg on secreted protein, acidic, cysteine-rich (Osteonectin/BM-C) (SPARC), thrombospondin (TSP), rho-A (a Ras superfamily member) intracellular adhesion molecule-2 (TCAM-2) and/or von Willebrand Factor (vWF) RNA or polypeptide expression, or expression of heterologous RNA or expression of beterologous RNA or expression of Erg or of Erg RNA in a given expression system, determining whether or not a group being screened modulates the cypeation of Erg RNA in a given expression system, determining whether or not a group being screened modulates binding of Erg to a nucleic acid comprising an Erg binding site, determining whether or not a mucleic acid comprising an Erg binding site, determining whether or not a mucleic acid hybridises with DNA of an Erg gene or its transcription product or determining whether or not a mucleic acid knocks out or confect acid comprising whether or not a mucleic acid hybridises with DNA of an Erg gene or its transcription produces expression of Erg Erg based probes can be used in the diagnosis of a disorder such as a disorder in which angiogenesis is involved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inflammatory disorder, developmental disorder, wound, menstrual disorder involving cell proliferation, a disorder that can be treated by tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      remodeling, cancer, cancer metastasis, rheumatoid arthritis, atherosclerosis, diabetic retinopathy, restenosis, osteoporosis, cataract, diabetes mellitus, glomerulonephritis, inflammatory glomerular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brg, which is not tumor necrosis factor-alpha or interleukin-1, for treating cancer, rheumatoid arthritis, atherosclerosis, restenosis, and
                                                                                                                                                                                                                                                                                                                                                                                                                      menstrual disorder; cancer; rheumatoid arthritis; atherosclerosis; diabetic retinopathy; restenosis; osteoporosis; cataract; diabetes mellitus; glomerulonephritis; inflammatory glomerular disease; vasculitis; retinopathy; liver fibrosis; haemoglobinopathy;
                                                                                                                                                                                                                                                                                                                          Human; Erg; transcription factor; tumour necrosis factor-alpha;
TNF-alpha; interleukin-1 (IL-1); SPARC; thrombospondin; TSP; rho-A;
intracellular adhesion molecule-2; ICAM-2; von Willebrand Factor; vWF;
                                                                                                                                                                                                                                                                                                                                                                                               angiogenesis; inflammatory disorder; developmental disorder; wound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New modulator of a member of the Ets family
                                                                                                                                                                                                                                                                                Human thrombospondin 1, TSP-1, protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 55-58; 75pp; English.
                                                                                                                                   AAU75315 standard; protein; 1170 AA.
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301 VTEENKELANELR 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Crohn's disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        osteoporosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Predicting, diagnosing or prognosing chronic lung disease, by detecting a chronic obstructive pulmonary disease (COPD) gene in a biological sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; chronic obstructive pulmonary disease; COPD; chronic lung disease.
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disease, vasculitis, retinopathy, liver fibrosis, haemoglobinopathy or Crohn's disease. The modulator is useful in the preparation of a medicament for treating a disorder which involves aberrant expression of SPARC, TSP, Tho A, ICAM-2 or WFP. A group that modulates the effect of Brg or a therapeutically active agent is useful for the preparation of medicament for treating the above mentioned disorders. The present sequence is the amino acid sequence of human TSP-1
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                                                                                                                                                                                Length 1170;
                                                                                                                                                                     , DB 5; Lens.
. 9.8e+02;
3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kallabis H, Hall R, Schulze T,
                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human COPD related protein SEQ ID NO:30.
                                                                                                                                                                                   Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 8; Page 120-125; 214pp; English
                                                                                                                                                                                                                                                                                                                                                                                  ABP96780 standard; protein; 1170 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-MAY-2002; 2002WO-EP005835.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-MAY-2001; 2001GB-00013266.
                                                                                                                                                                                 67.7%;
61.5%;
                                                                                                                                                                                                                                                                                        301 VTĖĖNKĖLANELR 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUN-2003 (first entry)
                                                                                                                                                                                                                                                       1 ILEENKELENALK 13
                                                                                                                                                                                   Query Match
Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gehrmann M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2003-140492/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1170 AA;
                                                                                                                                                Sequence 1170 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (FARE ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ACC46751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200297127-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oellers N,
                                                                                                                                                                                                                                                                                                                                                                                                                     ABP96780;
                                                                                                                                                                                                                                                                                                                                                                ABP96780
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Gaps

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Score 42; DB 6; Length 1170; Pred. No. 9.8e+02; 2; Mismatches 3; Indels

67.7%; 61.5%;

Query Match Best Local Similarity

2; Mismatches

1 ILEENKELENALK 13

8

8; Conservative

Matches

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Matches
   RESULT 46
                     ABG74673
                                                                           The present invention relates to methods and compositions for detecting an anglogenesis-associated transcript in a cell in a patient. The method involves contacting a biological sample from the patient with a polynucleotide that selectively hybridises to a sequence at least 80% identical to any of the angiogenesis-associated human polynucleotide sequences given in the specification. These angiogenesis-associated polynucleotide sequences comprise genes that exhibit changes in expression levels as a function of time in tissue undergoing carponesis. The method and the polynucleotide sequences of the invention are useful for diagnosing and treating angiogenesis and angiogenesis-associated diseases e.g. cancer. The polynucleotide sequences are also useful in the gene therapy of such disorders. The sequences are also useful in the gene therapy of such disorders. The sequences are also useful to the gene therapy of such disorders. The sequences are useful as a vaccine for therapeutic and prophylactic immunisation. ABU03456-ABU03569 represent anglogenesis-associated protein sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detecting angiogenesis-associated transcript in a cell for diagnosing and treating cancer by contacting a sample with a polynucleotide that exhibits changes in expression level as a function of time in tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 42; DB 6; Length 1170;
Pred. No. 9.8e+02;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                 Human, anglogenesis-associated transcript, anglogenesis, anglogenesis-associated disease, cancer, cytostatic.
                                                                                                                                                                                                                             Angiogenesis-associated human protein sequence #19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aziz N;
                                                                                                                ABU03474 standard; protein; 1170 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Page 199; 291pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Watson SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (EOSB-) EOS BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-FEB-2001, 2001US-00784356.
22-FEB-2001; 2001US-00791390.
19-APR-2001, 2001US-0285475P.
03-AUG-2001; 2001US-0350666P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-NOV-2001; 2001US-0350666P.
29-NOV-2001; 2001US-0334244P.
                                                                                                                                                                                                                                                                                                                                                                                                                                      14-FEB-2002, 2002WO-US004915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative
: |||||| | |:
301 VTEENKELANELR 313
                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 undergoing angiogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murray R, Glynne R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-040681/03.
N-PSDB; ABX08757.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1170 AA;
                                                                                                                                                                                                                                                                                                                                                              WO200279492-A2.
                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                            21-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                   10-OCT-2002
                                                                                                                                                       ABU03474;
                                                                               RESULT 49
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This invention describes a novel method for identifying a subject as a candidate for a particular course of therapy to treat a vascular disease or disorder. The method comprises determining the identity of the nucleotide present at specific positions, or their complements, and identifying the subject as a candidate for a particular clinical course of therapy based on the identity of the nucleotide present in that specific position. The method can be used for identifying a subject who is a candidate for further diagnostic evaluation of a vascular disease or disorder and selecting a clinical course of therapy. The products of the invention have cardiant, antiateriosclerotic and cerebroprotective cinvention have cardiant, antiateriosclerotic and cerebroprotective activity and can be used for gene therapy. The methods disclosed are activity and can be used for gene therapy. The methods disclosed are cartery disease, myocardial infarction, ischaemia, stroke, peripheral coursel in a fingerprint for detecting different individuals watchin the same species applicable in forensic studies and paternity cesting. This sequence represents the human THBSI gene represented in course invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying a subject as a candidate for a particular course of therapy to treat a vascular disease or disorder, e.g. stroke, myocardial infarction or ischemia by determining the identity of the nucleotide
                                                                                                                                                                                                                                                                                              Human; THBS1; vascular disease; cardiant; antiarteriosclerotic; stroke; cerebroprotective; gene therapy; coronary artery disease; ischaemia; myocardial infarction; peripheral vascular disease; pulmonary embolism; venous thromboembolism; forensic; paternity testing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67.7%; Score 42; DB 6; Length 117
61.5%; Pred. No. 9.8e+02;
tive 2; Mismatches 3; Indels
ABG74673 standard; protein; 1170 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 12; 568pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present at specific positions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-AUG-2001; 2001US-0313097P.
05-OCT-2001; 2001US-0327485P.
14-DEC-2001; 2001US-00020141.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-AUG-2002; 2002WO-US026343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : ||||| | |:
301 VTEENKELANELR 313
                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ILEENKELENALK 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mccarthy J, Ableson A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (VITI-) VITIVITY INC
                                                                                                                                                                                                                               Human THBS1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-300617/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1170 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ABQ77405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2003016494-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                     10-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-FEB-2003.
                                                                              ABG74673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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RESULT 47

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Gaps . 0

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1 ILEENKELENALK 13

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AAE36228

07-AUG-2003

single

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New nucleic acid molecule comprising first nucleic acid sequence encoding at least one CD36 binding domain, and a second nucleic acid sequence encoding at least one immunogenic amino acid sequence, useful for eliciting immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid molecule encoding an immunogenic chimeric polypeptide. The isolated nucleic acid molecule comprises at least a first nucleic acid sequence encoding at least one immunogenic amino acid sequence, where the introduction of the nucleic acid molecule in a cell results in expression of the immunogenic chimeric polypeptide. The nucleic acid molecule is useful for eliciting an immune response. The present sequence represents a human thrombospondin 1 (TSP1) polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; differential expression; cancer; angiogenic disorder; fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis; inflammatory disease; autoimmune disease; retinal neovascularistaion syndrome; scarring; uterine fibroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C222
            ISP1; immunogenic; CD36; immunomodulator; vaccine; gene therapy;
immune response; human; thrombospondin 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1170;
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Pred. No. 9.8e+02
                                                                                                                                                                                                          447. .452
/note= "CD36 binding domain"
504. .511
/note= "CD36 binding domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                   l. .31
'note= "signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADN39852 standard; protein; 1170 AA.
                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Fig 1A; 59pp; English.
                                                                                                                                                                                          /note= "mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Goebel
                                                                                                                                                                                                                                                                                                                                                                                          12-DEC-2002; 2002WO-US039885.
                                                                                                                                                                                                                                                                                                                                                                                                                                 12-DEC-2001; 2001US-0341771P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.7%;
61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 VTEENKELANELR 313
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                                                                                                                                                                      .1170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AVET ) AVENTIS PASTEUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alexander JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-513975/48.
N-PSDB; ACC84978.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1170 AA;
                                                                                                                                                                                                                                                                                                             WO2003050268-A2.
                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                    19-JUN-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADN39852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cox WI,
                                                                                                                                 Peptide
                                                                                                                                                                        Protein
                                                                                                                                                                                                                Domain
                                                                                                                                                                                                                                                       Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention is based at least in part on the discovery of polymorphisms within the thrombospondin 1 (THBS1) or THBS4 genes. The invention also provides a nucleic acid comprising allelic variant of polymorphic region of THBS1 or THBS4 gene. The method is useful for identifying a subject as a candidate for a particular clinical course of therapy or to treat a vascular disease or disorder and for selecting a clinical course of therapy to treat a subject who is at risk for developing a vascular disease or disorder. The present sequence is human THBS1 reference protein. Note: This sequence is said to be encoded by SEQ ID NO: 1 (AADS5693). However this does not appear to be the case
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated nucleic acid comprising allelic variant of polymorphic region of thrombospondin 1 or 4 gene, useful for identifying predisposition of subject to develop vascular disease associated with the allelic variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                           /note= "This residue is changed to Ser during single nucleotide polymorphism (SNP)"
                                                                                                                                                       vascular disease; therapy; SNP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 6; Length 1170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67.7%; Score 42; DB 6; Length 117
61.5%; Pred. No. 9.8e+02;
ive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (VITI-) VITIVITY INC. (WHED ) WHITEHEAD INST BIOMEDICAL RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABR62059 standard; protein; 1170 AA.
  AAE36228 standard; protein; 1170 AA.
                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Fig 2; 338pp; English.
                                                                                                                                                     thrombospondin 1; THBS1; nucleotide polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human thrombospondin 1 (TSP1)
                                                                                                                 Human THBS1 reference protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-SEP-2001; 2001US-0317033P.
17-OCT-2001; 2001US-0330248P.
14-DEC-2001; 2001US-00017721.
                                                                                                                                                                                                                                                                                                                                                                                                                                     04-SEP-2002; 2002WO-US028281
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                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Daley G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-312992/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1170 AA;
                                                                                                                                                                                                                                                           Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                          WO2003020120-A2
                                                                                                                                                                                                                  Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-OCT-2003
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Mccarthy J,

13-MAR-2003

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Gaps

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ABR62059;

BXXXXB

RESULT 48 **ABR62059** 

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RESULT 50

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The invention relates to nucleic acids and proteins (ADN38683-ADN40064)

whose expression is upregulated or downregulated in specific cancers or other diseases such as angiogenic or fibratic disorders, and to methods of determining the presence or absence of a pathological cell in a conferenting the presence or absence of a pathological cell in a conferenting the presence or absence of a pathological cell in a conferenting a nucleic acid at least 80% identical to those of the invention or by detecting a polypeptide of the invention. The conclet acid of the invention, antibodies which specifically bind a conclet acid of the invention, use of such antibodies for drug targeting; and methods of screening for modulators of activity or expression of the polypeptides and nucleic acids. The nucleic acids, polypeptides, antibodies and methods are useful for diagnosing, prognosing and treating cancer and other conditions such as psoriasis, ischaemia, heart disease, attentable acids inflammatory diseases, autonimune diseases, ratinal neovascularistation syndromes, scarring and uterine fibroids. They may also be useful in wound healing and in contraception. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.
detection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; vulnerary; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glynne R, Hevezi PA;
3, Zlotnik A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gish KC, Gly
Wilson KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 12; SEQ ID NO C222; 1385pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aziz N, Ginsburg WM,
Murray R, Watson SR,
                                                                                                                                                                                                         2001US-0350666P.
2001US-0332464P.
2001US-0334393P.
2001US-0335394P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (EOSB-) EOS BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                                                               10-JAN-2002; 2002US-0347349P.
08-FEB-2002; 2002US-0355250P.
13-FEB-2002; 2002US-0356714P.
20-FEB-2002; 2002US-0359077P.
                                                                                                                                                                                                                                                                               2001US-0340376P.
2002US-0347211P.
                                                                                                                                                                                                                                                                                                                                                                                     2002US-0368809P.
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                                                                                                                                                                          2002WO-US036810
                                                                                                                                                                                                                                                                                                                                                                                                     2002US-0370110P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2003-468649/44.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aziz N,
                                                                                                          WO2003042661-A2.
                                                                                                                                                                                                                                                                               14-DEC-2001;
08-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                                                     29-MAR-2002;
04-APR-2002;
                                                                       Homo sapiens
                                                                                                                                                                          13-NOV-2002;
                                                                                                                                                                                                                             21-NOV-2001;
29-NOV-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                       12-APR-2002;
                                                                                                                                            22-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Afar D, 1
Mack DH,
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The present invention describes a method of testing for bronchial asthma or chronic obstructive pulmonary disease. The method comprises determining the expression level of a marker gene in a biological sample from a biological sample from a subject, comparing the expression level determined with the expression level of the marker gene in a biological sample from a healthy cubicity pulmonary disease. The marker gene comprises: (a) a group of genes (S1) whose expression levels increase when respiratory epithelial colls are stimulated with interleukin-13; or (b) a group of genes (S2) whose expression levels discrease when respiratory epithelial colls are stimulated with interleukin-13. Also described: (1) a reagent (1) for testing for bronchial asthma or chronic obstructive pulmonary disease; (2) a kit for screening for a candidate compound for a therapeutic agent to treat bronchial asthma or chronic obstructive pulmonary disease; (4) an inducer that induces bronchial asthma or chronic obstructive pulmonary disease; (4) an inducer that induces bronchial asthma or chronic obstructive pulmonary disease; (c) asthma or chronic obstructive pulmonary disease; (b) a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease, (c) a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease, (c) a marker gene, a ribozyme, a polynucleotide that suppresses the expression of the gene through an RNAi effect or an antibody recognising conchial asthma or a chronic obstructive pulmonary disease, on which a probe has been immobilised to assay a marker gene, and can be used in gene therapy. The method is useful for testing for or screening for a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease. The present cy sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Testing for bronchial asthma or chronic obstructive pulmonary disease by comparing the expression level of a marker gene in a biological sample from a subject with the expression level of the gene in a sample from a
                                                                                                                                                                                   bronchial asthma; chronic obstructive pulmonary disease; respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic; gene therapy; marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Izuhara K;
                                                                                                                                             Marker gene related amino acid sequence SEQ ID NO:548.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nagai H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 11; SEQ ID NO 548; 241pp; English.
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                    ADJ75296 standard; protein; 1170 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-AUG-2002; 2002JP-00229312.
20-MAR-2003; 2003JP-00077212.
                                                                                                                                                                                                                                                                                                                                                                                                           04-AUG-2003; 2003EP-00254857.
                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GENO-) GENOX RES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ohtani N, Sugita Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-193155/19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       healthy subject.
                                                                                                                                                                                                                                                                                                                          EP1394274-A2.
                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                    03-MAR-2004.
                                                                                                         20-MAY-2004
                                                              ADJ75296;
ADJ75296
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Length 1170;

Score 42; DB 8; Pred. No. 9.8e+02;

67.7%; 61.5%;

Query Match Best Local Similarity

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Gaps .

Score 42; DB 7; Length 1170; Pred. No. 9.8e+02; 2; Mismatches 3; Indels

67.7%; 61.5%;

Best Local Similarity

Query Match Matches

301 VTEENKELANELR 313 1 ILEENKELENALK 13 8; Conservative

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Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          New purified thrombospondin fragment extracted from a body fluid, useful for diagnosing cancer e.g. adenoma, adenocarcinoma, carcinoma, lymphoma or leukemia or as calibrators, indicators, immunogens and analytes.
 Gaps
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 Indels
                                                                                                                   Human; thrombospondin-1; epitope; cancer; diagnosis.
                                                                                                                                                                                                                                              = Interchain_disulfide_bonds
                                                                                                                                                                                                                                                                        "Collagen V binding region"
                                                                                                                                                                                                                                "Fibrinogen binding region"
 <u>ښ</u>
                                                                                                                                                                                                      "Heparin binding region"
                                                                                                                                                                                                                   "Heparin binding region"
                                                                                                                                                                                                                                                     181. .378
| label = Procollagen_homology
 Mismatches
                                                                                                                                                                                                                                                                                                            16. .943
|abel = Type-III_repeats
                                                                                                                                                                                                                                                                                                    - Type-II_repeats
                                                                                                                                                                    9. .1170
| label= Thrombospondin-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 38; 76pp; English.
                                                                                                                                                                                                                                                                                       Type-I_repeats
                                                                                                                                                       . . 18
|abel= Signal_peptide
                                                              ADL70639 standard; protein; 1170 AA.
                                                                                                                                               .ocation/Qualifiers
                                                                                                                                                                                       = N-terminal
                                                                                                                                                                                                                                                                                                                         )44. .1170
/label = C-terminal
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                                                                                                                                                                                                                                                                                                                                                                                      23-AUG-2002; 2002US-0405494P.
21-APR-2003; 2003US-00419462.
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/label = 7
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548.
/label = 7
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301 VTEENKELANELR 313
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/note= ""5
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              1 ILEENKELENALK 13
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 8; Conservative
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                                                                                                       Human thrombospondin-1
                                                                                                                                                                                                                                                                                                                                                                                                           (WILL/) WILLIAMS K J.
                                                                                                                                                                                                                                                                                                                                                                                                                                             REFSEQ, NP 003237.1.
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                                                                                                                                                                                                                                                                                                                                                                                                                         Williams KJ;
                                                                                                                                   Homo sapiens
                                                                                         20-MAY-2004
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                                                                            ADL70639;
                                                                                                                                                      Peptide
                                                                                                                                                                    Protein
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                                                 RESULT 51
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mol.wt.) found in plasma, and their use in clinical assays for cancer and for generation of antibodies and other binding agents. A method that distinguishes TSP from a TSP fragment or portion involves: (1) using an epitope shared by TSP and the TSP fragment or portion involves: (1) using an epitope shared by TSP and the TSP fragment or portion of TSP plus TSP plus TSP fragment or portion; (2) using an antibody, to obtain a quantitation of TSP plus TSP fragment or portion; (2) using the difference between (1) and (2) as a quantitation of the amount of TSP fragment or portion. Suitable epitopes are provided ADL70602-

CC using the difference between (1) and (2) as a quantitation of the amount of TSP fragment or portion is performed in order to detect the presence, or monitor the course, of a close or condition selected from cancer, renal failure, renal disease, of a close or ordition selected from cancer, renal failure, renal disease, close architels, vasculitis, acute vasculitis, renal allograft, asthma, close architels, rename to the TSP fragment or portion is performed in order to detect the presence, or monitor the course, of a close acutivitis, vasculitis, vasculitis, juvenile returnatomyositis, polyarteritis nodosa, systemic lupus erythematoctay. CC dermatomyositis, polyarteritis nodosa, systemic lupus erythematocty condition, a condition associated with intravascular condition, a condition associated with nother activation, a condition associated with products on and/or release of thrombospondin and/or a thrombospondin or condition, intravascular coagulation, extravascular coagulation, intravascular coagulation, a condition associated with a cryoglobulin, and condition associated with a cryoglobulin, and condition associated with a cryoglobulin, and condition associated with a cryoglobulin, and a condition associated with a cryoglobulin, and a condition associated with a cryoglobulin, and a condition associated with a cryoglobulin, and a condition associated with a cryoglobulin, and endocarround and and an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tissue, endodermal tissue, a teratoma, a poorly-differentiated cancer, a well-differentiated cancer, a moderately differentiated cancer, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a cancer with vascular invasion, internal cancer, skin cancer, cancer of the respiratory system, circulatory system, musculoskeletal system, nuascle, bone, a joint, tendon or ligament, digestive system, liver or biliary system, nances, k.a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           biliary system, pancreas, head, neck, endocrine system, reproductive system (male or female), genitourinary system, kidney, urinary tract, sensory system, nervous system, lymphoid organ, blood, a gland, mammary gland, prostate gland, endometrial tissue, mesodermal tissue, ectoderma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 9.8e+02;
2; Mismatches 3; Indels
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61.5%;
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301 VTEENKELANELR 313
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Best Local Similarity 61.5.
Best Local 8; Conservative
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WO2004056386-A2

08-JUL-2004

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Microvaecular permeability-modifying disorder;

Microvaecular permeability-modifying disorder;

Microvaecular permeability-modifying disorder;

Alzhelmer's disease; vascular-related dementia;

Alzhelmer's disease; bovine spongiform encephalopathy;

Microvaecular permeability multiple seclerosis;

Microvaecular disease; bovine spongiform encephalopathy;

Microvaecular disorder; septic shock; hepatic encephalopathy;

Microvaecular disorder; depression; autism; schizophrenia; psychosis;

Microvaecular disorder; depression; autism; schizophrenia; psychosis;

Microvaecular disorder; proliferative vitreoretinopathy;

Microvaecular disease; mountain sickness; ALDS-related dementia;

Microvaecular disease; proliferative vitreoretinopathy;

Microvaecular disease; proliferative vitreoretinopathy;

Microvaecular disease; phonomenon; inflammacory vascularisation;

Microvaecular disease; Approxemention;

Microvaecular disease; phonomenon; inflammacory vasculitides;

Microvaecular disease; phonomenon; aneurysm; arterial restenosis;

Microvaecular disease; phonomenon; aneurysm; arterial restenosis;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a novel method for identifying a compound that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying a compound that modulates angiogenesis for treating e.g., cancer comprises contacting the compound with a nucleic acid or polypeptide and determining the functional effect of the compound upon the nucleic acid or polypeptide.
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Pred. No. 9.8e+02;
2; Mismatches 3; Indels
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02-SEP-2003; 2003WO-US027523.
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                                                                                                 30-AUG-2002; 2002US-00231956
                                                                                                                                                                                                                                                                                                                   Lorens JB, Bogenberger J,
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301 VTEENKELANELR 313
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Best Local Similarity 61.5.
Best Local 8; Conservative
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                                                                                                                                                                                                             (RIGE-) RIGEL PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-239116/22.
N-PSDB; ADL35873.
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This sequence represents thrombospondin 1 encoded by the TH881 gene. This protein supregulated in BCEC (brain capillary endochelial cells) by protein sequence may be used in the enclod of the invention for modulating the permeability of the invention for modulating the permeability of the invention for modulating the permeability of the invention for modulating the permeability of the invention for modulating the permeability of the invention for modulating the permeability of the activity or the steady-state level of a pro-barrier (PB) polypeptide amino acid sequence elected from ADO26047AD02605AAD02605AAD02605AAD02605AAD02605AAD02605AAD02605AAD02605AAD02605AAD02605AAD02605AAD02605AAD02605AAD02605AAD02605AAD02605AAD02605AAD02605AAD02605AAD02605AAD02605AAD02605AAD02605AAD02605AAD02605AAD02605AAD02605AAD02605AAD02605AAD02605AAD02605AAD02605AAD02605AAD02605AAD02605AAD02605AAD02605AAD02605AAD02605AAD02605AAD02605AAD02605AAD02605AAD02606AAD02605AAD02606AAD02605AAD02606AAD02606AAD02606AAD02606AAD02606AAD02606AAD02606AAD02606AAD02606AAD02606AAD02606AAD02606AAD02606AAD02606AAD02606AAD02606AAD02606AAD02606AAD02606AAD02606AAD02606AAD02606AAD02606AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02609AAD02600AAD02600AAD02600AAD02600AAD02600AAD02600AAD
                                                                                                                                                                                                                                                                                                                           Modulating the permeability of endothelial cells, useful for treating or preventing e.g. neurodegenerative disorders, comprises altering in the endothelial cells the activity or the steady-state level of a pro-barrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  reperfusion injury, angina, myocardial infarctions, chronic heart conditions, or osteoporosis). The PB polypeptide may also be used in the manufacture of a composition for reversibly increasing the microvascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Pred. No. 9.8e+02;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 24; 222pp; English.
                                                                                                                                                                                                                                        Brink A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67.7%;
61.5%;
                                                                                19-DEC-2003; 2003WO-NL000915.
                                                                                                                            19-DEC-2002; 2002EP-00080503
25-APR-2003; 2003US-0465234P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 61.5
les 8; Conservative
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                                                                                                                                                                                                                                        Gaillard PJ,
                                                                                                                                                                                                                                                                                                                                                                                                  polypeptide.
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Best Local S
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g

sapiens

Homo

Length 1170;

antiarthritic;

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The present invention describes an isolated PRO nucleic acid (1). Also described: (1) a vector comprising (1); (2) a host cell comprising the vector of (1); (3) a process for producing a PRO polypeptides; (4) an isolated PRO polypeptide; (5) a chimeric molecule comprising the composition of matter comprising a polypeptide of (4); (7) a composition of matter comprising a polypeptide of (4); (7) a composition of matter comprising a polypeptide of (4); (7) a composition of matter comprising a polypeptide of (4); (7) a comprising a container, a label on the container and a composition of matter of (1); (9) a method of treating an immune related disease in a command; (10) a method for determining the presence of a PRO polypeptide in a sample suspected of having the polypeptide; (11) a method of disease or an inflammatory immune response in mammal; (12) a method of identifying a compound that inhibits or minics the activity of or expression of a gene encoding a PRO polypeptide; and (13) a method of simulating the immune response in a mammal. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New PRO polynucleotides and polypeptides, useful in useful in diagnosing and treating an immune related disease, e.g. systemic lupus erythematosus, rheumatoid arthritis, diabetes mellitus or asthma and in stimulating an immune response.
                                                                                                                                                                                                                                              haemostatic; hepatotropic; immunostimulant; immunosuppressive; muscular; nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRO sequences have antiallering antianaemic, antiarthritic, antiasthmatic, antidiabetic, antiantantory, antipsoriatic, antiathmatic, antityroid, CNS, dermatological, gastrointestinal, haemostatic, hepatotropic, immunostimulant, immunosuppressive, muscular, nephrotropic, neuroprotective, osteopathic, respiratory, vasotropic and virucide activities, and can be used in gene therapy. The nucleic acid (1) and the encoded polypeptides, compositions, kits and methods are
                                                                                                                                                          human; PRO; immune related disease; inflammatory immune response; immune response stimulation; antiallergic; antianaemic; antiarthrit antiasthmatic; antidiabetic; antiinflammatory; antipsoriatic; antirheumatic; antithyrold; CNS; dermatological; gastrointestinal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gurney AL, Schoenfeld J, Williams PM;
                                                                                                                        protein sequence SEQ ID NO:155.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 155; 3009pp; English.
ADP54179 standard; protein; 1170 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-OCT-2003; 2003WO-US034381.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-OCT-2002; 2002US-0422472P.
                                                                                 (first entry)
                                                                                                                                                                                                                                                                                             virucide; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clark H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GETH ) GENENTECH INC
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Wood WI, Wu TD;
                                                                                                                                                                                                                                                                                                                                                                            WO2004039956-A2
                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                 18-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                       13-MAY-2004
                                                                                                                          Human PRO
                                          ADP54179;
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useful in diagnosing and treating an immune related disease and in stimulating an immune response. The present sequence represents a human PRO protein from the present invention.

Sequence 1170 AA;

Life inversion creates to a novel method for the comprises detecting a single nucleotide polymorphism (SNP) in any one of comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification; in the individual's nucleotide acids, where the presence of the SNP is correlated with an altered risk for myocardial infarction in the individual. The invention altered risk for myocardial infarction in the individual. The invention cates comprises; an isolated nucleic acid molecule comprising at least of contiguous nucleotides where one of the nucleotides is an SNP given in the specification or its complement and encoding any one of the amino acid sequences given in the specification, an amino acid sequence given in the specification, an amino acid sequence given in the specification, an amino acid sequence given in the specification and which is between about 16 and 1000 nucleotides in specification and which is between about 16 and 1000 nucleotides in conprising the conclete acid molecule; a method of detecting a variant polypeptide; and a nucleic acid molecule; a method of detecting a variant polypeptide; and a myocardial infarction. The novel detection method has cardiant activity. The nucleic acids of the invention may be used in gene therapy. The method is useful in identifying an individual who has an increased or method is useful in identifying an individual who has an increased or method is useful in identifying an individual who has an increased or method is useful in identifying an individual who has an increased or method is useful in identifying an individual who has an increased or method is useful in identifying an individual who has an increased or method is useful and an increased or method is useful and an increased or method is useful and an increased or method is useful and an increased or method is useful and an increased or method is useful and an increase and an increase and an increased or method is useful and an increase and an increase and composition for treating or preventing myocardial infarction. This sequence represents the protein of a human myocardial infarctionassociated gene containing one or more SNP's of the invention. Note: This Human myocardial infarction-associated gene derived protein, SEQ ID 1021. the invention relates to a novel method for identifying an individual who Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in the individual's nucleic acids. Myocardial infarction; detection; single nucleotide polymorphism; SNP; decreased risk for developing myocardial infarction and for preparing composition for treating or preventing myocardial infarction. This Gaps ö Score 42; DB 8; Length 117 Pred. No. 9.8e+02; ; Mismatches 3; Indels Claim 10; SEQ ID NO 1021; 145pp; English. Iakoubova 0; ADQ39358 standard; protein; 1170 AA cardiant; gene therapy; human. 20-DEC-2002; 2002US-0434778P. 10-MAR-2003; 2003US-0453135P. 30-APR-2003; 2003US-0466112P. 23-SEP-2003; 2003US-0504955P. 22-DEC-2003; 2003WO-US040978. 67.7%; 61.5%; 301 VTEENKELANELR 313 (first entry) 1 ILEENKELENALK 13 Conservative Devlin JJ, (APPL-) APPLERA CORP WPI; 2004-533949/51. Query Match Best Local Similarity N-PSDB; ADQ38530. WO2004058052-A2. Homo sapiens. 18-NOV-2004 15-JUL-2004. 8 Cargill M, ADQ39358; Matches RESULT 55 ADQ39358 ò 셤

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ADQ39355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single nuclectide polymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual's nucleic acids, where the presence of the SNP is correlated with an altered risk for myocardial infarction in the individual's cureled risk for myocardial infarction in the individual. The invention altered risk for myocardial infarction in the individual. The invention correlates an isolated nucleic acid molecule comprising at least so contiguous nucleotides where one of the nucleotides is an SNP given in the specification any one of the amino comprising an amino acid sequence given in the specification; an antibody that specification and which is between about 16 and 1000 nucleotides in specification and which is between about 16 and 1000 nucleotides in specification and which is between about 16 and 1000 nucleotides in specification and which is between about 16 and 1000 nucleotides in clength; a kit for detecting an SNP in a nucleic acid molecule; a method of detecting an SNP in a nucleic acid molecule; a method of detecting an agent useful in treating or preventing method for identifying an agent useful in treating or preventing method has cardiant activity.
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                                                                                                                                                                                                                                                                                                    Human myocardial infarction-associated gene derived protein, SEQ ID 1019
sequence was not shown in the specification. The sequence has come from an electronic sequence listing downloaded from the WIPO website.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in the individual's nucleic acids.
                                                                                                                                                                                                                                                                                                                               Myocardial infarction; detection; single nucleotide polymorphism; SNP;
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                                                                     8; Length 1170;
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                                                                     Score 42; DB 8; I
Pred. No. 9.8e+02;
                                                            67.7%; Scor.
61.5%; Pred. No. 2..
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Iakoubova 0;
                                                                                                                                                                                                                       ADQ39356 standard; protein; 1170 AA.
                                                                                                                                                                                                                                                                                                                                               cardiant; gene therapy; human.
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30-APR-2003; 2003US-0466412P.
23-SEP-2003; 2003US-0504955P.
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                                                                                                                                                   301 VTEENKELANELR 313
                                                                                                                                                                                                                                                                             (first entry)
                                                         Query Match
Best Local Similarity 61.57
                                                                                                                           1 ILEENKELENALK 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cargill M, Devlin JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (APPL-) APPLERA CORP
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N-PSDB; ADQ38528.
                                           Sequence 1170 AA
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                                                                                                                                                                                               RESULT 56
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The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual's nucleotide acids, where the presence of the SNP is correlated with an altered risk for myocardial infarction in the individual. The invention altered risk for myocardial infarction in the individual. The invention curter comprises: an isolated nucleic acid molecule comprising at least sometiguous nucleotides where one of the nucleotides is an SNP given in the specification or its complement and encoding any one of the amino acid sequences given in the specification; an isolated polypeptide comprising an amino acid sequence given in the specification; an amplified polynucleotide or its antigen-binding the fragment; an amplified polynucleotide containing an SNP given in the specification and which is between about 16 and 1000 nucleotides in length; a kit for detecting an SNP in a nucleic acid, comprising the
                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                    This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human myocardial infarction-associated gene derived protein, SEQ ID 1018.
                                  decreased risk for developing myocardial infarction and for preparing a composition for treating or preventing myocardial infarction. This sequence represents the protein of a human myocardial infarction-associated gene containing one or more SNP's of the invention. Note: This sequence was not shown in the specification. The sequence has come from an electronic sequence listing downloaded from the WIPO website.
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is useful in identifying an individual who has an increased
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                                                                                                                                                                                                                                                                                                                                          Score 42; DB 8; Length Ling
Pred. No. 9.8e+02;
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10-MAR-2003; 2003US-0453135P.
30-APR-2003; 2003US-066412P.
23-SEP-2003; 2003US-0504955P.
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301 VTEENKELANELR 313
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nes 8; Conservative
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N-PSDB; ADQ38527.
                                                                                                                                                                                                                                                                                                            Sequence 1170 AA;
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polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a nucleic acid molecule; a method of detecting a variant polypeptide; and. a method for identifying an agent useful in treating or preventing myocardial infarction. The novel detection method has cardiant activity. The nucleic acids of the invention may be used in gene therapy. The method is useful in identifying an individual who has an increased or decreased risk for developing myocardial infarction and for preparing a sequence represents the protein of a human myocardial infarction. This sequence was not shown in the specification. The sequence was not shown in the specification. The sequence has come from an electronic sequence listing downloaded from the MIPO website. 

Sequence 1170 AA;

Gaps ö DB 8; Length 1170; 67.7%; Score 42; DB 8; Lengua .... 61.5%; Pred. No. 9.88+02; "" "" "" " Indels Best Local Similarity 61.5 Matches 8; Conservative Query Match

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ADZ21688;

ADZ21688 standard; protein; 1170 AA (first entry) 30-JUN-2005 

Thrombospondin 1, rheumatoid arthritis marker.

Rheumatoid arthritis, antirheumatic, antiarthritic, inflammation, antiinflammatory, diagnosis, thrombospondin.

Ното варіепв

WO2005032328-A2

14-APR-2005

20-MAY-2004; 2004WO-US015761

21-MAY-2003; 2003US-0472330P

(MILL-) MILLENNIUM PHARM INC.

Zolg JW; ₩u J, Jones MD, Liao H, Guild BC,

WPI; 2005-295995/30.

N-PSDB; ADZ21687

Assessing whether a patient is afflicted with rheumatoid arthritis comprises determining the level of expression of one or more markers in patient sample.

Disclosure; SEQ ID NO 44; 182pp; English.

The invention is directed to methods of determining or diagnosing whether patients are inflicted with inflammatory disorders, e.g. joint disorders, especially rheumatoid arthritis (RA). These methods involve obtaining a sample of a patient's body fluid, e.g. blood serum, determining the level of expression of one or more markers in the fluid, and identifying whether the patient's body fluid has a pattern or profile of expression of a selected marker of marker set which correlates with the presence of the inflammatory disorder. The invention also provides methods for determining or diagnosing whether patients are afflicted with a particular form of arthritis, such as erosive RA. The markers whose expression correlates with the presence or absence of RA were identified by the sequencing of peptides derived from proteins in the sera of healthy, non-erosive and erosive patients by mass spectroscopy. Markers

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The present invention provides a method for analyzing differential protein expression associated with histopathological features of breast protein expression associated with histopathological features of breast disease, in particular breast tumors, e.g. breast carcinomas, comprising detecting the overexpression or underexpression of a pool of proteins in breast tissues or cells. The pool comprises all or part of a protein set comprising: afadin, aurora A, alpha-catenin, beta-catenin, BCL2, cyclin CC D1, cyclin E, cytokeratin 5/6, cytokeratin 8/18, E-cadherin, BCR2, cyclin CC D1, cyclin E, cytokeratin 5/6, cytokeratin 18/18, angl, aurora B, BCRP1, FTHT, GATA3, Ki67, mucin 1, p53, CC Cytokeratin 18, angl, aurora B, BCRP1, cathepain D, CD10, CD44, CK14, CC Cytokeratin 18, angl, aurora B, BCRP1, cathepain D, CD10, CD44, CK14, CC Cox2, fibroblast growth factor 2 (FGF2), GATA4, hifla, matrix CC Cox2, fibroblast growth factor 2 (FGF2), GATA4, hifla, matrix CC Cox2, fibroblast growth factor 2 (FGF2), GATA4, hifla, matrix CC Cox2, fibroblast growth factor 2 (FGF2), GATA4, hifla, matrix CC CC CX2, fibroblast Growth SCRIBBLE, smooth muscle actin, CC CC Thrombospondin (THBS) 1, tissue-inhibitors of matrix metalloprotease (WMP) 2 (TIMP1). The measuring of over- or underexpression of proteins is carried cout on tissue microarray, by immunohistochemistry (IHC) technologies. The method may involve comparing expression levels of the protein set in a
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    over-expressed
were identified that are newly associated with RA and are over-expressed in patients diagnosed with erosive or non-erosive RA. The present sequence is theprotein sequence of marker M590, which was identified as
                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Breast tumor; breast disease; endocrine disease; gynecology and obstetrics; neoplasm; prognosis; tumor marker; DNA library; microarray; expression; thrombospondin 1.
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Pred. No. 9.8e+02;
; Mismatches 3; Indels
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(PAOL-) INST PAOLI CALMETTES.
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cultion many also involve detecting the over- or underexpression of nucleic acids coding for the proteins. Also claimed are a protein library and a mucleic acid library useful for the molecular characterization of histopathological features of breast disease. The method is useful for analyzing differential protein expression associated with useful for histopathological features of breast disease. It is also is useful for carecting, diagnosing, staging, monitoring, predicting, and preventing conditions associated with breast cancer, predicting clinical outcome of breast cancer, predicting occurrence of metastatic relapse, and for a patient can be based on the analysis of the differential protein carperssion profile. Breast cancers can be classified into prognostically relevant subclasses, and appropriate doses and/or schedule of chemotherapeutics and/or biopharmaceuticals and/or radiation therapy can be elected to circumvent toxicities in a patient. The method is also useful in assessing breast cancer heterogeneity and prognosis in patients the present sequence is that of
control sample to levels of equivalent proteins in a tissue sample.
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Score 42; DB 9; Length 1170; Pred. No. 9.8e+02; 2; Mismatches 3; Indels 67.7%; : |||||| | |: 301 VTEENKELANELR 313 1 ILEENKELENALK 13 Query Match 67.7 Best Local Similarity 61.5 Matches 8; Conservative 임 ઠે

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Gaps

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AEB46751 standard; protein; 1170 AA. 20-OCT-2005 (first entry) Human thrombpspondin 1. AEB46751; RESULT 60 AEB4675 

Thrombospondin; gastrointestinal proliferative factor; GIPF; mucositis; enterocolitis; inflammatory bowel disease; Crohns disease; short-bowel syndrome; proliferation; epithelial cell; wound healing; burns; ocular disease; ophthalmological; antiinflammatory; gastrointestinal-gen.; vulnerary; immunosuppressive; chemotherapy; radiotherapy; B-lymphocyte; transgenic animal.

Ното варіелв

WO2005072419-A2.

11-AUG-2005.

27-JAN-2005; 2005WO-US002996.

27-JAN-2004; 2004US-0539605P. 15-OCT-2004; 2004US-0619241P.

(NUVE-) NUVELO INC. (KIRI ) KIRIN BEER KK.

Boyle BJ, Funk W, | Yagi M, Tomizuka K;

New composition comprising a gastrointestinal proliferative factor (GIPF) polypeptide, its fragment or analogue, and a carrier, useful for treating mucositis, inflammatory bowel disease or short bowel syndrome. WPI; 2005-555619/56.

Tang TY;

Kakitani M, Oshima T, Park EJ,

Disclosure; SEQ ID NO 28; 377pp; English

The invention relates to a composition comprising a gastrointestinal proliferative factor (GIPF) polypeptide, itse fragment or analogue, and a proliferative factor (GIPF) polypeptide (comprising a biologyteally active fragment of GIPF and a caritar, also included are applacably active fragment of GIPF and a caritar, a method of stimulating optihalial cell proliferation, a method of treating a disease (chosen from mucositis, inflammatory bowel (sease or short bowel syndrome, comprising administering to the composition), a method of treating a disease or short bowel syndrome, comprising administering to the composition, a method for treating a patient at mammalian subject the composition), a method for treating a patient that has undergone radiation therapy/chemotherapy by administering the composition, a method for treating a patient that has undergone radiation therapy/chemotherapy by administering the composition, a method for treating a patient that has undergone radiation therapy/chemotherapy by administering the composition, a method for construct comprising associated with an expression control sequence) construct comprising associated with an expression control sequence.

CC foretruct comprising numbered with an expression control sequence of size expression in B-cells), a transgenic mouse that produces in the Eaguence encoding GIPF protein, operably linked to transcriptional regulatory sequences directing its expression vector comprising expression regulatory sequences directing its expression vector comprising expression regulatory sequences directing its expression vector comprising expression regulatory collogorated virth the polympetide perpendence directing its expression vector comprising expression regulatory collogorated with the polymucleotide, an expression vector comprising expression regulatory collogoration and a polypeptide perpendence directing its expression of the polympetide methods of producing a patient the polympetide perpendence with the polympetide perpendence of SEC ID No. 4, wher administering the composition. The present sequence represents a human protein showing some sequence similarity to GIPF. 

Sequence 1170 AA;

Gарв ö Length 1170; Score 42; DB 9; Length 117 Pred. No. 9.8e+02; 2; Mismatches 3; Indels 2; 67.7%; Conservative Local Similarity hes 8; Conservat Query Match Matches

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Search completed: March 11, 2006, 12:18:52 Job time : 138.447 secs alanine\_tRNA ligas hypothetical prote giantin - human conserved hypothet clusterin - sheep hypothetical 16.2K hypothetical prote Regulatory protein Lysk-family regula hypothetical prote

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al prote	R; Scanla	, M.J.	, Raj, 1	B.; Cal	0,	B.; Garin-(	loncasi,	M.P.; Healey, J.; Ol
-isoprop	Proc. Na	Ll. Acad	d. Sci.	U.S.A.	6:4	, 5657-5661 hroblest act	alnha a	member of the serin
ar proce	A;Refere	nce num	ber: 130	8593; N	dio.	:94261645; 1	,	
louridine	A, Accession: I38593	ion: I3	8593					
al prote	A; Status: preliminary	preli	minary					
ranscrip	A;MOIECUIE LYDE: MKNA A:Regidues: 1-759 <res></res>	1e cype	: MKNA 59 KRES	^				
SC transp	A;Cross-	referen	ces: UN.	IPARC:U	IPI 0	000175B7D; 1	A; Cross-references: UNIPARC: UP10000175B7D; EMBL: U09278; NID: 9507749;	; PID:9507750
de trans	C, Genetic	38:						
rase III	A;Gene: GDB:FAP	3DB:FAP	100 · Bar	9.37418	. 4	OMTM - 600403		•
ipoprote	A; Map po	sition:	2q23-20	q23	-	A;Map position: 2q23-2q23		
ipoprote	C; Superf	amily: (	dipeption	âyl-pe⊧	tid	аве ІV		
ipoprote	C;Keywords:	de: tra	nsmembr	ane pro	tei	<b>s</b>		
.ipoprote regulator	Ouery	ŭ		100	.0	Score	, DB 2; Length 759;	
erase li	Best Loc	al	Similarity 100	y 100.0%;	.0	Pred.	037;	0.0
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UNIPARC: UPI00000531CD; EMBL: Z71297; NID: 91301850; PI
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R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Vature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A;Reference number: A71800; MUID:99120557; PMID:9923682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Restdues: 1-806 <ARN>
A;Cross-references: UNIPROT:Q9ZMZ9; UNIPARC:UPI00000D7152; GB:AE001445; GB:AE001439; NI·
A;Experimental source: strain J99
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C;Datesion: B64528
R;Tomb. J. F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenn son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:024906; UNIPARC:UPI000000308C; GB:AE000528; GB:AE000511; NI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          conserved hypothetical ATP-binding protein HP0066 - Helicobacter pylori (strain 26695)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein jhp0061 - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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F;373-380/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 43; DB 2
Pred. No. 48;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 41;
1; Mismatches
                                                                                                                                                                                                                             A;Cross-references: SGD:S0004966; MIPS:YNL021w
A;Map position: 14L
F;51-388/Domain: RPD3/acuc homology <RAH1>
                                                                                                                                                                                                                                                                                                                                                Score 43;
Pred. No.
                  A,Accession: S62933
A,Molecule type: DNA
A,Residues: 1-706 cAND>
A,Cross-references: UNIPROT:P53973;
A,Experimental source: strain S288C
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                   69.4%;
81.8%;
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155 ILTESKEIEEALK 167
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Best Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 LEENKEEENSL 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 LEENKELENAL 12
A; Reference number: S62920
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                       A;Gene: SGD:HDA1
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A;Experimental source: strain 972h-; cosmid c1884
B;Eyne, M; Rajandream, M.A.; Barrell, B.G.; Bothe, G.; Pohl, T.
Submitted to the EMBL Data Library, October 1998
A;Reference number: Z22003
                                                                                                                                                                                                                                                                                                                                                                                                                           A;Accession: T41592
A;Status: translated from GB/EMBL/DDBJ
A;Atatus: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 83-405 <LYN>
A;Cross-treferences: UNIPARC:UPI00001690B6; EMBL:AL031825; NID:g3702633; PIDN:CAA21226.1;
A;Experimental source: strain 972h-; cosmid c757
C;Genetics:
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A;Cross-references: UNIPROT:Q97WW8; UNIPARC:UPI000064631; GB:AE006641; NID:g13815271;
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: H90365
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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N;Alternate names: hypothetical protein N2819
C;Species: Saccharomyces cerevisiae
C;Decies: Sarcharomyces cerevisiae
C;Decies: Sarcharomyces cerevisiae
C;Decession: S62933
R;Andre, B.; Iraqui Houssaini, I.; Urrestarazu, L.A.; Vissers, S. submitted to the Protein Sequence Database, April 1996
                     C;Date: 20-Oct-2000 #sequence_revision 08-Dec-2000 #text_change 09-Jul-2004 C;Accession: T41194; T41592 R;Bothe, G; Pohl, T.; Wood, V.; Rajandream, M.A.; Barrell, B.G. abubmitted to the EMBL Data Library, September 1998 A;Reference number: Z21977 A;Accession: T41194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 405;
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66.7%; Pred. No. 4.1;
iive 3; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 47; DB 2;
Pred. No. 5.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Map position: 3
C;Superfamily: nickel transport protein YPO2673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: SPDB: SPCC1884.02; SPDB: SPCC757.01
                                                                                                                                                                                                    Status: translated from GB/EMBL/DDBJ
      C;Species: Schizosaccharomyces pombe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 75.8%;
Best Local Similarity 69.2%;
Matches 9; Conservative :
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24 LEENKKIENEIK 35
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Best Local Similarity
Matches 8; Conserv
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RiLawler, J.; Hynes, R.O.
7. Cell Biol. 103. 1635-1648, 1986
A.Title: The structure of human thrombospondin, an adhesive glycoprotein with multiple c
A.Reference number: A26155; MUID:87057617; PMID:2430973
                                                                                                                                                                                                                                                                                                                                                                                                                     A)Residues: 1-1170 <LAW>
A)Residues: 1-1170 <LAW>
A)Cross-references: UNIPROT:P07996; UNIPARC:UPI0000046821; GB:X04665; NID:g37137; PIDN:C
A)Cross-references: UNIPROT:P07996; UNIPARC:UPI0000046821; GB:X04665; NID:g37137; PIDN:C
A)Rote: parts of this sequence, including the amino end of the mature protein, were determed to the including the determinent of the promoter region of the human thrombospondin gene. DNA 8:A)Reference number: A34274; MUID:89291870; PMID:2544587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: UNIPARC:UP100001742BF; GB:J04835
A;Cross-references: UNIPARC:UP100001742BF; GB:J04835
A;Cross-references: UNIPARC:UP100001742BF; GB:J04835
A;Title: Complete thrombospondin mRNA sequence includes potential regulatory sites in the A; Reference number: A00140; MUID:89139590; PMID:2918029
A;Reference number: A00140
A;Accession: A30140
 MUID:8715592; PMID:3030396
A;Accession: A25812.
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A;Residues 1.83,'A',85-397 <KOB>
A;Cross references: UNIPARC:UDIO00016B0CA; GB:M25631; NID:g538353; PIDN:AAA36741.1; PID:
R;Dixit, V.M.; Hennessy, S.W.; Grant, G.A.; Rotwein, P.; Frazier, W.A.
R;Dixit, V.M.; Hennessy, S.W.; Grant, G.A.; Rotwein, P.; Frazier, W.A.
A;Reference number: A05172; MUID:86287276; PMID:3461443
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A; Residues: 1-83, A', 85-374, 'RC' < DIX>
A; Residues: 1-83, A', 85-374, 'RC' < DIX>
A; Cross-references: UNIPARC:UP1000016B140; GB:M14326; NID:g340005; PIDN:AAA61237.1; PID:
A; More: parts of this sequence, including the amino end of the mature protein, were deter
R; Sun, X.; Skorstengaard, K.; Mosher, D.F.
A; Call Balo. 118, 693-704, 1993
A; Title: Disulfides modulate RGD-inhibitable cell adhesive activity of thrombospondin.
A; Reference number: A42927; MUID:92348511; PMID:1379247
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F;19-1170/Product: thrombospondin 1 #status predicted <MAT.>
F;19-1170/Product: thrombospondin 1 #status predicted <MAT.>
F;19-1375/Domain: von Willebrand factor type C repeat homology <VWC.>
F;378-429/Domain: thrombospondin type 1 repeat homology <THR1.>
F;491-497/Domain: thrombospondin type 1 repeat homology <THR2.>
F;551-586/Domain: EGF homology <EGF2.>
C;Species: Homo sapiens (man)
C;Date: 23-Aug-1987 #sequence revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: A26155; A34274; Ā30140; A25812; A05172; A42927
R;Lawler, J.; Hynes, R.Q.
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A;Cross-references: GDB:120438; OMIM:188060
A;Map position: 15q15-15q15
A;Introns: 23/1
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A;Residues: 987-1003 <SUN>
A;Cross-references: UNIPARC:UPI00001742C0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-166 <LAH>
                                                                                                                                                                                                                                                                                                                                                                                         A, Molecule type: mRNA
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C; Species: Rickettsia prowazekii
C; Species: Rickettsia prowazekii
C; Species: Rickettsia prowazekii
C; Date: 21. Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
C; Accession: H71647
R; Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, U Nature 396, 133-140, 1998
A; Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria. A; Reference number: A71619
A; Accession: H71647
A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Residues: 1-877 < AND-A; A; Cross-references: UNIPROT:Q92CA4; UNIPARC:UPI0000136321; GB:AJ235273; GB:AJ235269; NIE A; Experimental source: strain Madrid E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cipecies: Pyrococcus horikoshii
Cipate: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004
Cipate: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004
Cipate: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004
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A; Note: this accession replaces an interim accession for a sequence replaced by GenBank
C; Genetics:
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C;Superfamily: alanyl-tRNA ligase
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                              DB 2; Length 831;
49;
                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein PH1595 - Pyrococcus horikoshii C; Species: Pyrococcus horikoshii
                                                                                                                                                             2; Mismatches
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                                                                       Score 43;
Pred. No.
                                                                       69.4%;
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178 ILTESKEIEEALK 190
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                                                              Query Match
Best Local Similarity 69.2
Matches 9; Conservative
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Matches 9; Conservative
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Matches 9; Conserv
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thrombospondin 1 precursor - human

RESULT 9

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2; Indels

Length 294;

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A;Residues: 1.294 <GLA>
A;Residues: 1.294 <GLA>
A;Cross.references: UNIPROT: Q8Y7W9; UNIPARC: UPI0000054CCF; GB: NC_003210; PIDN: CAC99228.1
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmol150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: G72210
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sea A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: G72210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: UNIPROT: 09X2C2; UNIPARC: UP10000C11F6; GB: AE001817; GB: AE000512; NIF
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Pred. No. 34;
1; Mismatches
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                                                                                                                                                                                                                                                                                                            66.1%;
72.7%;
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Best Local Similarity 61.5%;
Matches 8; Conservative
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Best Local Similarity 72.7
Matches 8; Conservative
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A; Residues: 1-847 < TOM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-546 <ARN>
                                                                 A; Molecule type: DNA
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A, Accession: AF1218
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Cispecies: Listeria monocytogenes
Cispecies: Listeria monocytogenes
Cispecies: Listeria monocytogenes
Cispecies: Listeria monocytogenes
Cispecies: Listeria monocytogenes
Cispecies: Listeria monocytogenes
Cispecies: Listeria monocytogenes
Cispecies: Listeria monocytogenes
Richaer, 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
Richaer, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J. Domingues-Bernal, G.; Duchaud, E.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mah, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species
A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A.Residues: 17291 cROU>
A.Gross-references: UNIPROT:080435; UNIPARC:UPI00000A8813; EMBL:AC003028; NID:g3335356;
A.Experimental source: cultivar Columbia
A.Experimental source: cultivar Columbia
R:ibin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shea, T.P.; Banito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shea, T.P.; Banito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shea, J.A.; Salzberg, S.E.; Umayam, L.; Tallon, L.
Nature 402, 761-768, 1999
A.Aitle: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A.Reference number: A84420; MuID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: T01241; G84800
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, July 1998
A;Description: Arabidopsis thaliana chromosome II BAC F16M14 genomic sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: UNIPARC: UP100000A8813; GB: AE002093; NID: g3335378; PIDN: AAC27179.1; C; Genetics:
                         F:171-232/Disulfide bonds: #status predicted
F:248,360,708,1067/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:270,274/Disulfide bonds: interchain #status predicted
F:610/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
F:610/Modified site: carbohydrate (Asn) (covalent) #status absent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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Species: Arabidopsis thaliana (mouse-ear cress)
Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 05-Oct-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        obable MYB family transcription factor [imported] - Arabidopsis thaliana
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       F;926-928/Region: cell attachment (R-G-D) motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: T01241
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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301 VTEENKELANELR 313
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A;Map position: 2
                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 8; Conserv
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A;Residues: 1-291 <STO>
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A; Status: preliminary
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A,Introns: 142/2
F:14-68/Domain:
                                                                                                                                                                                                                                                          Query Match
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R.Tomb. J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKennrason, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
A.Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A; Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A.Reference number: A64520; MUID:97394467; PMID:9252185
A.Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:P56452; UNIPARC:UPI0000136308; GB:AE000629; GB:AE000511; NII
C;Superfamily: alanyl-tRNA ligase
C;Keywords: ligase
                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alanine-tRNA ligase (EC 6.1.1.7) - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
                                                                                                                                                                                        Gaps
                                                                                                                                                                                        ö
                                                                                                        2; Length 546;
A;Gene: TM1802
C;Superfamily: Thermotoga maritima hypothetical protein TM1802
                                                                                                                                                                                        1; Indels
                                                                                                        Score 41; DB 2
Pred. No. 66;
4; Mismatches
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Gaps ö

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A; Molecule type: DNA
A; Residues: 1.340 <ANG>
A; Residues: 1.340 <ANG>
A; Residues: 1.340 <ANG>
A; Cross-references: UNIPROT: P48296; UNIPPARC: UPI000013353D; GB: L20680; NID: G461416; PIDN: A; Cross-references: UNIPROT: P48296; UNIPPARC: UPI00013353D; GB: L20680; NID: G461416; PIDN: A; Experimental source: strain YT-1

R; Wetmur, J.G.; Wong, D.M.; Ortiz, B.; Tong, J.; Reichert, F.; Gelfand, D.H.
A; Title: Chem. 269, 25928-25935, 1994
A; Title: Cloning, sequencing, and expression of RecA proteins from three distantly relat. A; Reference number: A55020; MUID: 95014407; PMID: 7929298
A; A; Accession: B55020
A; A; Accession: B55020
A; Molecule type: DNA
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A,Reference number: A72200; MUID:99287316; PMID:10360571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:Q9WYS8; UNIPARC:UPI0000D3A00; GB:AE001723; GB:AE000512; NID
A;Experimental source: strain MSB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: phosphoribosylaminoimidazole carboxylase carbon dioxide-fixation chain; pl
C;Keywords: carbon-carbon lyase; carboxy-lyase
F;15-349/Domain: phosphoribosylaminoimidazole carboxylase carbon dioxide-fixation chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            conserved hypothetical protein SP0741 [imported] - Streptococcus pneumoniae (strain TIGR) C;Species: Streptococcus pneumoniae C;Species: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Residues: 1-340 <WET>
A,Cross-references: UNIPARC:UP1000013353D; GB:L20095; NID:g349150; PIDN:AAA27502.1; PID:
                   A,Title: The recA gene from the thermophile Thermus aquaticus YT-1: cloning, expression, A,Reference number: A53378, MUID:94156846; PMID:8113181
A,Accession: A53378
A,Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hickey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable phosphoribosylaminoimidazole carboxylase (EC 4.1.1.21) carbon dioxide-fixation
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C.Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 40; DB 2;
Pred. No. 66;
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Bacteriol. 176, 1405-1412, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64.5%;
53.8%;
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Matches 10; Conservative
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les 7; Conservé
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-380 <ARN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession: H72374
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                                                                                                                                                                                           alanine-tRNA ligase (EC 6.1.1.7) - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: F71842
C;Accession: F71842
C;Accession: F71842
C;Accession: F71842
C;Accession: F71842
C;Accession: F71842
C;Accession: F71842
A;Reference number: A71800; MUD:99120557; PMID:9923682
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A;Reference number: A71800; MUD:99120557; PMID:9923682
A;Status: preliminary
A;Molecule type: DNA
A;References: UNIPROT:Q92JY5; UNIPARC:UPI0000136307; GB:AE001543; GB:AE001439; NIE
A;Experimental source: strain J99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C, Accession: 371116
R, Adachi, T.; Schamel, W.W.A.; Kim, K.M.; Watanabe, T.; Becker, B.; Nielsen, P.J.; Reth, ENBO J. 15, 1534-1541, 1996
A, Title: The specificity of association of the IgD molecule with the accessory proteins A, Reference number: S71116; MUID:96203070; PMID:8612576
A, Residues: 1-245 ADA
A, Residues: 1-245 ADA
A, Cross-references: UNIPROT:Q61335; UNIPARC:UPI0000161CC5; EMBL:X81816; NID:g1487985; PI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BCR-essociated protein BAP31 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
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,Superfamily: alanyl-tRNA ligase
,Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.1%; Score 41; DB 2; Length 847; 88.9%; Pred. No. 1.1e+02; ive 1; Mismatches 0; Indels
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2; Mismatches
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Pred. No.
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66.7%;
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Best Local Similarity 88.7
Lag 8; Conservative
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177 LEENKSLKNDLR 188
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Best Local Similarity 66.7
Matches 8; Conservative
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699 EENKELKNA 707
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                                 EENKELENA
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A,Map position: X
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myosin-like coiled-coil protein sp8 (imported) - fission yeast (Schizosaccharomyces pom
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C;Species: Bacillus subtilis phage SPBC2
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accession: T12796; A6931
R;Lazarevic, V.; Duesterhoeft, A.; Soldo, B.; Hilbert, H.; Mauel, C.; Karamata, D. submitted to the EMBL Data Library, August 1997
A;Description: The complete nucleotide sequence of the Bacillus subtilis SPbetac2 proph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-1727 <MCD>
A;Cross-references: UNIPROT:Q9UTKS; UNIPARC:UPI00001258AA; EMBL:AL133357; PIDN:CAB62414
A;Experimental source: strain 972h(-); cosmid c1486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Schizosaccharomyces pombe
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
C;Accession: T50073
A;McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Seeger, K.; Harris, D.
submitted to the EMBL Data Library, December 1999
A;Reference number: Z25034
                                                                                                                                                                                                                                                                                                                                   Species: Schizosacchāromyces pombe
Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 04-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-1173 <JIM>
A;Cross-references: UNIPARC:UPI00001687F2; EMBL:AF010473; PIDN:AAB65416.1
A;Experimental source: strain 972h(-)
                                                                                                                                                                                                                                                                                                        (Schizosaccharomyces pombe) (fragment)
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                                                                      Indels
                     Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                     C.Species: Schizosaccharomyces powbe
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #t.
C;Accession: T43527
K:Jimenez, M.; Goday, C.
Submitted to the EMBL Data Library, June 1997
A;Description: Schizosaccharomyces powbe myosin-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 40; DB 2; I
Pred. No. 3.3e+02;
L; Mismatches 3;
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Pred. No. 2.2e+02;
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66.7%;
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66.7%;
                                           53.8%;
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Best Local Similarity 66...
Best Local Similarity 66...
                                                                                                                                                                         853 LLOETKELKNEIK 865
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                                                                                                                         1 ILEENKELENALK 13
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                                                                           Conservative
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                                        Best Local Similarity
Matches 7; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                sp8 protein -
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on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E. Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Althors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Accession: G95085
A;Accession: G95085
A;Accession: G95085
A;Residues: prelimity
A;Residues: 1-391 <KUR>
A;Cross-references: UNIPROT:Q97RQ7; UNIPARC:UPI0000051578; GB:AE005672; PIDN:AAK74880.1; A;Genetics:
A;Genetics:
A;Genetics:
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R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; F e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, B.J.; Lu, J.; Matsushima, P.; McAhren, S.; My, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, S709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    conserved hypothetical protein spr0651 [imported] - Streptococcus pneumoniae (strain R6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cross-references: UNIPROT:QBDQ17; UNIPARC:UP100000E34C3; GB:AE007317; PIDN:AAK99455.1;
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A;Cross-references: UNIPROT:P41542; UNIPARC:UP1000016829C; GB:U15589; NID:9558474; PIDN
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Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Species: Streptococcus pneumoniae
Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
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Proc. Natl. Acad. Sci. U.S.A. 92, 527-531, 1995
A;Title: Transcytosis-associated protein (TAP)/pl15 is a A;Reference number: A55913; MUID:95132633; PMID:7831324
A;Accession: A55913
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68;
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Pred. No. 6
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Pred. No.
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Best Local Similarity 71.4%;
Matches 10; Conservative
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269 LEENREKSLKNALK 282
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Best Local Similarity 71.4 Matches 10; Conservative
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A; Residues: 1-397 < KUR>
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A;Residues: 1-959 <BAR>
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C;Species: Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 31-Dec-2004
C;Accession: B97074
C;Accession: B97074
R;Nolling, J: Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
Blaly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A;Reference number: A96900; MUID:21359325; PMID:21359325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Cross-references: UNIPROT:P44241, UNIPARC:UPI000013859F; GB:U32828; GB:L42023; NID:g15
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                                                                                                                                                                                                                                                                                                    Clayton, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, R.Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.; Science 269, 496-512, 1995
A;Authors: Genhw, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Authors: Genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: H64034
A;Accession: H64034
A;Molecule type: DNA
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C,Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
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C;Superfamily: ribosomal protein serine N-acetyltransferase
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41;
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Pred. No. 40;
0; Mismatches
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Pred. No. 41;
4; Mismatches
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69.2%;
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53.8%;
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Best Local Similarity 53.0
T; Conservative
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VLEEREFIENAIK 55
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                                                                        EENDELENSL 937
                                                                                                                                                                                                                      hypothetical protein HI1521
                  3 EENKELENAL 12
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Best Local Similarity
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A,Status: preliminary
A,Molecule type: DNA
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hypochetical protein T12DB.1 - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Decies: T2-1899
Rs; McMurray, A.
submitted to the EMBL Data Library, October 1996
A; Recession: T24864
A; Accession: T24864
A; Accession: T24864
A; Residues: L2461
A; McCession: T24864
A; Coss-references: UNIPROT: O46025; UNIPARC: UP1000007A66F; EMBL: Z81120; PIDN: CAB03348.1;
A; Esperimental source: clone T12D8
R; Steward, C.
submitted to the EMBL Data Library, November 1996
A; Retrence number: Z20436
A; Retrence number: Z20436
A; Retrence number: Z20436
A; Retrence number: L2561
A; Molecule type: DNA
A; Residues: L-2561
A; Cross-references: UNIPARC: UP1000007A66F; EMBL: Z82094; PIDN: CAB055024.1; GSPDB: GN00021;
A; Experimental source: clone ZK525
C; Generices: Constant A; Consta
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A;Map position: 3
A;Introns: 44/3; 78/3; 104/2; 251/2; 466/3; 504/3; 548/3; 662/2; 747/1; 962/1; 1355/3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64.5%; Score 40; DB 2; Length 2285; 61.5%; Pred. No. 4.4e+02;
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847 ILKTNKELEKAIE 859
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Matches 8; Conservative
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nes 8; Conserv
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probable carboxynorspermidine decarboxylase - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
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A;Experimental source: strain J99
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C;Gsecies: Pyrococcus horikoshii norikoshii nor
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A;Residues: 1-42 <KRW>
A;Cross-references: UNIPROT:O58688; UNIPARC:UPI000062F42; GB:AP000004; NID:g3236131; Pi
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
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maltose-binding periplasmic protein precursor (maltodextrin-binding protein) (mmbp) PAB
C;Species: Pyrococcus abyssi
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Pred. No. 1.1e+02;
2; Mismatches 2; Indels
Length 405;
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Pred. No. 1e+02;
DB 2;
         Score 39; DB 2;
Pred. No. 1e+02;
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121 ILDKNKQLEN 130
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                                     Similarity 7; Conserve
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Best Local Similarity
Matches 7; Conserv
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         Query Match
Best Local S
Matches 7
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C; Genetics:
A; Gene: nspC
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                                                        Nature 408, 816-820, 2000
A; Authors: Huncer, J.L.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. A; Authors: Huncer, J.L.; Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Southwick, A.M.; Sun, H.; Tallon, A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A; Authors: Salzberg, S.L.; Fraser, C.M.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A; Reference and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719; PMID:11130712.
A; Residues: Drawley: DNA
A; Residues: 1-230 <STO>
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A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
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C;Genetics:
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R;Bolocin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehr:
R;Bolocme Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis A;Reference number: A66625; MUID:21235186; PMID:11337471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cell shape determining protein [imported] - Lactococcus lactis subsp. lacti
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C;Accession: G86903
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Pred. No. 72;
1; Mismatches
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56;
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Pred. No.
                       ansen, N.F.; Hughes, B.; Huizar, L.
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ENKELKKALK 111
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71 QEEKELEKALK 81
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Matches 8
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Pred. No. 1.6e+02;
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72.7%;
  58.3%;
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218 LEDNPELENEIR 229
                                  Conservative
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416 ILEEAKELDNS 426
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Matches 8; Conserv
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A;Status: preliminary
A;Molecule type: DNA
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C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C;Accession: A71023
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Rese S, 55-76, 1998
A;Tille: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A;Reference number: A71020
A;Reference number: A71020
A;Reference number: A71020
A;Reference number: A71020
A;Reference number: A71020
A;Reference number: A7103
A;Nolecule type: DNA
A;References: UNIPROT: O59147; UNIPARC: UP1000013665C; GB:AP000006; NID:g3236133; PI
A;Experimental source: strain O73
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
C;Genetics:
A;Gene: PH1478
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: F75206
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A;Reference number: A75001
A;Accession: F75206
A;Status: preliminary
A;Accession: F75206
A;Status: Draliminary
A;Residuss: 1-453 <AMM>
A;Residuss: 1-453 <AMM>
A;Residuss: 1-453 <AMM>
A;Access-references: UNIPROT:Q9V297; UNIPARC:UPI000012EB47; GB:AJ248283; GB:AL096836; NIC
A;Gene: malE; PAB0119
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CiSpecides: Adelaide River virus
CiSpecides: Adelaide River virus
CiSpecides: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
CiAccession: T02769
RiWang, Y:, Walker, P.J.
Virology 195, 719-731, 1993
A;Title: Adelaide river rhabdovirus expresses consecutive glycoprotein genes as polycist
A;Reference number: Z14732; MUID:93331730; PMID:8337841
A;Accession: T02769
A;Accession: T02769
A;Accession: T02769
A;Accession: T02769
A;Accession: T02769
A;Residues: Leon GB/EMBL/DDBJ
A;Residues: Leon GB/EMBL/DDBJ
A;Residues: Leon GB/EMBL/DBJ
A;Residues: Leon GB/EMBL/DBJ
A;Residues: Leon GB/EMBL/DBJ
A;Cross-references: UNIPROT:089904; UNIPARC:UPI00000F4A64; EMBL:L09206; NID:9348027; PII
C;Superfamily: Adelaide River virus Gns protein
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Pred. No. 1.6e+02;
3; Mismatches 2; Indels
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58.3%;
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Best Local Similarity 53.8%;
Matches 7; Conservative
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111 VFEQKPDLENALK 123
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187 LESNKKLDNTVK 198
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Best Local Similarity 58.3
Matches 7; Conservative
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C;Accession: A12402
R;Kanako, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anaì
A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: DNA
A;Mosidues: 1-656 «KUR»
A;Cross-references: UNIPROT:08YMZ8; UNIPARC:UPI0000CEC4C; GB:BA000019; PIDN:BAB76475.1;
A;Experimental source: strain PCC 7120
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C,Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Riesad, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Notlaic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
                                                                                                                                                                                                                                                                                                                                                                         cell division protein [imported] - Nostoc sp. (strain PCC 7120)
C.Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C.Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
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C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
    Gaps
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62.9%; Score 39; DB 2; Length 629;

Query Match

Gaps

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C,Accession: A99604

R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I., Nucleic Acids Res. 29, 2145-2153, 2001

A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pul.
A;Reference number: A99512; MUID:21267165; PMID:11353084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cjaccession: I52300
RjsOnda, M.; Misumi, Y.; Fujiwara, T.; Nishioka, M.; Ikehara, Y.
Bjochem. Biophys. Res. Commun. 205, 1399-1408, 1994
A;Title: Molecular cloning and sequence analysis of a human 372-kDA protein localized in
A;Reference number: I52300; MUID:95100974; PMID:7802676
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A;Aclecule type: mRNA
A;Residues: 1-3225 <RES>
A;Cross-references: UNIPROT:Q14789; UNIPARC:UPI000016A987; GB:D25542; NID:g662389; PIDN
C;Superfamily: giantin
                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-991 -KUR>
A;Essidues: 1-991 -KUR>
A;Experimental source: UNIPROT: 098PI5; UNIPARC: UPI00000C8105; GB:AL445566; PID:g14090152;
C;Genetics:
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C;Date: 19-Oct-1995 #sequence_revision 26-Jan-1996 #text_change 09-Jul-2004
C;Date: 19-Oct-1995 #sequence_revision 26-Jan-1996 #text_change 09-Jul-2004
C;Accession: A56519; 837536
R;Seelig, H.P.; Schranz, P.; Schroeter, H.; Wiemann, C.; Griffiths, G.; Renz, M.
Mol. Cell. Biol. 14, 2564-2576, 1994
A;Title: Molecular genetic analyses of a 376-kilodalton Golgi complex membrane protein
                                                                                                                                                                                           RESULT 40
A99604
hypothetical protein MYPU_7370 [imported] - Mycoplasm<u>a</u> pulmonis (strain UAB CTIP)
                                                                                                                                                                                                                                                                           Species: Mycoplasma pulmonis
Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
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C;Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
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Pred. No. 9.3e+02;
2; Mismatches 0
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Pred. No. 2.6e+02
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     Mismatches
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73
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53.8%;
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Best Local Similarity 77.8%;
Matches 7; Conservative
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738 ILERNKEVEKELE 750
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N;Alternate names: macrogolgin
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                                                         1 ILEENKELENALK 13
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Best Local Similarity 53.8
Matches 7; Conservative
     Conservative
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2525 LQQNKELEN 2533
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A;Genetic code: SGC3
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A,Experimental source: strain J138
C,Genetics:
A,Gene: CPJ0726
                                                                                                                                            A;Accession: F72044
A;Status: preliminary
A;Actus: preliminary
A;Actus: preliminary
A;Actus: preliminary
A;Actus: 1-831 cARN>
A;Cross-references: UNIPROT:Q9Z7H9; UNIPARC:UPI0000D3815; GB:AE001653; GB:AE001363; NIC
C;Genetics:
A;Gene: CPn0726
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Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349; PMID:10871362
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                                   'n.
                                   L.; Grimwood,
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R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson,
Science 293, 2093-2098, 2001
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A,Accession: G97865
A,Status: preliminary
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;Species: Rickettsia conorii
;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
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                              R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, Nature Genet. 21, 385-389, 1999
A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis. A;Reference number: A72000; MUID:99206606; PMID:10192388
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Pred. No. 2.2e+02;
2; Mismatches 1; Indels
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Pred. No. 2.2e+02;
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2; Mismatches . 1; Indels
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Pred. No. 2.3e+02;
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Best Local Similarity 72.7
Matches 8; Conservative
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A;Residues: 1-831 <STO>
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C; Superfamily
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Length 82; 0; Indels

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hypothetical 16.2K protein - phage SPP1
N'Alternate names: hypothetical protein 42
Sispecies: phage SPP1
C;Species: phage SPP1
C;Species: phage SPP1
C;Accession: JN0729; S43816; S41190; T42347; S21429
C;Accession: JN0729; S43816; S41190; T42347; S21429
C;Accession: JN0729; S43816; S41190; Trautner, T.A.; Alonso, J.C.
Gene 129, 41-49, 1993
A;Title: Sequence analysis of the left end of the Bacillus subtilis bacteriophage SPP1
A;Reference number: JN0729; MUID:93328123; PMID:8335259
A,Cross-references: UNIPARC:UP100001777B1; UNIPARC:UP100001777B2
A,Accession: $10672
A,Molecule type: protein
A,Residues: 62-82 <182>
                                                                                                         A;Cross references: UNIPARC:UP100001777B1; UNIPARC:UP100001777B2
C;Superfamily: clusterin
C;Keywords: glycoprotein; testis
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Pred. No. 27;
2; Mismatches
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77.8%;
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Matches 7; Conservative
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21 NKEIKNALK 29
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A;Residues: 3-133 <ALO>
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A;Molecule type: DNA
A;Residues: 1-67 <PED>
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A; Residues: 3-67 <PE2>
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  A;Reference number: A56539; MUID:94187728; PMID:7511208
A;Accession: A56539
A;Molecule type: mRNA
A;Molecule: L3259 eSEB>
A;Cross-references: UNIPROT:Q14789; UNIPARC:UP1000012B42C; EMBL:X75304; NID:g405714; PID
C;Genetics:
A;Gene: GDB:GGLGB1; GCP; GCP371
A;Cross-references: GDB:454558
A;Map position: 3q13.31-3q13.31
C;Superfamily: ajantin
C;Superfamily: ajantin
C;Superfamily: ajantin
C;Keywords: coiled coll; Golgi apparatus; transmembrane protein
F;3238-3254/Domain: transmembrane #status predicted <TMN>
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R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:O66700; UNIPARC:UPI000056337; GB:AE000687; NID:g2983050; A;Experimental source: strain VF5 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clusterin - sheep (fragments)

Clusterin - sheep (fragments)

NiAlternate names: SGP2; sulfated glycoprotein 2

Cispecies: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

Cispecies: Ovis orientalis aries, Ovis ammon aries (location orientalis aries)

Cibate: 30-Sep-1993 #sequence revition 30-Sep-1993 #text_change 19-Oct-1995

Ciaccession: A60457; S10671; S10672

Right Sisperial No. D.; Sishop, P.D.; Kim, K.H.; Ping, R.; Siiteri, J.E.; Morales, C. Ann. N. Y. Acad. Sci. 564, 154-172, 1999

A;Title: Function of vitamin A in normal and synchronized seminiferous tubules.

A;Accession: A60457

A;Molecule type: protein

A;Reference number: NIPARC:UP10000177780

R;Tsuruta, J.K.; Wong, K.; Fritz, I.B.; Griswold, M.D.

Biochem. J. 268, 571-578, 1990

A;Title: Structural analysis of sulphated glycoprotein 2 from amino acid sequence. R
A;Reference number: S10671; MUID:90303244; PMID:2363694

A;Recession: S10671

A;Residues: 4-26;41-49 <TSU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Tatle: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Accession: H70333
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: H70333
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Pred. No. 9.4e+02;
2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 conserved hypothetical protein aq 378 - Aquifex aeolicus
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Pred. No. 1.4e+02;
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77.8%;
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75.0%;
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Best Local Similarity 75.v.
Pest Local 9; Conservative
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432 EQNKEKIENALK 443
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Best Local Similarity
Matches 7; Conserva
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A; Molecule type: DNA
A; Molecule type: DNA
A; Rossides: 1-133 <CHA>
A; Cross-references: UNIPROT:Q38070; UNIPARC:UPI000009B0FE; EMBL:X65941; NID:g14843; PIDN
A; Cross-references: UNIPROT:Q38070; UNIPARC:UPI000009B0FE; EMBL:X65941; NID:g14843; PIDN
R; Pedre, X.; Weise, F.; Chai, S.; Lueder, G.; Alonso, J.C.
J. Mol. Biol. 236, 1324-1340, 1994
A; Title: Analysis of cis and trans acting elements required for the initiation of DNA re
A; Reference number: S43798; MUID:94172631; PMID:8126723
                                                                                                                                                                                                                                                                                                                                                                                                                               A,Cross-references: UNIPARC:UP100001798BD; EMBL:X67865
R;Pedre, X.; Chai, S.; Lueder, G.; Traucner, T.A.; Alonso, J.C.
Bubmitted to the EMBL Data Library, July 1992
A;Description: DNA replication studies with the Bacillus subtilis bacteriophage SPP1. The A;Reference number: S41172
A;Accession: S41190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPARC:UP1000016D74F; EMBD:X67865; NID:g472886; PIDN:CAA48065.1; PJ R;Alonso, J.C.; Luder, G.; Stiege, A.C.; Chai, S.; Weise, F.; Trautner, T.A. Gene 204, 201-212, 1997
A;Title: The complete nucleotide sequence and functional organization of Bacillus subtil A;Reference number: Z22137; MUID:98094274; PMID:9434185
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hypothetical protein MJECS01 - Methanococcus jannaschii plasmid pURB801
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C;Superfamily: phage SPP1 hypothetical 16.2K protein
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45;
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Pred. No.
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A;Accession: AB0078
A;Status: preliminary
A;Molecule type: DMA
A;Residues: 1-310 «KUR»
A;Cross-references: UNIPROT:Q8Z180; UNIPARC:UPI0000DCE05; GB:AL590842; PIDN:CAC89485.1
A;Cross-references: UNIPROT:Q8Z180; UNIPARC:UPI0000DCE05; CB:AL590842; PIDN:CAC89485.1
A;Genetics:
A;Genetics:
C;Superfamily: conserved hypothetical protein HI1364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein F36H12.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Date: 29-Oct-1999 #sequence Of C: Blanchard, M: Stellyes, L.
submitted to the EMBL Data Library, July 1998
A;Description: The sequence of C: elegans cosmid F36H12.
A;Reference number: 221346
A;Accession: T33458
A;Accession: T33458
A;Accession: T336 - SLA>
A;Accession: U350 - SLA>
A;Residues: 1-350 - SLA>
A;Residues: 1-350 - SLA>
A;Cross-references: UNIPROT:O76720; UNIPARC:UPI000007FBA7; EMBL:AF078790; PIDN:AAC26929
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C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
B;JACcession: G71917
B;JALm, R.A., Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, O.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
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A;Experimental source: strain J99
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                                                                                                                                                                                                                                                                                   Length 310;
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Pred. No. 1.4e+02;
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Pred. No. 1.1e+02;
1; Mismatches 3;
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Pred. No. 1.3e+02;
1; Mismatches 4,
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C;Superfamily: 5-aminolevulinate synthae
C;Keywords: acyltransferase; coenzyme A
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A, Introns: 24/2; 172/3; 222/1; 312/2
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69.2%;
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Best Local Similarity 61.5%;
Matches 8; Conservative
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Best Local Similarity 69.2.
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72 ILQEIDELEGALK 84
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A;Molecule type: DNA
A;Residues: 1-373 <ARN>
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                                                                 CyAccession: A64516
RyBult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Pleischmann, R.D.; Sutton, G.G.; Blake, R. Hutte, O.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberte, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996
A; Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, G. A; Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii A; Reference number: A64300, MUID:96337999; PMID:8688087
A; Rocession: A64516
A; Status: prediminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-276 & BUL>
A; Cross-references: UNIPROT:Q60300; UNIPARC:UPI000013C255; GB:L77119; NID:g1500688; TIGR
C; Genetics:
A; Map position: ECSREV1259-429
A; Genome: plasmid
A; Note: this stable 16-kilobase pair plasmid is also designated ECS (small extrachromosc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kiglaser, F. Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, S. Sominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U. Science 252, 2001
A.Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; MaOk, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Reference number: AB1077; MUID:21537279; PMID:11679669
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A; Residues: 1-294 <GLA>
A; Cross-references: UNIPROT: Q92CQ7; UNIPARC: UPI0000CC47D; GB: AL592022; PIDN: CAC96345.1;
A; Experimental source: strain Clip11262
C; Genetics:
A; Gene: lin1114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Regulatory protein Salmonella typhimurium PocR protein homolog lin1114 [imported] - List
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: A<u>1</u>1571
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A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
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Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
                                       Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 276;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 38; DB 2;
Pred. No. 98;
0; Mismatches 3
                C;Species: Methanococcus jannaschii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 61.3%;
Best Local Similarity 72.7%;
Matches 8; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |:|||: |||
188 EDNKEIRKALK 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 EENKELENALK 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Accession: AB0078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 47
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C;Accession: A35744
R;Palmer, D.J.; Christie, D.L.
N. Biol. Chem. 265, 6617-6623, 1990
A;Title: The primary structure of glycoprotein III from bovine adrenal medullary chromaf A;Reference number: A35744; MUID:90216681; PMID:1691174
                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-439 cPAL-
A; Cross-references: UNIPROT: P17697; UNIPARC: UP10000127BA3; GB:J05391; NID:g163114; PIDN:
A; Cross-references: UNIPROT: P17697; UNIPARC: UP10000127BA3; GB:J05391; NID:g163114; PIDN:
A; Note: parts of this sequence, including the amino ends of the alpha and beta chains, w
C; Superfamily: clusterin
C; Superfamily: clusterin sequence #status predicted <SIG>
F; 1-19/Domain: signal sequence #status predicted <SIG>
F; 20-221, 202-439/product: clusterin heta chain #status experimental <BCH>
F; 222-439/pomain: clusterin alpha chain #status experimental <ACH>
F; 222-439/pomain: clusterin alpha chain #status experimental <ACH>
F; 20-231, 222-439/pomain: clusterin alpha chain #status experimental <ACH>
F; 20-231, 20-33, 320, 346, 366/Binding site: carbohydrate (Asn) (covalent) #status predicte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cyaccession: A4018

Ribartmann, K.; Rauch, J.; Urban, J.; Parczyk, K.; Diel, P.; Pilarsky, C.; Appel, D.; Hai Ribartmann, K.; Rauch, J.; Urban, J.; Parczyk, K.; Diel, P.; Pilarsky, C.; Appel, D.; Hai A; Hitle: Molecular cloning of gp 80, a glycoprotein complex secreted by kidney cells in A; Reference number: A40018; MUID:91236776; PMID:2033078

A; Reference number: A40018

A; Rocession: A40018

A; Rocession: A40018

A; Rocession: A40018

A; Rocession: A40018

C; Roperfamily: clusterin
C; Reywords: apoptosis; disulfide bond; glycoprotein
C; Reywords: apoptosis; disulfide bond; glycoprotein
C; Reywords: apoptosis; disulfide bond; glycoprotein
C; Roymords: signal sequence #status predicted <SIG>
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C;Keywords: apoptosis; disulfide bond; glycoprotein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-226/Domain: clusterin beta chain #status experimental <MAT>
F;227-445/Pomain: clusterin alpha chain #status experimental <ACH>
F;227-445/Domain: clusterin alpha chain #status experimental <ACH>
F;86,103,145,277,287,350,370/Binding site: carbohydrate (Asn) (covalent) #status predict
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NyAlternate names: complement cytolysis inhibitor; CP40 protein
C;Species as scrofa domestica (domestic pig)
C;Date: 04-Mar-1993 #sequence revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A42108; JC5535; PC4475
C;Accession: A42108; JC5535; PC4475
C;Accession: A52708; M: Baglioni, C.; Millis, A.J.
J;Bhomer, V; Hoyle, M: Baglioni, C.; Millis, A.J.
A;Ditle: Expression of porcine complement cytolysis inhibitor mRNA in cultured aortic sn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N.Alternate names: 80k secreted glycoprotein, renal, complement cytolysis inhibitor C.Species: Canis lupus familiaris (dog)
C.Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 09-Jul-2004
                                   C;Species: Bos primigenius taurus (cattle)
C;Date: 05-Oct-1990 #sequence_revision 05-Oct-1990 #text_change 09-Jul-2004
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Best Local Similarity 77.8%; Pred. No. 1.6e+02;
Matches 7; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
N; Contains: clusterin alpha chain; clusterin beta chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
61.3%; Score 38; DB 2; I
Best Local Similarity 77.8%; Pred. No. 1.6e+02;
Matches 7; Conservative 2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37 NKEIKNALK 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 NKELENALK 13
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43 NKEIKNALK
                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq A;Reference number: A72200; MUD:99287316; PMID:10360571
A;Accession: D72319
A;Accession: D73319
A;Residuator
A;Molecule type: DNA
A;Residuas: 1-395 cARN-
A;Residuas: 1-395 cARN-
A;Cross-references: UNIPROT:Q9WZU6; UNIPARC:UPI00000C13A0; GB:AE001744; GB:AE000512; NID
A;Experimental source: strain MSB8
A;Experimental source: strain MSB8
A;Genesics:
A;Genesics:
A;Genesics:
C;Superfamily: Thermotoga maritima hypothetical protein TM0737
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A; Accession: D72324
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-430 cARN>
A; Cross-references: UNIPROT: Q9WZY4; UNIPARC: UPI00000D396B; GB: AE001753; GB: AE000512; NIE
A; Experimental source: strain MSB8
A; Conselred: TW0882
C; Genetics:
C; Superfamily: cystathionine gamma-synthase
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R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
                                                                                                                                                                                                                                                                                                                                               C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: D72339
R;Nelson, KE.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 38; DB 2; Length 395;
Pred. No. 1.4e+02;
3; Mismatches 0; Indels
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       Indels
                                                                                                                                                                                                                                                                                                                   hypothetical protein - Thermotoga maritima (strain MSB8)
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73
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ilarity 69.2%; Pred. No. 1.6e+02;
Conservative 0; Mismatches 4;
       Mismatches
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70.0%;
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          8; Conservative
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350 LEDTKELANAL 360
                                                                          2 LEENKELENAL 12
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109 KNKKLONALK 118
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Les 9, Conserv
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Best Local S:
Matches 9
              Matches
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-448 <ARN>
A;Residues: 1-448 <ARN>
A;Cross-references: UNIPROT:O84028; UNIPARC:UPI00000D32E4; GB:AE001277; GB:AE001273; NIi
A;Experimental source: serotype D, strain UW-3/Cx
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein 1 - fruit fly (Drosophila subobscura) transposable element P C; Species: Drosophila subobscura C; Species: Drosophila subobscura C; Species: Drosophila subobscura C; Species: Drosophila subobscura C; Species: O' S.22594
R; Paricio, N.; Perez-Alonso, M.; Martinez-Sebastian, M.J.; de Frutos, R. Mucleic Paquences Of Species Specie
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A;Experimental source: strain Bristol N2; clone R0853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Map position: X
A;Introns: 17/2; 38/2; 75/3; 118/1; 155/3; 244/3; 285/3; 323/3; 357/3; 426/3; 437/3; 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Cross-references: UNIPROT: Q24662; UNIPARC: UP10000075F17; EMBL:X60436; NID:911017; PIC
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia A;Reference number: A71570; MUID:99000809; PMID:9784136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein R08E3.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Ocr-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Description: The sequence of C. elegans cosmid R08E3.
A;Reference number: Z20536
                                                                                                                                                                                                                                                                                                                                                                            C;Superfamily: signal recognition particle 54K protein C;Keywords: nucleotide binding; P-loop F;106-113/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 38; DB 2; I
Pred. No. 1.6e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                December 1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: T28878
R;Hawkins, J.
submitted to the EMBL Data Library,
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80.0%;
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70.0%;
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les 8; Conservative
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Les 7; Conserv
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                                                                                    A; Accession: D71566
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A;Cross-references: UNIPROT:Q9PL14; UNIPARC:UPI000057886; GB:AE002297; GB:AE002160; NID
A;Experimental source: strain Nigg (MoPn)
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Science 282, 754-759, 1998
                                                                                                                                          A;Cross-references: UNIPROT:029549; UNIPARC:UPI0000127BA8; GB:M84639; NID:g164408; PIDN: A;Experimental source: aortic smooth muscle cells
A;Note: sequence extracted from NCBI backbone (NCBIN:87354, NCBIP:87356)
R;Ogawa, S.; Ishibashi, Y.; Sakamoto, Y.; Kitamura, K.; Kubo, M.; Sakai, T.; Inoue, K. Biochem. Biophys. Res. Commun. 234, 712-718, 1997
A;Title: The glycoproteins that occur in the colloids of senescent porcine pituitary glaA;Reference number: JC5535; MUID:97318844; PMID:9175781
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A;Reference number: A81500; MUID:20150255; PMID:10684935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 - Chlamydia muridarum (strain Nigg)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
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F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-227/Domain: clusterin beta chain #status predicted <BCH>
F;23-227,228-446/Product: clusterin #status predicted <MAT>
F;228-446/Domain: clusterin alpha chain #status predicted <ACH>
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Pred. No. 1.6e+02;
2; Mismatches 0; Indels
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   A;Reference number: A42108; MUID:92184774; PMID:1544909
A;Accession: A42108
A;Molecule type: mRNA
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A;Gene: TC0294
C;Superfamily: signal recognition particle 54K protein
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Pred. No. 1.6e+02;
0; Mismatches 2.
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Residues: 58-66;68-77;229-247;249-251;408-436
;Cross-references: UNIPARC:UP10000127BA8
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80.0%;
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Best Local Similarity 77.8
Matches 7; Conservative
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Best Local Similarity 80.0
Matches 8; Conservative
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NKEIKNALK 51
                                                                                                                          Residues: 1-446 <DIE>
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Residues: 1-446 <OGA>
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A; Status: preliminary
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Accession: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Species: Drosophila subobscura
C;Bate: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: $22594
C;Accession: $22594
A;Title: P sequences of Drosophila subobscura lack exon 3 and may encode a 66 kd repress
A;Title: P sequences of Drosophila subobscura lack exon 3 and may encode a 66 kd repress
A;Reference number: $22594; MUID:92107652; PMID:1662362
A;Recession: $22595
A;Recession: $22595
A;Recession: $22595
A;Recession: $22595
A;Recession: $22595
A;Recession: $22595
A;Recession: $22596
A;Recession: $22597
A;Rocession: $22597
A;Molecule type: DNA
A;Residues: 1-575 cPAR>
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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Pfam; PF00326; Peptidase S9; 1.
ProSiTE; PS00708; PRO_ENDOPEP_SER; 1.
3D-structure; Alternative splicing; Direct protein sequencing; Glycoprotein; Hydrolase; Polymorphism; Protease; Serine protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Signal-anchor for type II membrane protein (Potential). Extracellular (Potential).
                                                                                                                                                                                                                                                                                 MIM; 600403; -.. Gintegral to plasma membrane; TAS. GO; GO:0030027; C:integral to plasma membrane; TAS. GO; GO:0030027; C:lamellipodium; IDA. GO; GO:0005886; C:plasma membrane; NAS. GO; GO:0004222; F:metalloendopeptidase IV activity; NAS. GO; GO:0004222; F:metalloendopeptidase activity; TAS. GO; GO:0004222; F:protein homodimerization activity; NAS. InterPro; IPR001371; Pept S9_AS. InterPro; IPR001375; Peptidase_S9. InterPro; IPR001375; Peptidase_S9. InterPro; IPR001379; Ser_estra. Pfam; PF00930; DPPIV_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 62; DB 1; Length 760; 100.0%; Pred. No. 0.4;
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R -> T (in dbSNP:1126507).
/FTId=VAR 019691.
P -> A (in Ref. 2 and 5).
K -> T (in Ref. 2 and 5).
i, AOD34B4801BE07EA CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                              PDB; 1268; X-ray; A=39-757, B=-.
MEROPS; S09.007; -.
Ensembl; ENSG00000078098; Homo sapiens
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                                                                                                                     EMBL; U09278; AAB49652.1; -; mRNA.
EMBL; U7683; AAC51668.1; -; mRNA.
EMBL; BC07822; AAF21600.1; -; mRNA.
EMBL; BC026250; AAH26250.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transmembrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QS3TPS_HUMAN PRELIMINARY; '
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CARBOHYD
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CARBOHYD
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1D QS
AC QS
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Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altauner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A blatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Brownstein M.J., Usdin T.B., Toobhyuki S., Carninci P., Prange C.,
A Brownstein M.J., Usdin T.B., Toobhyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Bask S.A., McKernan R.J., Mackernan R.J., Mala S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Wilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glbbs R.A.,
A Helton B.K. Retreman M., Madan A., Rodrigues S., Sanchez A.,
A Mhiting M., Madan A., Young A.C., Schwuchenko Y., Bouffard G.G.,
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
Butterfield W. A., Schein J.E., Jones B.J.M., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEIN SEQUENCE OF 192-208; 220-240 AND 510-521.
MEDLINE=94327249; PubMed=7519584;
MEDLINE=94327249; PubMed=7519584;
MEtting W.J., Su S.L., Fortunato S.R., Scanlan M.J., Raj B.K.M.,
Gardin-Chesa P., Healey J.H., Old L.J.;
"Fibroblast activation protein: purification, epitope mapping and
induction by growth factors.";
Int. J. Cancer 58:385-392 (1994).
Int. J. Cancer 58:385-392 (1994).
Int. Way have a role in tissue remodeling during development
and wound healing, and may contribute to invasiveness in malignant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    type I and
agen. Does
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- INDUCTION: In fibroblasts at times and sites of tissue remodeling during development, tissue repair, and carcinogenesis.
-i- PTM: N-glycosylated.
-i- PTM: The N-terminus may be blocked.
-i- SIMILARITY: Belongs to the peptidase S9B family.
                                                                                                                                                                                                                                    Goldstein L.A., Chen W.T.;
"Identification of an alternatively spliced seprase mRNA that encodes a novel intracellular isoform.";
J. Biol. Chem. 275:2554-2559(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Type II membrane protein. Found in cell surface lamellipodia, invadopodia and on shed vesicles. ALTERNATIVE PRODUCTS:
                                                                                                   "Identification of the 170-kDa melanoma membrane-bound gelatinase (seprase) as a serine integral membrane protease."; J. Biol. Chem. 272:7595-7601(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      type IV collagen, but not native type I or type IV collagen. not cleave laminin, fibronectin, fibrin or casein. SUBUNIT: Homodimer, or heterodimer with DPP4. The monomer is
                            TISSUE=Melanoma;
MEDLINE=97218181; PubMed=9065413; DOI=10.1074/jbc.272.12.7595;
Pineiro-Sanchez M.L., Goldstein L.A., Dodt J., Howard L., Yeh Y.,
                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1), AND VARIANT
                                                                                                                                                                                                                        MEDLINE=20112818; PubMed=10644713; DOI=10.1074/jbc.275.4.2554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATALYTIC ACTIVITY: Degrades gelatin and heat-denatured
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=2; Synonyms=S, Truncated;
IsoId=Q12884-2; Sequence=VSP_005367;
TISSUE SPECIFICITY: Fibroblast specific.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=Q12884-1; Sequence=Displayed;
                                                                                                                                                                                    NUCLEOTIDE SEQUENCE (ISOFORM 2).
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          461-472 AND 511-518.
                                                                                                                                                                                                      TISSUE=Melanoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and mouse cDNA
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                                                                                       Chen W.
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Gaps

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Interbro; IPR001375; Peptidase_S9.
Interbro; IPR002469; Peptidase_S9B.
Interbro; IPR00079; Ser_estra.
Pfam; PF0030; DPPIV N; I.
Pfam; PF00326; Peptidase S9; 1.
PROSITE; PS00708; PRO_ENDORPP_SER; 1.
Hydrolase; Transmembrane.
SEQUENCE 761 AA; B7843 MW; EB214BBE4BB14F2C CRC64;
                                                                                                                                                                                                                                                                                                                1 ILEENKELENALK 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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Matches
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Rattus.
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Wilson R.K.;

Wilson R.K.;

Wilson R.K.;

Submitted (ARR-2005) to the EMBL/GenBank/DDBJ databases.

Submitted (ARR-2005) to the EMBL/GenBank/DDBJ databases.

GO; GO: 0016020; C: membrane; IEA.

GO; GO: 0004274; F: catalytic activity; IEA.

GO; GO: 0004274; F: prolyl oligopetidase IV activity; IEA.

GO; GO: 0004287; F: prolyl oligopetidase activity; IEA.

RO; GO: 0006508; P: proteolysis and peptidolysis; IEA.

RINCEPPO; IPR002471; Pept. 89_AS.

InterPro; IPR002479; Ser_estrs.

RINCEPPO; IPR002479; Ser_estrs.

RINCEPPO; IPR00379; Ser_estrs.

R Pfam; PF00326; Peptidase S9; 1.

R Pfam; PF00326; Peptidase S9; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 62; DB 2; Length 760; 100.0%; Pred. No. 0.4; cive 0; Mismatches 0; Indels
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0004177; F:aminopeptidase activity; IEA.
GO; GO:0004274; F:dipeptidyl-peptidase IV activity; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0004287; F:hydrolase activity; IEA.
GO; GO:0006508; P:procelyals and peptidolysis; IEA.
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF493782; AAM11677.1; -; mRNA.
HSSP; P27487; 1PPQ.
                                                                      Cotton M., Maupin R., Hawkins M., Harkins R.; "The sequence of Homo sapiens BAC clone RP11-576116."; Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                    to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                          to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein; Transmembrane.
760 AA; 87713 MW; 7FF817B5A4F75142 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Fibroblast activation protein alpha subunit.
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GO; GO:0004287; F:prolyl oligope
GO; GO:0006508; P:proteolysis an
InterPro; IPR002471; Pept_S9_AS.
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QBR492;
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                                                                                                                                                                                       Waterston R.H.;
Submitted (OCT-1999)
                                                                                                                                                                                                                                                                      Waterston R.;
Submitted (OCT-2000)
                                                       NUCLEOTIDE SEQUENCE.
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Best Local Similarity
Matches 13; Conserv
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               NCBI_TaxID=9606;
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TISSUB-Mammary gland;

XX TISSUB-Mammary gland;

XX Strausberg R.L. Feingold E.A., Grouse L.H., Derge J.G.,

XI Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

XI Strausberg R.L., Zeeberg B., Wagner L., Shemen C.M., Schuler G.D.,

XA Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haich F.,

XA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

XA Stapleton M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

XA Stapleton M.J., Wedernan K.J., Malek J.A., Gunaratne P.H.,

Raha S.A., McEwan P.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

XA Nichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

XA Halton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

XA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S. N., Krzywinski M.I., Skalaka U., Smailus D.E.,

XA Butterfield Y.S. N., Krzywinski M.I., Skalaka U., Smailus D.E.,

XA Butterfield Y.S. N., Krzywinski M.I., Skalaka U., Smailus D.E.,

XA Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
- Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
- PUNCTION: May have a role in tissue remodeling during development and wound healing, and contribute to invasiveness in malignant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Seprase (EC 3.4.21.-) (Fibroblast activation protein alpha) (Integral membrane serine protease).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Niedermeyer J., Scanlan M.J., Garin-Chesa P., Daiber C., Flebig H.H., Old L.J., Rettig W.J., Schnapp A.; "Mouse fibroblast activation protein: molecular cloning, alternative splicing and expression in the reactive stroma of epithelial
                                                                                              Gaps
                                                                                         ;
0
    Length 761;
                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
93.5%; Score 58; DB 2;
84.6%; Pred. No. 1.8;
tive 2; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      761 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE (ISOFORMS 1; 2 AND 3).
STRAIN=BALB/c; TISSUE=Embryo;
MEDLINE=97284459; PubMed=9139873;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Int. J. Cancer 71:383-389(1997).
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Hypothetical protein.
ORFNames-Chro.70572;
Cryptosporidium hominis.
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Cryptosporidiidae; Cryptosporidium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00693; LUM BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80.6%;
90.9%;
                                                                                                                                                                                                                                                                                               Best Local Similarity 90.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                               |||||||||||
183 LEENKQLENAL 193
                                                                                                                                                                                                                                                                                                                                              2 LEENKELENAL 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1624 AA;
                                                                                                        NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                     Q5CXS4
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                                                                                                                                                                                                                         This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                   Isola-P97321-3; Sequence=VSP 005369;
TISSUE SPECIFICITY: Detected in fibroblasts, in placenta, uterus, embryos from day 7-19 and in new-born mice (Pl).
SIMILARITY: Belongs to the peptidase S9B family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Charge relay system (By similarity).
Charge relay system (By similarity).
Charge relay system (By similarity).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
Missing (in isoform 3).
       inactive (By similarity).
-!- SUBCELLULAR LOCATION: Type II membrane protein (By similarity)
-!- ALTERNATIVE PRODUCTS:
   -!- SUBUNIT: Homodimer, or heterodimer with DPP4. The monomer is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytoplasmic (Potential).
Signal-anchor for type II membrane
protein (Potential).
Extracellular (Potential).
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Pred. No. 5.3;
), Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002411; Pept 59 AS.
InterPro; IPR001375; Peptidase_S9.
InterPro; IPR001375; Peptidase_S9.
InterPro; IPR001379; Ser_estrs.
Pfam; PF00910; DPPIV N; I.
PROSITE; PS00708; PRO_ENDOPEP SER; 1
Alternative splicing; Glycoprotein; Hydrolase; Protease; Series of Series protease; Signal-anchor; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -> L (in Ref. 2).
9174C3AEDA213B25 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Missing (In isoform 2) /Frid=VSP_005368.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                             Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       005369.
                                                                                                                                                                                                                                                                                                                                                                                               MGI; MGI:109608; Fap.
GO; GO:0016021; C:integral to membrane; TAS.
                                                                                                                         IsoId=P97321-2; Sequence=VSP_005368;
                                                                                                                                                                                                                                                                                                                                                                              Ensembl; ENSMUSG00000000392; Mus musculus.
                                                                                          IsoId=P97321-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FTIG=VSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Missing
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                                                                                                                                                                                                                                                                                                                   EMBL; Y10007; CAA71116.1; -; mRNA.
EMBL; BC019190; AAH19190.1; -; mRNA.
HSSP; P27487; 1PFQ.
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76.98;
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Best Local Similarity 76.5.
-heg 10; Conservative
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QSCDS3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ILEENKELENALK 13
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                                                                                                                                                                                                                                                                                                                                                                  MEROPS: S09.007;
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                                                                                                           Name=2
                                                                                                                                          Name=3
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ACT_SITE
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ACT_SITE
ACT_SITE
CARBOHYD
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CARBOHYD
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CARBOHYD
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ID OS
AC OS
DT 10
DT 10
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STRAIN=TUS02;
Xu P., Widmer G., Wang Y., Ozaki L.S., Alves J.M., Serrano M.G.,
Yu P., Widmer G., Akiyoshi D., Mackey A.J., Pearson W.R., Dear P.H.,
Bankler A.T., Peterson D.L., Abrahamsen M.S., Kapur V., Tzipori S.,
Buck G.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Iowa type II;
PubMcd=15044751; DOI=10.1126/science.1094786;
Abrahanten M.S., Templeton T.J., Enomoto S., Abrahante J.E., Zhu G. Lancto C.A., Deng M., Liu C., Widmer G., Tzipori S., Buck G.A., Xu Bankier A.T., Dear P.H., Konfortov B.A., Spriggs H.F., Iyer L., Anantharaman V., Aravind L., Kapur V.;
"Complete genome sequence of the apicomplexan, Cryptosporidium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 which is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GACKS4_CRYPV
05CXS4_CRYPV PRELIMINARY; PRT; 1624 AA.
05CXS4;
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Hypothetical low complexity protein with coiled coil regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 50; DB 2; Length 1624; Pred. No. 74;
                                                                                                                                                                                                                                                                                                                                                         80.6%; Score 50; DB 2; Length 352; 90.9%; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        parvum.";
Science 304:441-445(2004).
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORFNames=cgd7_5130;
Cryptosporidium parvum,
Bukaryota; Alveolata; Apicomplexa; Coccidia; Eimerlida;
Cryptosporididae; Cryptosporidium.
                                                                                                                                                        "The genome of Cryptosporidium hominis.";
Nature 431:1107-1112(2004).
BMBL; AAELO1000939; EAL34754.1; -; Genomic_DNA.
Hypothetical protein:
SEQUENCE 352 AA; 41011 MW; 83BE269AD8026310 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAEE01000001; EAK90470.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
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InterPro; IPR000888; dTDP Sugar isom.
InterPro; IPR011992; EF Hand type.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR0100259; Fimbrial.
InterPro; IPR0110486; HdeA.
InterPro; IPR012287; Homeodomain-rel.
InterPro; IPR001783; Lum_binding.
InterPro; IPR001931; Wing_hlx_DNA_bd.
InterPro; IPR011991; Wing_hlx_DNA_bd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bind.
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GeneDB_Spombe; SPCC1884.02;
                        1 ILEENKELENALK 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa (japonica cultivar-group).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bopermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria, Spirochaetes, Spirochaetales, Spirochaetaceae, Borrelia,
Borrelia burgdorferi group.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
79.0%; Score 49; DB 2; Length 653;
Best Local Similarity 69.2%; Pred. No. 41;
Matches 9; Conservative 3; Mismatches 1; Indels
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GTOCKNET G., Schilhabel M., Lehmann R., Platzer M.;
GTOCKNET G., Schilhabel M., Lehmann R., Platzer M.;
GLOCKNET G., Schilhabel M., Lehmann R., Platzer M.;
SUDMITTEG (SES-2014) ALUS6078.1; -; Genomic DNA.
GO; GO:0006313; P:DNA transposition; IEA.
Hypothetical protein.

SEQUENCE 147 AA; 17320 MW; 2FB3455E2732018E CRC64;
   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
SEQUENCE 653 AA; 73039 MW; F680E30FCF8C8225 CRC64;
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Last sequence update)
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                                                                                                                                                                                                                                                                     653 AA
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      Mismatches
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01-MAR-2003 (TrEMBLrel. 23, Last sequ
01-MAR-2003 (TrEMBLrell. 23, Last sequ
Hypothetical protein OSJNBb0043C10.4.
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25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
Hypothetical protein.
ORFNames=BGP227;
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QSXYQ4;
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                                                                                                                                                                                                                                    7 ORYSA
QBH7V7 ORYSA PRELIMINARY;
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                                                                                                                   1455 LEENKQLENAL 1465
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      10; Conservative
                                                            2 LEENKELENAL 12
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Best Local Similarity
Matches 9; Conserv
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      Matches
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Q5XYQ4_BO
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RK MEDLINE=2184801; PubMed=11859360; DOI=10.1038/nature724;

KN MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;

KN MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;

KN MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;

RA Sgourcs J.G., Peat N., Hayles J., Baker S.G., Basham D., Bowman S.,

RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

RA Gentles S., Goble A., Hamlin N., Harris D.E., Hidalgo J., Hodgson G.,

RA HOLFOYG S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

RA HOLFOY S., Jones L., Jones M., Leather S., McDonald S., McLean J.,

RA James K.D., Jones L., Jones M., Leather S., McDonald S., McLean J.,

RA Jones K.D., Jones L., Gress M., Seeger K., Saeger K., Saeger K.,

RA Mooney P., Moule S., Mungall K.L., Murphy L.D., Niblett D., Odell C.,

RA Taylor K., Taylor R.G., Tivey A., Walsh S., K., Warren T., Whitehead S.,

RA Taylor K., Taylor R.G., Tivey A., Walsh S., Stevens K.,

RA Taylor K., Taylor R.C., Tivey A., Walsh S., Schaefer M., Mueller-Auer S.,

RA Hilbert H., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R.,

RA Hilbert H., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R.,

RA Galibert R., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

Loas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,

Lower T., Mcrenc Z., Sanchez M., dalzon A., Thode G.,

RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., dal Rey F., Benito J.,

RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,

Nature A., Reyder M., Rochelt J., Moreno S., Armare Componer M.,

RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,

Nature A., Reyder M., Rochel M., Rochel M., Medler M., Nature A.,

RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         biosynthesis.";
J. Biol. Chem. 275:18029-18033(2000).
-!- FUNCTION: High-affinity nickel transporter responsible for nickel
uptake. Required for urease biosynthesis.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
-!- SIMILARITY: Belongs to the NiCoT transporter (TC 2.A.52) family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20309746; PubMed=10748059; DOI=10.1074/jbc.M001978200; Eitinger T., Degen O., Bohnke U., Muller M.; "Niclp, a relative of bacterial transition metal permeases in Schizosaccharomyces pombe, provides nickel ion for urease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
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                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
High-affinity nickel transport protein nicl.
Name=nicl; ORFNames=SPCC1884.02, SPCC757.01;
Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
                                                                                                                                                                                                                                                                                          405 AA
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EMBL; AL031825; CAA21226.1; -; Genomic_DNA.
PIR; T41194; T41194.
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27 VIEENKILKNALK 39
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                                                                                                                                                                                                                                                                                          STANDARD;
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ORFNames=RCJMB04_29921;
ORFNames=RCJMB04_29921;
ORINIUS gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianidae;
                          Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
James K., Rutherford K., Harris B., Harris D., Churcher C.,
Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
Bidwell S.L., Rajandream M.A., Carucci D.J, Yates J.R., Kafatos F.C.,
Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
"A comprehensive survey of the Plasmodium life cycle by genomic,
transcriptomic, and proteomic analyses.";
Science 307.82-86(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.

Kehrenberg C., Ojo K.K., Schwarz S.;

"Nucleotide sequence and organization of the multiresistance plasmid pSCTS1 from Staphylococcus sciuri.";

DSCTS1 from Staphylococcus sciuri.";

J. Antimicrob. Chemother. 54:936-939(2004).

EMBL; AJ579365; CAE18150.1; -; Genomic_DNA.
                                                                                                                                                                                                      -i- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                            Score 45; DB 2; Length 219;
Pred. No. 57;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71.0%; Score 44; DB 2; Length 176; 61.5%; Pred. No. 66;
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                                                                                                                                                                                                                                                                   EMBL; CAAJ01007140; CAH84894.1; -; Genomic_DNA.
Hypothetical protein.
SEQUENCE 219 AA; 25862 MW; F44947037B46CAA6 CRC64;
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Last annotation update)
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Last annotation update)
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NCBI_TaxID=1296;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence
11-OCT-2004 (TrEMBLrel. 26, Last annotation
Putative recombinase/mobilization protein.
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Q5Z181_CHICK PRELIMINARY;

Q5Z181;

25-OCT-2004 (TrEMBLED. 28, L

25-OCT-2004 (TrEMBLED. 28, L

25-OCT-2004 (TrEMBLED. 28, L
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Best Local Similarity 61.5.
Best Local 8; Conservative
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Q7WVB4;
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61 VYQENKELKNELK 73
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nes 8; Conservative
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NCBI_TaxID=9031;
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Matches
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STRAIN-ATCC 35092 / DSM 1617 / P2;
STRAIN-ATCC 35092 / DSM 1617 / P2;
MEDLINE-21332296; PubMed=11427726; DOI=10.1073/pnas.141222098;
MASH Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
De Moors A., Erause G., Fletcher C., Gordon P.M.K.,
Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
Charlebois R.L., Doolittle W.F., Duguet M., Gast-Clobus solfataricus P2.;
The complete genome of the crenarchaeon Sulfolobus solfataricus P2.;
The complete Sci. U.S.A. 98:7835-7840(2001).

REMBL, AE006806; AAK42183.1; -; Genomic_DNA.
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Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein.
ORFNames=PC301291.00.0;
PRISMODIUM Chabaudi.
Bukaryota, Alveolata, Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5825;
                                                                                                                                                                                                                                  Score 47; DB 1; Length 405;
Pred. No. 52;
2; Mismatches 2; Indels
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SEQUENCE 162 AA; 18791 MW; 5F9595D273E868C8 CRC64;
                                                                                                                                                                            Potential.
44CCB1BE7D13EFC8 CRC64;
                                        Complete proteome; Nickel; Transmembrane; Transport.
TRANSMEM 35 55 Potential.
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Last annotation update)
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Potential.
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InterPro, IPR011541; Nico_transpt
                                                                                                                                                                                                45295 MW;
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                                                                                                                                                                                                                                                                                                                                            371 VLEKNKELENVSK 383
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Q97wwe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q4XDX5_PLACH PRELIMINARY;
                                                                                                                                                                                                                    Query Match
Best Local Similarity 69.2
Local 9; Conservative
                                                                                                                                                                                                                                                                                                                 1 ILEENKELENALK 13
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Matches 8; Conservative
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24 LEENKKIENEIK 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
                      Pfam; PF03824; NicO;
                                                                                                                                                                              330 3
405 AA;
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                                                                                                 TRANSMEM .
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SEQUENCE
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                                                                              TRANSMEM
                                                                                                                                       TRANSMEM
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Q4S9W6_TET
ID Q4S9W
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Sucgang R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,
A Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
Bankler A.T., Lehmann R., Hamilan N., Davies R., Gaudet P., Fey P.,
Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
Rethornou A., Nier K., Halla N., Anjard C., Hamphill L., Bason N.,
Rarborcher P., Desany B., Just E., Morio T., Rost R., Churcher C.,
Cooper J., Haydock S., Van Driessche N., Cronin A., Goodhead I.,
Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
Wardroper A., Felder M., Thangavelu M., Johnson D., Knights A.,
Loulseged H., Mungall K., Oliver K., Price C., Quail M.A.,
Unushihara H., Hernandez J., Rabbinowitsch E., Steffen D., Sanders M.,
Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
Sharp S., Simmonds M., Spiegler S., Tivey A.,
Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
Shaulsky G., Schleicher M., Weinercck G., Rosenthal A., Cox B.C.,
Alliams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;
"The genome of the social amoeba Dictyostelium discoideum.",
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
           STRAIN-CB; TISSUE-Bursa;
Caldwell R.B., Kierzek A.M., Arakawa H., Bezzubov Y., Zaim J.,
Fiedler P., Kutter S., Blagodateki A., Kostovska D., Koter M.,
Plachy J., Carninci P., Hayashizaki Y., Buerstedde J.M.;
"Full-length CDNAs from chicken bursal lymphocytes to facilitate
genefunction analysis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                    Genome Biol. 6:R6-R6(2005).

EMBL; AJ720903; CAG22562.1; -; mRNA.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0004177; F:aminopeptidase activity; IEA.

GO; GO:0004274; F:idipeptidyl-peptidase IV activity; IEA.

GO; GO:0004287; F:prolyl oligopeptidase activity; IEA.

GO; GO:0006289; F:prolyl oligopeptidase activity; IEA.

GO; GO:0006289; P:proteolysis and peptidolysis; IEA.

InterPro; IPR002471; Peptidase.

InterPro; IPR002471; Peptidase.

InterPro; IPR002469; Peptidase.

InterPro; IPR002469; Peptidase.
                                                                                                                                                                                                                                                                                                                                                                                                 71.0%; Score 44; DB 2; Length 759; 75.0%; Pred. No. 3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                   Interpro; IPR000379; Ser estrs.
Pfam; PF00930; DPPTV N; I.
Pfam; PF00126; Peptidase S9; I.
PROSITE; PS00706; PRO ENDOPEP SER; I.
Hydrolase; Hypothetical protein; Transmembrane.
SEQUENCE 759 Aa; 86343 MW; B9A0C38CCB8644AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dictyostelium discoideum (Slime mold).
Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein.
ORFNames=DDB0191988;
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EMBL; AAFI01000293; EAL60584.1; -; Genomic_DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 75.0
Matches 9; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Embryo;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                          Length 2110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 458;
Hypothetical protein.
SEQUENCE 2110 AA; 248356 MW; BB2FE3A6E2228424 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 458 AA, 52353 MW, B10D5E819C7D1611 CRC64;
                                                                                                                                                                                                                                                    05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
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Pred. No. 2.6e+02;
                                            Score 44; DB 2; I
Pred. No. 8.8e+02;
3; Mismatches 2;
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Ensembl; ENSDARG0000026834; Danio rerio.
ZFIN; ZDB-GENE-030131-8171; zgc:77462.
                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                   Hypothetical protein zgc:77462.
ORFNames=zgc:77462;
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                                     Query Match
Best Local Similarity 61.5%;
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                                                                                                                                          337 LLENNKKLENEIK 349
                                                                                                                                                                                   RESULT 15
QGNZT2 BRARE
ID QGNZT2_BRARE PRELIMINARY;
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Best Local Similarity
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NIH MGC Project;
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preliminary data.
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STRAIN=PEST;
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                                                                                                                                                            NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                     Local Similarity
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SEQUENCE
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Matches
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Maucali E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
Anthouard V., Jubin C., Castelli V., Ratinka M., Vacherie B.,
Biemont C., Skalli Z., Cattolic D., Poulain J., De Berardinis V.,
Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
Relis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
T. The early vertebrate proto-karyotype.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tetraodon nigroviridis (Green puffer).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                 Tetraodon nigroviridis (Green puffer).

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Erdinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes,
Tetradontoidea, Tetraodontidae, Tetraodon.
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last anotation update)
Chromosome undetermined SCAF14696, whole genome shotgun sequence.
                13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last amotation update)
Chromosome undetermined SCAF14694, whole genome shotgun sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
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61.5%; Pred. No. 2.7e+02;
w.emarches 1; Indels
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RR 469 469
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                                                                                       ORFNames=GSTENG00021713001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q4S9L4 TETNG
ID Q4S9L4 TETNG PRELIMINARY;
AC Q4S9L4;
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Matches 8, Conservative
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Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V., Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J., Parad G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S., Kellis M., Volff W., Guigo R., Zody M.C., Mesirov J., Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M., Laudet V., Scharhter V., Quetier F., Saurin W., Scarpelli C., Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.; "Genome duplication in the teleost fish Tetraodon nigroviridis reveals the early vertebrate proto-karyotype.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Culicidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The Anopheles gambiae Sequence Committee, Submitteed (APR-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                  Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FBB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Anopheles gambiae re-annotation.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
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532 AA; 59179 MW; EBBA3F7D277AA628 CRC64;
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 43; DB 2; I
Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAAE01014696; CAG02668.1; -; Genomic_DNA.
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InterPro; IPR002017; Spectrin.
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                                                                                                                                                                                                                                                                                        Nature 431:946-957(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :|| |||||::|:
51 LLERNKELEDSLQ 63
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Trust T.J.;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                 Philippsen P., Kleiner K., Pochlann R., Duesterhoeft A., Hamberg K., Alegemann J.H., Obermaier B., Urrestearazu L.A., Aert R., Albermann K., Altemann Y., Andre B., Baladron V., Ballesta J.P.G., Becam A.-M., Athermann R., Altemann R., Andrews B., Beinhauer J.D., Boskovic J., Bultrago M.J., Bussereau F., Coster F., Crozet M., D'Angelo M., Dal Pero F., De Antoni A., del Rey F., Doignon F., Domdey H., Dubois E., Fiedler T.A., Fleig U., Floeth M., Fritz C., Gaillardin C., Garcia-Cantalejo J.M., Glansdorff N., Goffeau A., Gueldener U., Herbert C.J., Heumann K., Heuss-Neitzel D., Hibbert H., Hinni K., Iraqui Houssaini I., Jacquet M., Jimenez A., Jonniaux J.-L., Karpfinger-Harl L., Lanfranchi G., Lepingle A., Levesque H., Lyck R., Maftahi M., Mallet L., Maurer C.T.C., Nicaud J.-M., Niedenthal R.K., Pandolfo D., Pieravadi E., Planta R.J., Niedenthal R.K., Pandolfo D., Pieravadi E., Planta R.J., Pohl T.M., Purnelle B., Rebischung C., Remacha M.A., Revuelta J.L., Saitzorello F., Scherens B., Sen-Gupta M., Soler-Mira A., Urbanue J.H.M., Volckaert G., Wach A., Verhasselt P., Mambutt R., Wedler H., Roller H., Sollner A., Hani, J.; Amming M., Hank, M., Manbutt R., Wedler H., Man, M., Hani, J.
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Ensembl; YNL021W; Saccharomyces cerevisiae.
Ensembl; YNL021W; Saccharomyces cerevisiae.
SGD; S000004966; HDA1.
GO; GO:0000118; C:histone deacetylase complex; IDA.
GO; GO:0004407; F:histone deacetylase activity; IDA.
GO; GO:000525; P:establishment and/or maintenance of chromat. . .; TAS.
GO; GO:0001308; P:loss of chromatin silencing during replicat. . .; IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "HDA1 and RPD3 are members of distinct yeast histone deacetylase complexes that regulate silencing and transcription."; wat. Acad. Sci. U.S.A. 93:14503-14508(1996).

Proc. Natl. Acad. Sci. U.S.A. 93:14503-14508(1996).

I stone deacetylation of lysine residues on the N-terminal part of the core histones (HDA, HDB, H3 and H4). Histone deacetylation gives a tag for epigenetic repression and plays an important role in transcriptional regulation, cell cycle progression and developmental events. Histone deacetylases act via the formation of large multiprotein complexes.

-1- SUBCELLULAR LOCATION: Nuclear.

-1- SIMILARITY: Belongs to the histone deacetylase family. Type 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The nucleotide sequence of Saccharomyces cerevisiae chromosome XIV
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MEDLINE=97121415; PubMed=8962081; DOI=10.1073/pnas.93.25.14503;
Rundlett S.E., Carmen A.A., Kobayashi R., Bavykin S., Turner B.M.,
                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                    Histone deacetylase HDA1.
Name=HDA1; OrderedLocusNames=YNL021W; ORFNames=N2819;
                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                   01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
10-WAY-2005 (Rel. 47, Last annotation update)
                                          706 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and its evolutionary implications."; Nature 387:93-98(1997).
                                          PRT;
                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97313269; PubMed=9169873;
                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IntAct; P53973; -. GermOnline; 143028; -.
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                                                                                                                                                                                                                                                                NCBI_TaxID=4932;
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                                        HDA1 YEAST
P53973;
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RESULT 19
HDA1_YEAST
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MEDLINE=99120557; PubMed=9923682; DOI=10.1038/16495;
Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C., Smith D.R., Noonan B., Guila B.C., deJonge B.L., Carmel G., Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C., Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAN-1998 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Conserved hypothetical ATP-binding protein.
OrderedLocusNames=HP0066;
Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
EMBL; AR01145; AAD05645.1; -; Genomic_DNA.
GO; GO:0006476; P:protein amino acid deacetylation; IDA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; TAS.
InterPro; IPR000286; His deacetylse.
PANTHER; PFHR10625; His deacetylse; 1.
Pfam; PF00850; Hist deacetyl; 1.
Pfam; PR01270; HDASUPER.
Chromatin regulator; Complete proteome; Hydrolase; Nuclear protein; Repressor; Transcription; Transcription; Transcription; Protein;
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Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales,
Helicobacteraceae, Helicobacter.
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                             Histone deacetylase.
By similarity.
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81.8%; Pred. No. 4.1e+02;
iive 1; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                706 AA; 80070 MW;
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155 ILTESKEIEEALK 167
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22 LEENKEEENSL 32
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Hypothetical protein.
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32 EENKOFENAL
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                                                                                                        MEDLINE=97394467; PubMede=952185; DOI=10.1038/41483;
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Peleischmann R.D., Kerchum K.A., Klenk H.-P., Gill S.R.,
Dougherty B.A., Nalson K.E., Quackenbush J., Zhou L., Kirkness B.F.,
Peterson S.N., Loftus B.J., Richardson D.L., Dodson R.J., Khalak H.G.,
Glodek A., McKenney K., FitzGerald L.M., Lee N., Adams M.D.,
Hickey B.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D.,
Watthey E.K., Mallin E., Hayes W.S., Borodovsky M., Karp P.D.,
Smith H.O., Fraser C.M., Venter J.C.,
"The complete genome sequence of the gastric pathogen Helicobacter
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GO; GO:000166; F:nucleotide binding; IEA.
GO; GO:0000166; F:nucleotide binding; IEA.
InterPro; IPR001543; AAA ATPase.
InterPro; IPR001543; FteK SpOIITE.
Ffam; PR01580; FteK SpOIITE; 1.
SNART; SM00182; AAA; 1.
Complete proteome.
SCOUENCE 831 AA; 95646 MW; F674CBA4A82AF587 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69.4%; Score 43; DB 2; Length 831
69.2%; Pred. No. 4.8e+02;
Linmarrhes 2; Indels
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SEQUENCE 172 AA, 19843 MW, SFSFDBD05EEAE7CA CRC64;
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Last annotation update)
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EMBL; BA000001; BAA30707.1; -; Genomic_DNA.

PIR; C71038; C71038.

INCEPPO; IPR000644; CBS.

PÉm; PF00571; CBS; 1.

SMART; SM00116; CBS; 2.
                                                                                                                                                                                                                                                                                                                                                                                  pylori.";
Nature 388:539-547(1997).
EMBL; AE000528; AAD07129.1; -; Genomic_DNA.
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Helicobacteraceae; Helicobacter
                                                                   NUCLEOTIDE SEQUENCE.
STRAIN=26695 / ATCC 700392;
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178 ILTESKEIEEALK 190
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059254;
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Best Local Similarity 69.2
Matches 9; Conservative
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TIGR; HP0066; -.
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                      NCBI_TaxID=210;
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                                                                                Gaps
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Eukaryota; Viridiplantes; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Malpighiales; Euphorbiaceae; Crotonoideae;
Micrandreae; Hevea.
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Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids, eurosids I; Malpighiales; Euphorbiaceae; Crotonoideae;
Micrandreae; Hevea.
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Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
L. SUBCELLULAR LOCATION: Nuclear (By similarity).
R. EMBL, AF229956; AAG444394.1; -; MRNA.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:00045449; P:regulation of transcription; IEA.
R. GO; GO:0045449; P:regulation of transcription; IEA.
R. InterPro; IPR012287; Homeodomain-rel.
R. InterPro; IPR012287; Homeodomain-rel.
R. InterPro; IPR00147; SHAGKYF—myb_bd.
R. Frank, FR00249; Myb_DNA_bd.
R. SMART; SM00717; SANY. 2.
R. SMART; SN00717; SANY. 2.
R. FIGRRAMS; TIGR01557; myb_SHAGKYF; 1.
R. PROSITE; PS50009; MYB_3; 2.
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                          Length 172;
Score 42; DB 2; Length 1/2, Pred, No. 1.3e+02;
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Last annotation update)
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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80.0%; Pred. No. 2.5e+02;
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                                                                                                                                                                                                                                                                                                                                               PRT;
                          67.7%;
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QGERNI;
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Q9FQF4;
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es 8; Conservative
                          Query Match 67.7
Best Local Similarity 69.2
Matches 9; Conservative
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1 ILEENKELENALK 13
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                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                              Name=HUMPPA;
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Matches
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Q4XEG4 PLA
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                                                                                       Venkatachalam P., Raghothama K.G., Thulaseedharan A.;
Venkatachalam P., Raghothama K.G., Thulaseedharan A.;
"Cloning and nucleotide sequence analysis of MYB transcription factor associated with TPD syndrome in rubber tree (Hevea brasiliensis).";
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.

C. !- SUDMCELLULAR LOCATION: Nuclear (By similarity).

REME, AY712938; AAU06309.1; -; Genomic_DNA.

G. GO: 0003673; F:DNA binding; IEA.

InterPro; IPR012287; Homeodomain-rel.

R interPro; IPR012287; Homeodomain-rel.

R interPro; IPR006447; SHAĞKYF_myb_bd.

R ffam; PF00249; Myb_DNA-binding; Z.

SMART; SM0717; SAÑT; Z.

R Ffam; PR0517; PS08 binding; Z.

R WIGHER PROSITE; PS0609; WYB_3; Z.

R Nuclear procein; Repeat.

SEQUENCE 310 AA; 35058 MW; 87F7A24821D87B74 CRC64;
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MEDLINE-2186394; PubMed=11889109;
MEDLINE-218640394; PubMed=11889109;

Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A., Battacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L., Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman B., Bernal A., Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R., Fonstein M., Kyrpides N.C., Overbeek R.;

"Genome sequence and analysis of the oral bacterium Fusobacterium nucleatum strain ATCC 25586 ",
J. Bacceriol. 184:2005-2018(2002).

EMBL, AE009551; AAL94814.1; -; Genomic_DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67.7%; Score 42; DB 2; Length 310;
80.0%; Pred. No. 2.5e+02;
iive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fusobacterium nucleatum (subsp. nucleatum).
Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Spermidine/putrescine-binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        342 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00909; SPERMDNBNDNG.
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Best Local Similarity 80.00,
Best Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QBRFR9 FUSNN PRELIMINARY;
QBRFR9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01547; SBP bac 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OrderedLocusNames=FN0618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 EENKELENAL 12
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                                                       NUCLEOTIDE SEQUENCE
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QBRFR9 FUSNN
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MEDLINE-2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE-2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
R trausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
R tlausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Richards S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Hakeeley R.W., Touchman J.W., Garen E.D., Dickson M.C.,
A Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
B. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 459;
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61.5%; Pred. No. 3.7e+02;
tive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH MGC Project;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC047534; AA447534.1; -; mRNA.
Ensembl; BC0360000109989; Homo sapiens.
SEQUENCE 459 AA; 52368 MW; 375796A4F0D7E764 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein (Fragment).
ORFNames-PC301191.00.0;
                                                                                                                                                                                                                                                                                             01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           523 AA.
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:|:::| ||||:|
261 VLKDSKHLENAMK 273
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                                                                                                                                                                                                                       Q86X02_HUMAN PRELIMINARY;
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les 8; Conservative
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Gaps

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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
Kawabbera A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Kawabbera A., Hikiji T., Kobatake N., Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.; Submitted (MGG-2000) to the EMBL/GenBank/DDBJ databases.
Submitted (AGG-2000) to the EMBL/GenBank/DDBJ databases.
BMBL, 34025632; BAB15196.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
11.3-SFP-2006 (Rel. 48, Last annotation update)
Alanyl-tRNA synthetase (EC 6.1.1.7) (Alanine--tRNA ligase) (AlaRS)
Name-alaS, OrderedLocusNames=RP856;
Rickettsia prowazekii.
NUCLECTIDE SEQUENCE.
Fathallah-Shaykh H.M., Finizio J., Ho A., Rosenblum M., Posner J.;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; LO2867; AAA91850.1; -; mRNA.
Ensembl; ENSG0000109089; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=9993949; PubMed=9823893; DOI=10.1038/24094; Andersson S.G.B., Zomorodipour A., Andersson J.O., Scheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K., Erikason A.-S., Winkler H.H., Kurland C.G.; "The genome sequence of Rickettsia prowazekii and the origin of mitochondria."; Nature 396:133-140(1998).
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Rickettsiaceae; Rickettsieae; Rickettsia; typhus group.
NCBI_TaxID=782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 720;
                                                                                                                                                             Length 535;
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                                                                                                                                                                                                      2; Indels
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                                                                                                                       535 AA; 58013 MW; 6C80A459E88BA1DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                             Score 42; DB 2; 1
Pred. No. 4.4e+02;
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Pred. No. 6e+02;
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                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein FLJ21979.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67.78;
53.88;
                                                                                                                                                             Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative
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108 LLERNKELEGSLQ 120
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les 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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SEQUENCE
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SEQUENCE
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Q9H6Q7_HUM
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                         Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
James K., Rutherford K., Harris B., Harris D., Churcher C.,
Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
Bladell S.L., Rajandream M.A., Carucci D.J. Yates J.R., Kafatos F.C.,
Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.,
"A comprehensive survey of the Plasmodium life cycle by genomic,
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Submitted (App.-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AYS0151; AAT012781. -; mRNA.
SEQUENCE 534 AA; 62429 WW; 44730BF32F13DB87 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                    transcriptomic, and proteomic analyses.";
Science 307:82-86(2005).
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

EMBL; CAAJ01007003; CAH84704.1; -; Genomic_DNA.
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                                                                                                                                                                                                                                                                                                                                                                                             Length 523;
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Pred. No. 4.3e+02;
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Pred. No. 4.4e+02;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                     523 AA; 61763 MW; 761E46033CBBBC6 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUL-2004 (TrEMBLrel. 27, C. 05-JUL-2004 (TrEMBLrel. 27, Le 05-JUL-2004 (TrEMBLrel. 27, Le Proetate cancer antigen T21. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67.7%;
53.8%;
                                                                                                                                                                                                                                                                                                                                                                                               67.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                  69.2%;
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Q15175;
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70 LVEENKQLEEGMK 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ILEENKELENALK 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 69.2
                                                                                                                                                                                                                                                                                                                 Appothetical protein.
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TISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
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[1]
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Q15175_HUM
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Caralle-Urboring Saccond Caracteristics of Strain-Urboring Saccond Caralle-Urboring Saccond Caralle-Urboring Saccond Caralle-Urboring Saccond Caralle-Urboring Caralle-Urboring Caralle-Urboring Caralle-Urboring Caralle-Urboring Caralle-Urboring Caralle-Urboring Caralle-Urboring Caralle-Urboring Caralle-Urboring Caralle-Urboring Caralle-Urboring
R HAMAP; MF 00036; -; 1.

R InterPro; IPR003156; Pesterase_DHHA1.

InterPro; IPR003156; Pesterase_DHHA1.

R InterPro; IPR012947; tRNA-synt_2c.

R Pfam; PF02272; DHHA1; 1.

R Pfam; PF0141; tRNA-synt_2c; 1.

R Pfam; PF0141; tRNA-synt_2c; 1.

R Pfam; PF0141; tRNA-synt_2c; 1.

R Pfam; PF0141; tRNA-synt_2c; 1.

R Pfam; PF0141; tRNA-synt_ac; 1.

R Pfam; PF0141; tRNA-synt-ac; 1.

R Pfam; PF0141; tRNA-syntheia.

R PR0251TE; PS50860; AA TRNA LIGAE II ALA; 1.

R Aminoacyl-tRNA synthetase; ATP-binding; Complete proteome; Ligase;

W Mulloclide-binding; Protein biosynthesis.

SEQUENCE 877 AA; 99125 MW; CF51798B7FC0016E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
Alanyl-tRNA syntherase (EC 6.1.1.7).
Name=alaS; OrderedLocusNames=RF_1353;
Rickettsia fells (Rickettsia azadi).
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae, Rickettsiace, spotted fever group.
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                                                                                                                                                                                                                                                                                                                                                                                   Score 42; DB 1; I
Pred. No. 7.4e+02;
1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67.7%; Score 42; DB 2; 1
69.2%; Pred. No. 7.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).
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                                                                                                                                                                                                                                                                                                                                                                                         67.7%;
                                                                                                                                                                                                                                                                                                                                                            Query Match
Query Local Similarity 69.44,
Best Local 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       738 ILERNKELEKELE 750
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ID TSP1_BOVIN
AC Q28178; Q28179;
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                                                                                                                                     This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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R HAMAP: MF 00036; -; 1.

R InterPro; IPR00316; Pesterase DHHAI.

R InterPro; IPR00129; FRNA-synt_2c.

R InterPro; IPR012947; KRNA-synt_2c.

R Pfam; PF02272; DHHAI; LRNA-synt_2c, 1.

R Pfam; PF0271; LRNA-synt_2c; 1.

R Pfam; PF0999; TRNA-synt_2c; 1.

R PRO91TE; PS0860; TRNASYNTHAIA.

R TIGRRAMS; TIGR0034; alas; 1.

R PRO91TE; PS0860; AA TRNA LIGASE II ALA; 1.

R PRO91TE; PS0860; AA TRNA LIGASE II ALA; 1.

R Maminoacyl-trNA synthetase; ATP-bIndIng; Complete protecome; Ligase; W Nucleocide-binding; Protein biosynthesis.

O SEQUENCE 877 AA; 99414 MW; 2BAB74099804379B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-MAY-2005 (Rel. 47, Created)
10-MAY-2005 (Rel. 47, Last sequence update)
113-SEP-2005 (Rel. 48, Last annotation update)
Alanyl-tRNA synthetase (EC 6.1.1.7) (Alanine--tRNA ligase) (AlaRS)
NamesalaS, OrderedLocusNames=RT0845;
Rickettsia typhi
           diphosphate + L-alanyl-tRNA(Ala).
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: Belongs to the class-II aminoacyl-tRNA synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Profeobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsiaae; Rickettsia; typhus group.
NCBI_TaxID=785;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h Score 42; DB 1; Length 877; Similarity 69.2%; Pred. No. 7.4e+02; 9; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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Best Local Similarity
Matches 9; Conserv
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Q68VQ7;
                                                                                             family
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RESULT 32

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TSP type-1 2.
TSP type-1 3.
EGF-like 1.
EGF-like 2.
EGF-like 2.
TSP type-3 1.
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   EGF-like domain; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GlcNAc. . .)
(GlcNAc. . .)
(GlcNAc. . .)
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Interchain (Probable)
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                                                       By similarity.
Thrombospondin-1.
TSP N-terminal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GlcNAc
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Calcium; Cell adhesion; EGF-like
Heparin-binding; Repeat; Signal.
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TSP1 HUMAN STANDARD; I
AC P07996; Q15667;
DT 01-AUG-1988 (Rel. 08, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Aortic endothelium;
Zafar R.S., Moll Y.D., Womack J.F., Walz D.A.;
"Cloning and sequencing of bovine thrombospondin stimulatory effect of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Adhesive glycoprotein that mediates cell-to-cell and cell-to-matrix interactions. Can bind to fibrinogen, fibronectin, laminin, type V collagen and integrins alpha-V/beta-1, alpha-V/beta-3 and alpha-IIb/beta-3. May play a role in dentinogenesis and/or maintenance of dentin and dental pulp.
-!- SUBUNIT: HOMOLYIMEY disulfide-linked.
                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
STRAIN=Holstein; TISSUE=Tooth;
MEDLINE=98173773; PubMed=5507054; DOI=10.1016/S0167-4838(97)00188-X;
Ueno A., Yamashita K., Nagata T., Tsurumi C., Miwa Y., Kitamura S.,
                                                                                                                     Name-THBS1; Synonyms-TSP-1, TSP1;
Bos taurus (Bovine)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "cDNA cloning of bovine thrombospondin 1 and its expression in odontoblasts and predentin."; Biochim. Biophys. Acta 1382:17-22(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - SIMILARITY: Belongs to the thrombospondin family.
- SIMILARITY: Contains 3 EGF-like domains.
- SIMILARITY: Contains 1 TSP C-terminal (TSPC) domain.
- SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
- SIMILARITY: Contains 3 TSP type-1 domains.
- SIMILARITY: Contains 7 TSP type-3 domains.
- SIMILARITY: Contains 1 WWFC domain.
   01-NOV-1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
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EGF_2: 1.
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EMBL; X87619; CAA60951.1; -; mRNA.
PIR; S55501; S55501.
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PF02412; TSP_3;
PF05735; TSP_C;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                   TISSUE-Endothelial cell;
MEDLINE-87057617; PubMed-2430973; DOI=10.1083/jcb.103.5.1635;
Lawler J., Hynes R.O.;
"The structure of human thrombospondin, an adhesive glycoprotein with multiple calcium-binding sites and homologies with several different
                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE OF 1-397.
MEDLINE-87157592; Pubmed-3030396;
Kobayashi S., Eden-Mccutchan F., Framson P., Bornstein P.;
"Partial amino acid sequence of human thrombospondin as determined by analysis of cDNA clones: homology to malarial circumsporozoite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDINE-56287276; PubMed-3461443;
Dixit V.M., Hennessy S.W., Grant G.A., Rotwein P., Frazier W.A.;
"Characterization of a cDNA encoding the heparin and collagen binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-89291870; PubMed-2544587;
Laherty C.D., Gierman T.M., Dixit V.M.;
"Characterization of the promoter region of the human thrombospondin gene. DNA sequences within the first intron increase transcription.";
J. Biol. Chem. 264:11222-11227(1989).
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MEDLINE=22338361; PubMed=12450399; DOI=10.1021/bi026463u;
Huwiler K.G., Vestling M.M., Annis D.S., Mosher D.F.;
Huwiler K.G., Vestling M.M., Annis D.S., Mosher D.F.;
"Biophysical characterization, including disulfide bond assignments,
of the anti-angiogenic type 1 domains of human thrombospondin-1.";
Biochemistry 41:14329-14339(2002).
-!- FUNCTION: Adhesive glycoprotein that mediates cell-to-cell and
cell-to-matrix interactions. Can bind to fibrinogen, fibronectin,
                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
MEDLINE=89139590; PubMed=2918029; DOI=10.1083/jcb.108.2.729;
Hennessy S.W., Frazier B.A., Kim D.D., Deckwerth T.L.,
Baumgartel D.M., Rowein P., Frazier W.A.;
"Complete thrombospondin mRNA sequence includes potential regulatory
sites in the 3' untranslated region.";
J. Cell Biol. 108:729-736(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 la Fleur M., Jobin C., Gauthier J., Kreis C.G.; Expression of thrombospondin in chronic inflammation: neutrophils from synovial fluids synthesize a novel 3.9 kb TSP mRNA."; Submitted (DEC-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIINE=11125860, PubMed=11067851; DOI=10.1074/jbc.M008073200; Hofsteenge J., Huwiler K.G., Macek B., Hess D., Lawler J., Mosher D.F., Peter-Katalinic J.; "C-mannosylation and O-fucosylation of the thrombospondin type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYDRATE-LINKAGE SITES TRP-385; SER-394; TRP-438; TRP-441; THR-450; TRP-498 AND THR-507.
TISSUE-Platelet;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              domains of human thrombospondin.";
Proc. Natl. Acad. Sci. U.S.A. 83:5449-5453(1986).
01-AUG-1988 (Rel. 08, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Thrombospondin-1 precursor.
Home = THBS1; Synonyms=TSP, TSP1;
Home sapiens (Human).
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                                                                                                                                                                                                                           proteins.";
J. Cell Biol. 103:1635-1648(1986).
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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PubMed=14654843; DOI=10.1038/nature02166;
Andersen J.S., Wilkinson C.J., Mayor T., Mortensen P., Nigg E.A.,
                                                    TISSUE=Aorta endothelial cell;
Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama
Ohara O., Nagame T., Kikuno F.R.;
"None Title.";
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Nature 426:570-574(2003).
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                                                                                   Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yoko Obara O., Nagase T., Kikuno F.R.;
"None Title.";
Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; AB209912; BAD93149.1; -; mRNA.
EMBL; AB209912; BAD93149.1; -; mRNA.
SNR; OSP899; 886-939; 889-1225.
GO; GO:0005576; F:calcium ion binding; IEA.
GO; GO:0007159; F:calcium ion binding; IEA.
GO; GO:0007159; F:calcium ion binding; IEA.
GO; GO:0007159; F:calcium ion binding; IEA.
InterPro; IPR001881; EGF Z.
InterPro; IPR001881; EGF Z.
InterPro; IPR001891; EGF Z.
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PROSITE; PS01208; VWFC 1; 1
PROSITE; PS50184; VWFC 2; 1
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InterPro; IPR003367; tsp 3.
InterPro; IPR008859; TSP C.
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PROSITE; PS50026; EGF_3; 2
PROSITE; PS50092; TSPI; 3.
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QGGGSB;
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SMART; SM00209; TSP<u>1</u>; 3
SMART; SM00210; TSPN; 1.
SMART; SM00214; VWC; 1.
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SMART; SM00181; EGF;
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  NCBI_TaxID=9606;
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
110-MAY-2005 (TrEMBLrel. 30, Last annotation update)
110-MAY-2005 (Human).
110-MAYOLO Sapiens (Human).
110-MAYOLO, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
110-MAMMMANIA; Euterchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
TSP type-3 1.
TSP type-3 2.
TSP type-3 3.
TSP type-3 4.
TSP type-3 6.
TSP type-3 7.
TSP type-3 7.
TSP Cterninal.
Heparin-binding (Potential).
Cell attachment site (Potential).
                                                                                                                                                                                                                                     N-linked (GlcNAc. ..).
N-linked (GlcNAc. ..) (Potential)
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3.9e+02;
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N-linked (GlcNAc. .)
N-linked (GlcNAc. .)
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O-linked (Fuc. .).
/FTIG=CAR 000206.
C-linked (Man).
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Interchain (Probable)
                                                                                                                                                                                                                                                                                                                                                                                                                                            /FTId=CAR 000208.
O-linked (Fuc. . . /FTId=CAR 000209.
C-linked (Man).
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Pred. No. 9
                                                                                                                                                                                                                                                                                   C-linked
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Local Similarity 61.5%;
les 8; Conservative
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059E99 HUMAN PRELIMINARY;
1D 059E99;
DT 10-MAY-2005 (TrEMBLrel. 30, DT 10-MAY-2005 (TrEMBLrel. 30, DT 10-MAY-2005 (TrEMBLrel. 30, DT 10-MAY-2005 (TrEMBLrel. 30, DT 10-MAY-2005 (TrEMBLrel. 30, DT 10-MAY-2005 (TrEMBLrel. 30, DT 10-MAY-2005 (TrEMBLrel. 30, DT 10-MAY-2005 (TrEMBLrel.) 30, DT 10-MAY-2005 (TrEMBLrel.) 30, DT 10-MAY-2005 (TrEMBLrel.) 30, DT 10-MAY-2005 (TrEMBLRel.) 30, DT 10-MAY-2005 (TrEMBLRel.) 30, DT 10-MAY-2005 (TrEMBLRel.) 30, DT 10-MAY-2005 (TrEMBLRel.) 30, DT 10-MAY-2005 (TrEMBLRel.) 30, DT 10-MAY-2005 (TrEMBLRel.) 30, DT 10-MAY-2005 (TrEMBLRel.) 30, DT 10-MAY-2005 (TrEMBLRel.) 30, DT 10-MAY-2005 (TrEMBLRel.) 30, DT 10-MAY-2005 (TrEMBLRel.) 30, DT 10-MAY-2005 (TrEMBLRel.) 30, DT 10-MAY-2005 (TrEMBLRel.) 30, DT 10-MAY-2005 (TrEMBLRel.) 30, DT 10-MAY-2005 (TrEMBLRel.) 30, DT 10-MAY-2005 (TrEMBLRel.) 30, DT 10-MAY-2005 (TrEMBLRel.) 30, DT 10-MAY-2005 (TrEMBLRel.) 30, DT 10-MAY-2005 (TrEMBLRel.) 30, DT 10-MAY-2005 (TrEMBLRel.) 30, DT 10-MAY-2005 (TrEMBLRel.) 30, DT 10-MAY-2005 (TrEMBLRel.) 30, DT 10-MAY-2005 (TrEMBLRel.) 30, DT 10-MAY-2005 (TrEMBLRel.) 30, DT 10-MAY-2005 (TrEMBLRel.) 30, DT 10-MAY-2005 (TrEMBLRel.) 30, DT 10-MAY-2005 (TrEMBLRel.) 30, DT 10-MAY-2005 (TREMBLRel.) 30, DT 10-MAY-2005 (TREMBLRel.) 30, DT 10-MAY-2005 (TREMBLRel.) 30, DT 10-MAY-2005 (TREMBLRel.) 30, DT 10-MAY-2005 (TREMBLRel.) 30, DT 10-MAY-2005 (TREMBLRel.) 30, DT 10-MAY-2005 (TREMBLRel.) 30, DT 10-MAY-2005 (TREMBLRel.) 30, DT 10-MAY-2005 (TREMBLRel.) 30, DT 10-MAY-2005 (TREMBLRel.) 30, DT 10-MAY-2005 (TREMBLRel.) 30, DT 10-MAY-2005 (TREMBLRel.) 30, DT 10-MAY-2005 (TREMBLRel.) 30, DT 10-MAY-2005 (TREMBLRel.) 30, DT 10-MAY-2005 (TREMBLRel.) 30, DT 10-MAY-2005 (TREMBLRel.) 30, DT 10-MAY-2005 (TREMBLRel.) 30, DT 10-MAY-2005 (TREMBLRel.) 30, DT 10-MAY-2005 (TREMBLRel.) 30, DT 10-MAY-2005 (TREMBLRel.) 30, DT 10-MAY-2005 (TREMBLRel.) 30, DT 10-MAY-2005 (TREMBLRel.) 30, DT 10-MAY-2005 (TREMBLRel.) 30, DT 10-MAY-2005 (TREMBLREL.) 30, DT 10-MAY-2005 (TREMBLREL.) 30, DT 10-MAY-2005 (TREMBLREL.) 30, DT 10-MAY-2005 (TREMBL
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PLASMID=PBC10987;
PubMed=14960714; DOI=10.1093/nar/gkh258;
Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L., Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L., Shoree K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F., Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
"The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic adaptations and a large plasmid related to Bacillus anthracis pXOI.";
Nucleic Acids Res. 32:977-988(2004).
EMBL; AE017274; AAS42659.1; -; Genomic_DNA.
FMRE, AE017195; AAS44852.1; -; Genomic_DNA.
TIGR; BCEA0002; -
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63.6%; Pred. No. 1.6e+02;
ive 4; Mismatches 0; Indels
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66.1%; Score 41; DB 2; Length 126
Best Local Similarity 72.7%; Pred. No. 1.46+02;
Matches 8; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                   Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus, Bacillus cereus group.
NCBI_TaxID=222523;
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Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; AY811299; AAX27188.1; -; mRNA.
EMBL; AY811299; AAX27188.1; -; mRNA.
InterPro; IPR011990; Cyt c b562.
InterPro; IPR011290; Fibrinogen G N.
InterPro; IPR011991; Wing_hlx_DNA_bd.
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                                                                                                                                                       05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Hypothetical protein.
Schistesoma japonicum (Blood fluke).
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Schistosomatoidea, Schistosomatidae, Schistosoma
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                                                                                                                                                                                                                               Tn554-related, transposase C.
OrderedLocusNames=BCE3149, BC
                                                              RESULT 39
Q735K3 BACC1
ID Q735K3_BACC1 PRELIMINARY;
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QSBZI7;
27 VLNENKILKNSLK 39
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76 EENKQLKNAIE 86
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140 AA; 10
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NUCLEOTIDE SEQUENCE.
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SEQUENCE 126 AA;
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SEQUENCE 14
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MEDLINE-98065943; PubMed-9403685; DOI=10.1038/37551;
Fraser C.M., Casjens S., Huang W.M., Sutron G.G., Clayton R.A.,
Lathigra R., White O., Ketchum K.A., Dodson R.J., Hickey E.K.,
Gwinn M.L., Dougherty B.A., Tomb J.-F., Fleischmann R.D.,
Richardson D.L., Peterson J.D., Kerlavage A.R., Quackenbush J.,
Salzberg S.L., Hanson M., van Vugt R., Palmer N., Adams M.D.,
Gocayne J.D., Weidman J.F., Utterback T.R., Watthey L., McDonald L.A.,
Artiach P., Bowman C., Garland S.A., Fujii C., Cotton M.D., Horst K.,
Roberts K.M., Hatch B., Smith H.O., Venter J.C.;
"Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=ATCC 35210 / B31;
MEDLINE=20139154; PubMed=10672174;
MEDLINE=20139154; PubMed=10672174;
Casjons S., Palmer N., Van Vugt R., Huang W.M., Stevenson B., Rosa P.,
Lathigra R., Sutton G.G., Peterson J.D., Dodson R.J., Haft D.H.,
Hickey E.K., Gwinn M.L., White O., Fraser C.M.,
"A becterial genome in L., white O., Fraser C.M.,
"A becterial genome in Liv: the twelve linear and nine circular
extrachromosomal DNAs in an infectious isolate of the Lyme disease
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Bacteria, Spirochaetes, Spirochaetales, Spirochaetaceae, Borrelia,
Borrelia burgdorferi group.
                            NUCLEOTIDE SEQUENCE.
Andersen J.S., Wilkinson C.J., Mayor T., Mortensen P., Nigg E.A.,
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                                                                                        Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases. EMBL; BK005587; DAA05591.1; -; mRNA. InterPro; IPR003900; KID_repeat. InterPro; IPR0039017; Spectrin. Pfam; PF02124; KID; Spectrin. SEQUENCE 2479 AA; 290328 MW; 8183C7E843CIF49C CRC64;
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EMBL, AE001581; AAM60782.1; -; Genomic_DNA.

EMBL, RE0010; C:membrane; IEA.

GO; GO:0005355; F:glucose transporter activity; IEA.

GO; GO:0006810; P:transport; IEA.
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SEQUENCE 73 AA; 8636 MW; FFF28C8E1A9984BF CRC64;
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01-0cT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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3; Mismatches
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Mol. Microbiol. 35:490-516(2000).
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640 LVBENKQLEEGMK 652
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QBKZ79 BORBU PRELIMINARY;
Q8KZ79;
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Matches 8; Conservative
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Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D.,
Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D.,
Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
Buckee C.O., Burrows C., Cherevach I.; Chillingworth C.,
Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,
Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,
Arnights T., Gobbe A., Goodhead I., Gwilliam R., Hannes Z.,
Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,
Humphray S., Jagels K., James K.D., Johnson D., Lennard N.,
Line A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
Line A., Maddison M., Mclean J., Mooney P., Moule S., Murphy L.,
Oliver K., Ormond D., Price C., Quail M.A., Rabbinowitsch E.,
Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,
Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,
Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,
Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13.";
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DOI=10.1128/IAI.68.3.1574-1586.2000;
Caimano M.J., Yang X., Popova T.G., Clawson M.L., Akins D.R.,
Caimano M.J., Yang X., Popova T.G., Clawson M.L., Akins D.R.,
Norgard M.V., Radolf J.D.;
"Molecular and evolutionary characterization of the cp32/18 family of supercoiled plasmids in Borrelia burgdorferi 297.";
Infect. Immun. 68:1574-1586 (2000).
EMBL, AF169008; AAF29799.1; -; Genomic_DNA.
GO; GO:0015077; F:DNA binding; IEA.
GO; GO:0015074; P:DNA integration; IEA.
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Borrelia burgdorferi group.
NCBI_TaxID=139;
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                                                                                                                                                                                                                                                                                                                                   Plasmodium falciparum (isolate 3D7).
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=36329;
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63.6%; Pred; No. 2.4e+02;
wiemarches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
SEQUENCE 211 AA; 25603 MW; 0EC18D131C82B334 CRC64;
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Last annotation update)
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein PFI0560c.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 419:527-531(2002).
EMBL; AL929356; CAD51798.1; -; Genomic_DNA.
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                                                                                                                            PRT;
                                                                 37_PLAF7
QB1337_PLAF7 PRELIMINARY;
QB1337;
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Q9L9M7;
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Best Local Similarity 63.0-
T, Conservative
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NUCLEOTIDE SEQUENCE.
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Q9L9M7 BOR
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STRAIN-ATCC 35210 / B31; PLASMID=cp32-8;

MEDLINE=98065943; PubMed=9403685; DOI=10.1038/37551;

Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,

Lathigra R., White O., Ketchum K.A., Dodson R.J., Hickey E.K.,

Gwinn M.L., Dougherty B.A., Tomb J.-F., Fleischmann R.D.,

Richardson D.L., Peterson J.D., Kerlavage A.R., Quackenbush J.,

Salzberg S.L., Hanson M., van Vugt R., Palmer N., Adams M.D.,

Gocayne J.D., Weidman J.F., Utterback T.R., Watthey L., McDonald L.A.,

Artiach P., Bowman C., Garland S.A., Fujii C., Cotton M.D., Horst K.,

Roberts K.M., Hatch B., Smith H.O., Venter J.C.;
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STRAIN=ATCC 35210 / B31; PLASMID=cp32-8;
MEDLINE=20138354; PubMed=10672174;
MEDLINE=20138354; PubMed=10672174;
Casjens S., Palmer N., van Vugt R., Huang W.M., Stevenson B., Rosa P., Lathlgra R., Sutton G.G., Peterson J.D., Dodson R.J., Haft D.H.,
Hickey E.K., Gwinn M.L., White O., Fraser C.M.;
"A bacterial genome in flux: the twelve linear and nine circular extrachromosomal DNas in an infectious isolate of the Lyme disease spirochete Borrelia burgdorferi.";
Mol. Microbiol. 35:499-516(2000).
                                                                                                                                                                                                                                                                            Gaps
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Borrella burgdorferi (Lyme disease spirochete).
Borrella burgdorferi (Lyme disease spirochete).
Balsamid op32-1, and Plasmid cp32-8.
Bacteria; Spirochaetes; Spirochaetales; Borrelia;
Borrelia burgdorferi group.
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MEDLINE=96256604; PubMed=8655548;
Stevenson B., Tilly K., Rosa P.A.;
A family of genes located on four separate 32-kilobase circular plasmids in Borrelia burgdorferi B31.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
STRAIN=B31; PLASMID=cp32-1;
STRAIN=97136624; PubMed=8982001;
Casjens S., van Vugt R., Tilly K., Rosa P.A., Stevenson B.;
"Homology throughout the multiple 32-kilobase circular plasmids
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                                                                                                                                                                                                        Score 41; DB 2; Length 258;
Pred. No. 3e+02;
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                                                                                                                                    258 AA; 30273 MW; 7B65A7771A1D42A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
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GO; GO:0006313; P:DNA transposition; IEA.
InterPro; IPR002104; Phage integrase.
Pfam; PF00589; Phage_integrase; 1.
Plasmid.
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J. Bacteriol. 179:217-227(1997).
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8; Conservative
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Stevenson B.;
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Q44780; Q7DFC7;
01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
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27 VLNENKILKNSLK 39
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                                                                                                                                                                                                                                 Local Similarity
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MEDLINE=98065943; PubMed=9403685; DOI=10.1038/37551;
Fraser C.M., Casjens S., Huang W.M., Sutron G.G., Clayton R.A.,
Lathigra R., White O., Ketchum K.A., Dodson R.J., Hickey E.K.,
Gwinn M.L., Dougherty B.A., Tomb J.-F., Fleischmann R.D.,
Richardson D.L., Peterson J.D., Kerlavage A.R., Quackenbush J.,
Salzberg S.L., Hanson M., van Vugt R., Palmer N., Adams M.D.,
Gocayne J.D., Weidman J.F., Utterback T.R., Watthey L., McDonald L.A.,
Artiach P., Bowman C., Garland S.A., Fujii C., Cotton M.D., Horst K.,
Roberts K.M., Hatch B., Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=ATCC 35210 / B31,
MEDLINE=20138354; PubMed=10672174;
Casjons S., Palmer N., van Vugt R., Huang W.M., Stevenson B., Rosa P.,
Lathigra R., Sutton G.G., Peterson J.D., Dodson R.J., Haft D.H.,
Hickey B.K., Gwinn M.L., White O., Fraser C.M.;
"A bacterial genome in flux: the twelve linear and nine circular
extrachromosomal DNAs in an infectious isolate of the Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia;
Borrelia burgdorferi group.
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                                                                                                                                                                                                                                                                                                                                                        Query Match 66.1%; Score 41; DB 2; Length 258; Best Local Similarity 61.5%; Pred. No. 3e+02; Matches 8; Conservative 3; Mismatches 2; Indels
  'Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30279 MW; 5300785231178FA4 CRC64;
                                                                                                                                                                                                                                                                                                      258 AA; 30267 MW; DBF069AEDC1B6E58 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Borrella burgdorferi (Lyme disease spirochete).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             258 AA.
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EMBL; AE001575; AAF07426.1; -; Genomic_DNA.
TIGR; BBP37; -.
                                    Nature 390:580-586(1997).
EMBL, U44912; AAC34924.1; -; Genomic DNA.
EMBL, AE001580; AAF07623.1; -; Genomic_DNA.
TIGR; BBL38; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0015074; P:DNA integration; IEA.
GO; GO:0006313; P:DNA transposition; IEA.
InterPro; IPR002104; Phage integrase.
Pfam; PF00589; Phage integrase; I.
Complete proteome; Plasmid.
SEQUENCE 258 AA; 30279 MM: 5100785221
                                                                                                                              TIGR, BBL38, --
O- GO-10016074; F:DNA binding; IEA.
GO; GO:0015074; P:DNA integration; IEA.
GO; GO:001513; P:DNA transposition; IEA.
GO; GO:006313; P:DNA transposition; IEA.
TheePro: IPROC2104; PROSE integrase.
Pfam; PF00589; Phage integrase.
Complete proteome; Plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 spirochete Borrelia burgdorferi.";
Mol. Microbiol. 35:490-516(2000).
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27 VLNENKILKNSLK 39
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                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosida; eurosida II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
Rounsley S.D., Kaul S., Lin X., Ketchum K.A., Crosby M.L.,
Rounsley S.D., Kaul S., Lin X., Ketchum K.A., Crosby M.L.,
Sandon R.C., Sykes S.M., Mason T.M., Kerlavage A.R., Adams M.D.,
Somerville C.R., Venter J.C.,
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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Length 258;
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Bacteria, Firmicutes, Bacillales, Listeriaceae; Listeria.
NCBI_TaxID=265669;
                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
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Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLUIAR LOCATION: Nuclear (By similarity).
EMBL; AC003028; AAC27179.1; -; Genomic_DNA.
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NAR-2004 (TrEMBLrel. 26, Last annotation update)
Putative MYB family transcription factor.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Pred. No. 3.4e+02;
1; Mismatches 1;
Score 41; DB 2;
Pred. No. 3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                     291 AA.
                                                                             3; Mismatches
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NUCLEOTIDE SEQUENCE.
PubMed=15115801; DOI=10.1093/nar/gkh562;
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80.0%;
66.1%;
61.5%;
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Q720T1;
                                                                                                                                                                                                  :| ||| |:||
27 VLNENKILKNSLK 39
                                                                                                                                                                                                                                                                                                                                                                                  15 ARATH
080435 ARATH PRELIMINARY;
080435;
                                                                                                                                                        1 ILEENKELENALK 13
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Matches 8; Conservative
                                                                                 Conservative
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                               Similarity
8; Conserva
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SEQUENCE 291 A
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factor).
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MEDLINE-21537279; PubMed=11679669; DOI=10.1126/science.1063447;
MEDLINE-21537279; PubMed=11679669; DOI=10.1126/science.1063447;
MEDLINE-21537279; PubMed=11679669; DOI=10.1126/science.1063447;
MEDLINE-21537279; PubMed=11679688 C., Mennid A.,
Meduero F., Berche P., Blocker H., Charkaborty T.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
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Charbit A., Chersen G., Modal P., Uthant E., Hauf J., Jackson D.,
A Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
A Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
Nordsiek G., Novella S., de Pablos B., Peræz-Diaz J.-C., Purcell R.,
A Varquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
Comparative genomics of Listeria species.";
Nelson K.E., Fouts D.E., Mongodin B.F., Ravel J., DeBoy R.T.,
Kolonay J.F., Rasko D.A., Angluoli S.V., Gill S.R., Paulsen I.T.,
Peterson J.D., White O., Nelson W.C., Nierman W.C., Beanan M.J.,
Brinkac L.M., Daugherty S.C., Dodson R.J., Durkin A.S., Madupu R.,
Haft D.H., Selengut J., Van Aken S.E., Khouri H.M., Fedorova N.,
Forberger H.A., Tran B., Kathariou S., Wonderling L.D., Uhlich G.A.,
Bayles D.O., Luchansky J.B., Fraser C.M.,
Whole genome comparisons of serotype 4b and 1/2a strains of the food-
borne pathogen Listeria monocytogenes reveal new insights into the
core genome components of this species ",
Nucleic Acids Res 32:2386-2395(2004).
EMBL, ARO17325, AAT03933.1, -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                               TIGR; LMO£2555.1157; --
GO; GO:0005622, C:intracellular; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
GO; GO:0006356; P:rranscription; IEA.
InterPro; IPR00005; HTHAraC.
PRINTS; PR000132; HTHARAC.
SMART; SM00342; HTHARAC.
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GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
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                                                                                                                                                                                                                                                                                                                 PROSITE; PS00041; HTH_ARAC_FAMILY_1; 1.
SKOSITE, PS01124; HTH_ARAC_FAMILY_2; 1.
Activator; Complete proteome; DNA-binding; Transcription; Transcription.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Regulatory protein similar to Salmonella typhimurium PocR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Listeria monocytogenes.
Bacteria, Firmicutes, Bacillales, Listeriaceae, Listeria.
                                                                                                                                                                                                                                                                                                                                                                          294 AA; 33836 MW; 491415EB91961469 CRC64;
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Q8Y7W9;
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 72.7
Matches 8; Conservative
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Ecker J.R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORFNames-At2g38090;
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Bubrayophyta; Virtipliplantes; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Putative MYB family transcription factor (MYB transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 41; DB 2; Length 298;
Pred. No. 3.5e+02;
1; Mismatches 1; Indels
                                                      PRINTS, PRODO312: HITHARAC.
SMART; SM00342; HTHARAC; 1.
PROSITE; PS0124; HTH ARAC FAMILY 1; 1.
ACTIVATOR; Complete proteome; DNA-binding; Transcription; Transcription. regulation.
SEQUENCE 294 AA; 33888 MW; 8ACF63B347B26349 CRC64;
                                                                                                                                                                                                                              Score 41; DB 2; Length 23*
Pred. No. 3.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Theologis A.; Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
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TIGRFAMS; TIGR01557; myb_3; 2.
Nuclear protein; Repeat.
SEQUENCE 298 Aa; 33251 MW; 812F4E21D6D8B440 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        298 AA
                                                                                                                                                                                                                                                                                                 1; Mismatches
InterPro; IPR012287; Homeodomain-rel.
InterPro; IPR000005; HTHAraC.
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72.7%;
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80.0%;
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                                          Pfam; PF00165; HTH AraC; 2.
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Best Local Similarity 72...,
Best Local Similarity 72...,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QBGXN7_ARATH PRELIMINARY;
QBGXN7;
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188 EENKEIRKALK 198
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NUCLEOTIDE SEQUENCE.
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Best Local Similarity
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NCBI_TaxID=59736;
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SEQUENCE
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Matches
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MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Straubsberg R.L., Felhagold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moorer T., Max S.L., Wang J., Haieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
                                                                                                                                                                                                                                                                        MEDLINE=22083941; PubMed=12089261;
DOI=10.1128/JCM.40.7.2452-2458.2002;
Rarjalainen T., Saumier N., Barc M.C., Delmee M., Collignon A.;
"Clostridium difficile genotyping based on slpA variable region in S-layer gene sequence: an alternative to serotyping.";
Jayer gene sequence: an alternative to serotyping.";
J. Clin. Microbiol. 40:2452-2458(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Hypothetical protein (Fragment).
Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                         Name=slpA;
Clostridium difficile.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 41; DB 2; Length 395;
Pred, No. 4.6e+02;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                      Karjalainen T.K., Saumier N.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, A4458878; AAM759421; -; Genomic_DNA.
InterPro; IRR07253; CW binding_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                395 395
395 AA; 42761 MW; 9FF83B300AD7B6FA CRC64;
                                                                                                                                    01-OCT-2002 (TrEMBLrel. 22, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                           S-layer protein variable domain SlpA (Fragment)
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                                                                                                                        Created)
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80.0%;
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                                                                                         QBKU29_CLODI PRELIMINARY;
Q8KU29;
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Best Local Similarity 80.0.
Local Similarity 80.0.
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149 EDKDLENALK 158
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EENKKFENAL 41
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            EENKELENAL
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                                                                                                                                                                                                                           NCBI_TaxID=1496;
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028EL9 BRA
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DT 10-MA
DT 10-MA
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STRAINCTCEBOT,

Numbed=15305603;

XI default of C.B., Camargo L.E.A., Van Sluys M.A.,

Monteiro-Vitorello C.B., do Amaral A.M., Harakava R.,

XI tajima J.P., Truffi D., do Amaral A.M., Harakava R.,

XI atiana J.C.F., Wood D., de Oliveira M.C., Miyaki C.Y.,

A Takita M.A., da Silva A.C.R., Furlan L.E., El-Dorry H.A.,

A lameida N.F. Jr., Carrer H., Coutinho L.E., El-Dorry H.A.,

Rerro M.I.T., Garliardi P.R., Giglioti E., Goldman M.H.S.,

A coldman G.H., Kimura B.T., Ferro E.S., Kuramae E.E., Lemos E.G.M.,

A numes L.R., Oliveira R.C., Pereira G.G., Siqueira W., de Souza A.A.,

Nunes L.R., Oliveira R.C., Pereira G.G., Siqueira W., de Souza A.A.,

Trai S.M., Zanca A.S., Simpson A.J.G., Brumbley S.M., Setubal J.C.,

RT "The genome sequence of the Gram-positive sugarcane pathogen Leifsonia

RT xyli subsp. xyli ",

Mol. Plant Microbe Interact. 17:827-836(2004)

Mol. Plant Microbe Interact. 17:827-836(2004)

C. -I. SIMILARITY: Belongs to the class III pyridoxal-phosphate-dependent

C. -I. SIMILARITY: Belongs to the class III pyridoxal-phosphate-dependent
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., García A.M., Gay L.J., Hulyk S.W., Villahon D.K., Muzny D.M., Sodergen E.J., Lu X., Gibbs R.A., Whiting M., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E., Grimwood J., Schmutz J., Myers R.M., Green E.D., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
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GO; GO:0003867; F:4-aminobutyrate transaminase activity; IEA.
GO; GO:000310; F:9-taminobutyrate transaminase activity; IEA.
GO; GO:000948; P:9-taminobutyric acid metabolism; IEA.
InterPro; IPR005814; Aminotrans 3.
InterPro; IPR004632; GABArrans bact.
PANTHER; PTHR11986; Aminotrans 3; 1.
Figh; PF00202; Aminotrans 3; 1.
TIGRFAMS; TIGR00700; GABĀtrnsam; 1.
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Micrococcineae; Microbacteriaceae; Leifsonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66.1%; Score 41; DB 2; Length 420
53.8%; Pred. No. 4.98+02; Lindels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases EMBL; BC091847; AAH91847.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  420 AA; 48404 MW; E1B329A48607B70E CRC64;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
4-aninobutyrate aminotransferase.
Name=goaG; OrderedLocusNames=Lxx12130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-Singapore local strain; TISSUE-Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences."
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QGAEY7;
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20 LLNENKEIEDLIK 32
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66.1%;
81.8%;
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Best Local Similarity 61.5%;
Matches 8; Conservative
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062319;
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Q9x2C2;
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STRAIN=VC1 / DSM 3638 / ATCC 43587 / JCM 8422;
Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
"The complete sequence of the Pyrococcus furiosus genome.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the class-III pyridoxal-phosphate-dependent aminotransferase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archaea, Euryarchaeota, Thermococci, Thermococcales, Thermococcaceae,
Pyrococcus.
                                                                                                                             Gaps
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Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
James K., Rutherford K., Harris B., Harris D., Churcher C.,
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                             Query Match
66.1%; Score 41; DB 2; Length 440;
Best Local Similarity 61.5%; Pred. No. 5.2e+02;
Matches 8; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 459;
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69.2%; Pred. No. 5.46+02; Landels
                      Complete proteome; Pyridoxal phosphate.
SEQUENCE 440 AA; 45909 MW; DA6F4F199BE29036 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4B7BD1DAE13D7DA0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2004 (TrEMBLrel. 21, Last sequence update)
Putative glutamate aminotransferase.
OrderedLocusNames=PF0513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0030170; F:pyridoxal phosphate binding; IEA.
GO; GO:0004813; F:transaminase activity; IEA.
InterPro; IPR005814; Aminotrans_3.
InterPro; IPR001760; Opsin.
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PROSITE; PS00600; AA TRANSPER CLASS 3; 1.
PROSITE; PS00238; OPSIN; UNKNOWN 1.
Complete proteome; Pyridoxal phosphate.
SEQUENCE 459 AA; 50554 MW; 4B7BDIDAEI
PROSITE; PS00600; AA TRANSFER CLASS 3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PANTHER; PTHR11986; Aminotrans_3; 1. Pfam; PF00202; Aminotran_3; 1.
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ORFNames=PC000508.00.0;
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Q4Y6Y2;
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QBU3F5;
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Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J., Bidwell S.L., Rajandream M.A., Carucot D.J. Yates J.R., Kafatos F.C., Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S., "A comprehensive survey of the Plasmodium life cycle by genomic,
                                                                                                                                                                                                                                                                            Gaps
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Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
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entry which
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein M04C3.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                transcriptomic, and proteomic analyses.";
Science 307:82-86(2005).
-!- CAUTION: The sequence shown here is derived f.
BMBL/GenBank/DDBJ whole genome shotgun (WGS).
prellminary data.
EMBL; CAAJ01000546; CAH75078.1; -; Genomic_DNA.
HyporHR 496 496
                                                                                                                                                                                                                                        Score 41; DB 2; I
Pred. No. 5.9e+02;
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Dictyostelium discoideum (Slime mold).
Bukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
NCBI_TaxID=44689;
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MEDLINE=22077258; PubMed=12081960;
MEDLINE=22077258; PubMed=12081960;
MEDLINE=22077258; PubMed=12081960;
DOI=10.1128/Jan.184.1386-3897.2002;
Calabi E., Fairweather N.,
"Patterns of sequence conservation in the S-Layer proteins and related sequences in Clostridium difficile.";
J. Bacteriol. 184:3886-3897 (2002).
EMBL, AF478570; AAM46789.1, -' Genomic_DNA.
InterPro; IPR007253; CW_binding_2.
Pfam; PF04122; CW_binding_2.
Pfam; PF04122; CW_binding_2.
SEQUENCE 610 AA; 64729 MW; 91CE9941ECA296CB CRC64;
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                                                                                                                                                                                                                                                            Gaps
                      Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239;
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                                                                                                    The C. elegans sequencing consortium;
"Genome sequence of the nematode C. elegans: a platform for investigating biology.";
Science 28::2012-2018(1998).
EMBL; 292808; CAB07266.2; -; Genomic_DNA.
PIR; T23701; T23701.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 66.1%; Score 41; DB 2; Length 610; Local Similarity 80.0%; Pred. No. 7.3e+02; e9 8; Conservative 2; Mismatches 0; Indels
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                                                                                                                                                                                WormBase, WBGene00010851; M04C3.2.
WormDep, M04C3.2; CB31973.
Complete protocome; Hypothetical protein.
SEQUENCE 606 AA; 70918 MW; DC4A18E9363754C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Surface layer protein A.
Clostridium difficile.
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Last annotation update)
                                                                    NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
                                                                                                                                                                                                                                                                                                                                                            610 AA
                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                      Ensembl; M04C3.2; Caenorhabditis elegans.
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                                                                               STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
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Q54CUS_DICDI PRELIMINARY;
Q54CUS_13-SEP-2005 (TrEMBLrel. 31, Le
13-SEP-2005 (TrEMBLrel. 31, Le
13-SEP-2005 (TrEMBLrel. 31, Le
Hypotherical protein.
ORFNames=DDB0184529;
                                                                                                                                                                                                                                      Similarity 61.5%;
8; Conservative ;
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Q8KTW2;
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165 EDKDLENALK 174
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               Caenorhabditis elegans
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Best Local Similarity
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Matches
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MEDLINE-20196006, PubMed=10731132; DOI=10.1126/ecience.287.5461.2185; MEDLINE-20196006, PubMed=10731132; DOI=10.1126/ecience.287.5461.2185; Andame M.D., Celniker S.E., Holt R.A., Evane C.A., Gocayne J.D., Amanarides P.G., Scherer S.E., Li P.W., Hookins K.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X., Ashandon R.C., Rogers Y.-H.C., Black M., Melfifer B.D., Handon R.C., Rogers Y.-H.C., Black M., Melse G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.W., Basu A., Barsendale J., Bayraktaroglu L., Beasley E.M., Besen K.Y., Benos P.V., Berman B.P., Bhandari D., Bolahakov S., Abrits K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Achery J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Chandra M. A. Deng Z., Mays A.D., Dew I., Dietz S.M., Abodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 0:0-0(2005).
-1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 784;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 41; DB 2; Length /07, Pred. No. 9.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
CG1962-PA, isoform A (CG1962-Pb, isoform b) (LD41224p)
ORFNames=CG1962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           784 AA; 91010 MW; A96EE5BCOFF445FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              preliminary data. ...... yenomue bnocgun (WGS EMBL; AAF101000269; EAL61150.1; -; Genomic_DNA. Hypothetical protein. SEQUENCE 784 AA; 91010 MW: A9GFEREDATER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               790 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
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QOVIKE;
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es 8; Conservative
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NUCLEOTIDE SEQUENCE.
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RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., RA Gong F., Gorrell J.H., Guz, Galbart W.M., Glasser K., Godek A., Gong F., Gorrell J.H., Guz, Glana P., Harias M., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J., RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Analai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kalush E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lang Y., Lei Y., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X., Rasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X., Rankloon D., R., McIntosh T.C., McLeod M.P., McPherson D., R., McHinna N.W., Mobarry C., Morris J., Moshrefi A., Nelson D.E., Ra Nelson D.R., Nelson D.E., Rangoon M., Murphy B., Murphy L., Murny D.M., Nelson D.E., Rangoon M., Stupsken D.R., Pacleder F., Shen H., Rangoon M., Stupskin M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T., Sylekas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Wellstock G.M., Waissenbach J., Milliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., A Zheng X.H., Zhong F.N., Zhou M., Zhu S., Zhu X., Smith H.O., A Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; Zhu X., Smith H.O., Chicales R.A., Myers E.W., Rubin G.M., Venter J.C.; Zhu X., Smith H.O., Received A. Chicales R.A., Myers E.W., Rubin G.M., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIINE=22426070; PubMed=12537573; Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R., Raminker J.S., Bergman C.M., Kronmiller B., Rubin G.M., Patel S., Fribe E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.; "The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22426065; PubMed=12537568;
Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinscock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; Finishing a whole-genome shotgun: release 3 of the Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLIRE-22426069; PubMed=12537572; Matthews B.B., Campbell K.S., Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P. Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., Harris N.L., Richter J. Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     George
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Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E.,
Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Drosophila melanogaster release 4 sequence.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         systematic review.";
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a genomics perspective.";
Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  melanogaster euchromatic genome sequence.";
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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Submitted (MAR-2005)
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
MEDLINE=99120557; PubMed=9923682; DOI=10.1038/16495;
Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
Smith D.R., Noonan B., Guild B.C., dedonge B.L., Carmel G.,
Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
31-MAY-2000 (Rel. 39, Last anguence update)
Alanyl-tRNA synthetase (EC 6.1.1.7) (Alanine--tRNA ligase) (AlaRS).
Name-alaS, OrderedLocusNames-1HP1162,
Helicobacter pylori J99 (Gampylobacter pylori J99).
Bacteria, Proteobacteria; Epsilonproteobacteria; Campylobacterales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               two unrelated isolates of the human
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Pfam; PF01411; tRNA-synt_2C; 1.
Pfam; PF01793; tRNA-SAD; 1.
PRINASYNTS, PR00980; TRNASYNTALA.
TIGRFAMS; TIGR00344; alaS; 1.
PROSTTE; PS50866; AA TRNA LIGASE II ALA; 1.
Aminoacyl-tRNA synthetase; ATP-bInding; Complete proteome; Ligase; Succeeded the synthetase; Secoution blosynthesis.
SEQUENCE 847 AA; 94978 MW; 714B10CA1F92D8F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diphosphate + L-alanyl-tRNA(Ala).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the class-II aminoacyl-tRNA synthetase
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K. Yu C., Lewis S.E., Rubin G.M., Celniker S., Submitted (Aug-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AR03567; AAF5312.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genomic sequence comparison of two unrelated isolates of the gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999)
-!- CATALYTIC ACTIVITY: ATP + L-alanine + tRNA(Ala) = AMP +
                                                                                                                                                                                                                                                          Length 790;
                                                                                                                                                                                                                                          Score 41; DB 2; Length />vePred, No. 9.5e+02;
                                                                                                                                                             IntAct; Q9VIK6; -
Ensemb; CG1962; Drosophila melanogaster.
FlyBase; FBGN0012876; CG1962.
SEQUENCE 790 AA; 89904 MW; DS8BADCC759607C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              847 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE011543; AAD06738.1; -; Genomic_DNA.
PIR; F71842; F71842.
                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HAMAR, MF 00036; -; 1.
InterPro; IPR003156; Pesterase DHHAl.
InterPro; IPR002318; tRNA-synt_2c.
InterPro; IPR012947; tRNA_SAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Helicobacteraceae, Helicobacter.
NCBI_TaxID=85963;
                                                                                                                                                                                                                                                              66.18;
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hes 8; Conservative
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                                                                                                                                                                                                                                                              Query Match
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SYA_HELPJ
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bloinformatics institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN=26695 / ATCC 700392;

KN MEDLINE=97394467; PubMed=2522185; DOI=10.1038/41483;

KN MEDLINE=97394467; PubMed=2522185; DOI=10.1038/41483;

KN MEDLINE=97394467; PubMed=2522185; DOI=10.1038/4183;

KN Fleisechmann R.D., Ketchum K.A., Klenk H.-P., Gill S.R.,

KN Pleisechmann R.D., Ketchum K.E., Quackenbush J., Zhou L., Kirkness E.F.,

KN Pougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness E.F.,

A Glodek A., McKenney K., FitzGerald L.M., Lee N., Adams M.D.,

Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D.,

KA Lley J.M., Cotton M.D., Weidman J.F., Rujii C., Bowman C.,

Matthey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D.,

Smith H.O., Fraser C.M., Venter J.C.,

The complete genome sequence of the gastric pathogen Helicobacter
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                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
13-SEP-2005 (Rel. 49, Last annotation update)
13-SEP-2005 (Rel. 49, Last annotation update)
13-SEP-2005 (Rel. 40, Last annotation update)
13-SEP-2005 (Rel. 40, Last annotation update)
13-SEP-2005 (Rel. 40, Last annotation update)
13-SEP-2005 (Rel. 40, Last annotation update)
13-SEP-2005 (Rel. 40, Last annotation update)
13-SEP-2005 (Rel. 40, Last annotation update)
13-SEP-2005 (Rel. 40, Last annotation update)
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13-SEP-2005 (Rel. 40, Last annotation u
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PEAM; PF07973; TRNA-Synt_2c; 1.
PEAM; PF07973; TRNA-SAD; 1.
PRINTS; PR00980; TRNASNTHALA.
TIGRFAMB; TIGR00344; alas; 1.
PROSTIE; PS50860; AA TRNA LIGASE II ALA; 1.
Aminoacyl-tRNA synthetase; ATP-binding; Complete proteome; Ligase; SEQUENCE 847 AA; 94700 MW; 56464EDB61FC8357 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diphosphate + L-alanyl-tRNA(Ala).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the class-II aminoacyl-tRNA synthetase
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Score 41; DB 1; Length 847;
Pred. No. 1e+03;
1; Mismatches 0; Indels
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Nature 388:539-547(1997).
-!- CATALYTIC ACTIVITY: ATP + L-alanine + tRNA(Ala) = AMP
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InterPro; IPR003156; Pesterase_DHHA1.
InterPro; IPR002318; tRNA-synt_2c.
InterPro; IPR012947; tRNA_SAD.
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         66.1%;
88.9%;
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Matches 8; Conservative
         Ouery Match
Best Local Similarity 88.5
Matches 8; Conservative
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                                                                                                                              3 EENKELENA 11
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TIGR; HP1241; -.
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15-JUL-1998
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US-09-248-796A-17798 Sequence 17798, A US-09-248-796A-24733 Sequence 24733, A US-09-248-796A-18403 Sequence 18403, A US-09-248-796A-16333 Sequence 16333, A	09-248-796A-19128 Sequence	.09-949-016-6779 Sequence	10-771-708-3 Sequence	.09-080-855-2 Sequence	.09-306-076-2 .08-973-462-8 Sequence	.09-949-016-11073 Sequence	08-487-826B-16 Sequence	.09-710-279-1080 Sequence	.09-134-001C-3275 Sequence	.09-270-767-60410 Semience	.08-676-782-7 Seguence	0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000	9000-013-000-013-00	ON-DIR-MANC-804/	09-27/0-/67-34ZI6 Sequence	09-2/0-/6/-49455 Sequence	.09-2/0-/6/-44935 sequence	.09-248-796A-18785 Sequence	.09-248-796A-15650 Seguence	.09-248-796A-14713 Segmence		anhac c6/c-1666-TC-60	.09-134-000C-5539 Sequence	.09-198-452A-1064 Sequence	97091 000 A381 050 000	DOCUMENTS OF CAMPAINS	.09-198-452A-85 Seguence	.09-438-1852-70 Segmence	00-140-101-01-01-01-01-01-01-01-01-01-01-01-0	-03-748-7368-73736 sednessce	.09-198-452A-627 Sequence	.09-830-230A-274 Sequence	- CO-CO-CO-CO-CO-CO-CO-CO-CO-CO-CO-CO-CO-C	.08-851-971-7 Sequence	-09-830-230A-273 Seguence	974-914-259-44	97. 37. 37. 37. 37. 37. 37. 37. 37. 37. 3	-09-902-540-15884 Sequence	.08-235-836C-92 Seguence		- 00-22-02-cc2-00	-08-235-836C-101 Sequence	-08-235-836C-142 Segmence	.08-235-836C-144 Semience		-08-23-83-6-39-6-108-108-108-108-108-108-108-108-108-108	.09-673-918A-8 Sequence	-09-914-259-45 Sequence	.09-248-796A-25350 Seguence	-09-710-279-66 Seguence	.00-710-279-746 Semience	פאריים פאריים פאריים פאריים פאריים פאריים פאריים פאריים פאריים פאריים פאריים פאריים פאריים פאריים פאריים פאריים	-09-248-/96A-1435/ sequence	-09-640-211A-2179 Sequence	-09-134-001C-3365 Seguence	- 24-0000-4665 - 134-0000-4665	20.101.000 1000 1000 1000 1000 1000 1000	-In-In4-04/-3424 sequence	-09-902-540-14910 sequence	-09-252-991A-17157 Sequence	-09-640-211A-624 Segmence	00-250-250-20	22.22.22.22.22.22.22.22.22.22.22.22.22.	-03-748-13931 sednence	-09-107-532A-6444 Sequence	-09-248-796A-14693 Sequence	.09-328-352-6791 Semience		-10-600-689-4 sequence	-09-134-000C-4961 sequence	-10-104-047-2664 Sequence	-09-949-016-11672 Sequence	10-104-047-3500 Segmence	10-104-04-0-00 acquest	-09-919-497-100 Sequence	-09-643-657-13 Sequence	-09-248-796A-19619 Sequence	00-013-0013-100-00-00-00-00-00-00-00-00-00-00-00-00	-09-252-99IA-19262 Sequence	-09-438-185A-587 Sequence
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Sequence 1144, Ap Sequence 1096, Ap Sequence 10, Appl Sequence 20, Appl Sequence 1142, Appl Sequence 1142, Appl Sequence 58, Appl Sequence 8, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl Sequence 934, Appl	equence 334 equence 334 equence 334 equence 334	equence 334 equence 334 equence 334 equence 2,	quence 22, quence 954	equence 23, equence 163	squence 44970,	duence 3	equence 1 equence 9 equence 2	equence equence	squence 1 squence 1 squence 2	equence 16013	squence squence	equence 8694, equence 8695,	equence 8635, equence 8675,	equence 8677, equence 8678,	aguence 8679, aguence 8680,	equence 8681, equence 8682,	equence 8683, equence 8684,	equence 8685, equence 8686,	equence 8687, equence 8688,	equence 8689, equence 8690,	equence 8691,	equence 2964,	equence 3139, equence 24, P	equence 18216 equence 18, A	Sequence 46195, A Sequence 18122, A Sequence 5, Appli	equence 5947,
equence 114 equence 105 equence 20, equence 114 equence 114 equence 18, equence 8,	- 136-457-334 Sequence 334 - 614-124B-334 Sequence 334 - 671-325-334 Sequence 334 - 589-184-334 Sequence 334 - 658-824-334 Sequence 334	17-754-334 Sequence 333-651-563-334 Sequence 333-515-642-334 Sequence 333-32-016-2 Sequence 2, 544-544-2	-556-419-22 Sequence 27, -949-016-9548 Sequence 95, -107-532A-6077 Sequence 60	-556-419-23 Sequence 23, -248-796A-16129 Sequence 16; -248-796A-18883 Sequence 186	-270-767-44970 Sequence 44970, -583-110-4043 Sequence 4043,	-10/-433-3/00 Sequence 3 -949-016-7268 Sequence 7 -836-687B-37 Sequence 3	-248-796A-15971 Sequence 1 -346-237-9 Sequence ·3 -248-796A-20613 Sequence 2	-585-858-13 Sequence 1-270-878-13 Sequence 1	-585-858-12 Sequence 1 -270-878-12 Sequence 1 -993-228-21 Sequence 2	-248-796A-16013 Sequence 16013 -949-016-9731 Sequence 9731,	-134-000C-6/43 Sequence 6/43, -902-540-14526 Sequence 14526 -949-016-8693 Sequence 8693,	-949-016-8695 Sequence 8695,	-949-016-8696 Sequence 8699, -949-016-8675 Sequence 8675, -040-016-8675 Sequence 8675,	-949-016-8677 Sequence 8677, -949-016-8678 Sequence 8679,	-949-016-8679 Sequence 8679, -949-016-8680 Sequence 8680,	-949-016-8681 Sequence 8681, -949-016-8682 Sequence 8682,	-949-016-8683 Seguence 8683, -949-016-8684 Seguence 8684,	949-016-8685 Sequence 8685, 949-016-8686 Sequence 8686,	949-016-8687 Sequence 8687, 949-016-8688 Sequence 8688,	949-016-8689 Sequence 8689, -949-016-8690 Sequence 8690,	-949-016-8691 Sequence 8691,	1-710-279-2964 Sequence 2964,	134-001C-3159 Sequence 3159, 8692-00282-24	-248-796A-18216 Sequence 18216 -305-856B-18 Sequence 18, P	270-767-46195 Sequence 46195 248-796A-18122 Sequence 18122 	-949-016-5947 Sequence 5947,
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ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 2.0 MB stc
COMPUTER: 1BM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Mordperfect
CURRENT APPLICATION DATA:
APPELICATION NUMBER: US/08/940,391
FILING DATE: 01-OCT-1997
CLASSIPRICATION 530
PRIOR APPLICATION BATA:
APPLICATION NUMBER: 08/619,280
FILING DATE: 18-MARCH-1996
APPLICATION NUMBER: 08/230,491
FILING DATE: 20-APRIL-1994
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 30,946
REGISTRATION NUMBER: 30,946
ATTORNEY/AGENT INFORMATION:
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 838-3884
INFORMATION: CANARALICE: CANARALICE: CANARALICE: CANARALICE: CANARALICE: CANARALICE: CANARALICE: CANARALICE: CANARALICE: CANARALICE: CANARALICE: CANARALICE: CANARALICE: CANARALICE: CANARALICE: CANARALICE: CANARALICE: CANARALICE: CANARALICE: CANARACTERISTICS:
UMBER: US/08/619,280A
18-MARCH-1996
                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/230,491
FILING DATE: 20-APRIL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5767242man D.
REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: LUD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 838-3884
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 760 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           487 ILEENKELENALK 499
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ADDRESSEE: Felfe & L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid;
; TOPOLOGY: linear
US-08-619-280A-2
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Matches 13; Conserv
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Sequence 2, Application US/08619280A

Patent No. 5767242

GENERAL INFORMATION:
APPLICANT: Zimmerman, Rainer; Park, John E.;
APPLICANT: Rettig, Wolfgang; Old, Lloyd J.

TITLE OF INVENTION: ISOLATED DIMERIC FIBROBLAST ACTIVATION PROTEIN
TITLE OF INVENTION: ALPHA, AND USES THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Rettig, Wolfgang J.; Scanlan, Matthew J.;
APPLICANT: Garin-Chesa, Pilar; Old, Lloyd J.
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE CODING FOR TITLE OF INVENTION: FIBROBLAST ACTIVATION PROTEIN 'AND USES TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 760
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MEDIUM TYPE: DISKETTE 3.5 inch 1.2 MB STORAGE
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 2.0 MB .storage
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: FELFE & LYNCH
STREET: 805 THIRD AVENUE
                                                                                                      Sequence 2, Application US/08230491A
Patent No. 5587299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 760 amino acids
amino acid
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Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wordperfect
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STATE:
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
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Gaps

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TITLE OF INVENTION: PROLYL PEPTIDASES AND METHODS OF USE
                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Mus musculus
US-09-518-550-26
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                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Zimmermann, Rainer; Park, John B.;
APPLICANT: Zimmermann, Rainer; Park, John B.;
APPLICANT: Estig, Wolfgang, Old, Lloyd J.
TITLE OF INVENTION: ALPHA, AND USES THEREOF
TITLE OF INVENTION: ALPHA, AND USES THEREOF
CORRESPONDENCE ADDRESS:
ADDRESSEE: Falfe & Lynch
STREET: 805 Third Avenue
CITY: New York
COUNTRY: USA
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                                       100.0%; Score 62; DB 1; Length 760; 100.0%; Pred. No. 0.11;
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                                                                               0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYRE Diskette, 3.5 inch, 2.0 MB
COMPUTER: 18M PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WOLOGEFAECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265,606
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                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Hanson, No. 6846910man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5330.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 838-3884
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 760 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/619,280
FILING DATE: 18-MARCH-1996
APPLICATION NUMBER: 08/230,491
FILING DATE: 20-APRIL-1994
ATTORNEY/AGENT INFORMATION:
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US-09-518-550-26

Sequence 26, Application US/09518550

PACENT NO. 6875851

GENERAL INFORMATION:

APPLICANT: TRAVIS, James

APPLICANT: BANBULA, Jan

APPLICANT: BANBULA, Agnieszka
                                                                                                                                                                                                                                                       Sequence 2, Application US/09265606
Patent No. 6846910
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Matches 13; Conservative
                                                                               13; Conservative
                                       Query Match
Best Local Similarity
Matches 13; Conserve
   US-08-940-391-2
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Sequence 82, Application US/10012819

| Sequence 82, Application US/10012819
| Sequence 82, Application US/10012819
| Sequence 82, Application US/10012819
| Patent No. 6916615
| GENERAL INFORMATION:
| APPLICANT: Legrain, Pierre
| APPLICANT: Rain, Jean-Christophe
| TITLE OF INVENTION: Dylori Protein-Protein Interactions and Applications thereof
| TITLE OF INVENTION: Dylori Protein-Protein Interactions and Applications thereof
| FILE REFERENCE: B5053
| CURRENT APPLICATION NUMBER: US/10/012,819
| FILE REFERENCE: B5053
| CURRENT APPLICATION NUMBER: EP 99401066.8
| PRIOR PILING DATE: 1999-04-30
| NUMBER OF SEQ ID NOS: 278
| SEQ ID NO 82
| LENGTH: 346
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; Sequence 649, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; TITLE OF INVENTION: Drotein-Protein Complexes and Method of Using Same
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; NUMBER OF SEQ ID NOS: 1387
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Pred. No. 42;
2; Mismatches
CURRENT APPLICATION NUMBER: US/09/518,550
CURRENT APPLICATION NUMBER: US/09/518,550
CURRENT FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: 60/123,148
PRIOR FILING DATE: 1999-03-05
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: 26
LENGTH: 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT;
CRGANISM: Helicobacter pylori
US-10-012-819-82
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 76.9%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 69.2%;
Matches 9; Conservative
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157 ILTESKEIBEALK 169
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APPLICANT: Cargill, Michele
APPLICANT: Cargill, Michele
APPLICANT: Cargill, Michele
APPLICANT: Ireland, James S.
APPLICANT: Ireland, James S.
APPLICANT: Bolk, Stacey
APPLICANT: Bolk, Stacey
APPLICANT: Mcarthy, Jeanette J.
TILLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
FILE REFERENCE: 2825.1027-001
CURRENT APPLICATION NUMBER: US/09/657,472
CURRENT APPLICATION NUMBER: US 60/153,357
PRIOR FILING DATE: 1999-09-10
PRIOR FILING DATE: 1999-09-10
PRIOR FILING DATE: 1999-09-10
PRIOR FILING DATE: 1090-09-10
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: US 60/225,724
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Pred. No. 2.2e+02;
                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40028-A-PCT-US
TELEPHONE: (212) 278-0400
TELEPHONE: (212) 391-0526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 42;
US/08/313,288B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 350, Application US/09949002; Patent No. 6900016; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09657472 Patent No. 6727063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: VENTER, J. Craig et al
                    January 5, 1995
                                                                                                                                                                                                                                                                                                                                                                                              67.7%;
61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67.7%;
61.5%;
                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 20
SEQUENCE CHARACTERISTICS:
LENGTH: 1170 amino acids
TYPE: amino acid
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Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Conservative
                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens
US-09-657-472-2
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                             STRANDEDNESS:
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US-09-949-002-350
                                                                                                                                                                                                                                                                                                                                                           US-08-313-288B-20
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US-09-657-472-2
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APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION

TITLE OF INVENTION: AND USES THEREOF

FILE REFERENCE: CL000790

CURRENT APPLICATION NUMBER: US/09/949,002

CURRENT FILING DATE: 2000-01-28

PRIOR FILING DATE: 2000-01-08

PRIOR FILING DATE: 2000-09-08
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                                                                                                                                                                                                                 Score 43; DB 2; Length 706;
Pred. No. 90;
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Patent No. 5750502
GENERAL INFORMATION:
TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A
TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN
                                                                              ORGANISM: Saccharomyces cerevisiae
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INPORMATION: Polypeptide Accession Number YNL021W
US-09-518-092-649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1185 Avenue of the Americas CITY: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 10823
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 482
LENCTH: 825
    SOFTWARE: CuraPatSeqFormatter Version 0.9
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 482, Application US/09949002
Patent No. 6900016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                     Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 67.7%;
Best Local Similarity 61.5%;
Matches 8; Conservative
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401 VTEENKELANELR 413
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper &
                                                                                                                                                                                                                                                                                                    2 LEENKELENAL 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
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ORGANISM: Human
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        SEQ ID NO 649
                                                                 TYPE: PRT
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ZIP: 19899
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US-09-033-524B-7
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            US-09-180-167A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
FITLE OF INVENTION: MUTH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
FILE REFERENCE: CLOO0790
CURRENT APPLICATION NUMBER: US/09/949,002
CURRENT FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/231,401
PRIOR APPLICATION NUMBER: 60/231,401
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 10823
SOFTWARES: PRAESEQ for Windows Version 4.0
SEQ ID NO 350
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US-09-270-767-42366
; Sequence 42366, Application US/09270767
; Sequence 42366, Application US/09270767
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION:
; FILE REPERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/08/270,767
; CURRENT PILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
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Pred. No. 2.2e+02;
2; Mismatches 3; Indels
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Patent No. 6558950

GENERAL INFORMATION:
APPLICATION
TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING
TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING
TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING
TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING
CURRENT APPLICATION NUMBER: US/09/180,167A
CURRENT APPLICATION NUMBER: CA 2,198,988
PRIOR PELING DATE: 1999-09-09
PRIOR APPLICATION NUMBER: PCT/1B98/00706
PRIOR APPLICATION NUMBER: PCT/1B98/00706
PRIOR FILING DATE: 1998-03-02
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FRAGESEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 62
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US-09-270-767-42366
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61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 VTEENKELANELR 313
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Best Local Similarity 61.5
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Human
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LENGTH: 317
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Patent No. 6607880

GENERAL INFORMATION:

APPLICANT: GOTON C. Shore et al.

TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING

TITLE OF INVENTION: APOPTOSIS

TITLE OF INVENTION: APOPTOSIS

TITLE OF INVENTION: NUMBER: US/09/033,524B

CURRENT APPLICATION NUMBER: US/09/033,524B

CURRENT FILING DATE: 1998-03-02

PRIOR FILING DATE: 1997-03-03

NUMBER OF SEQ ID NOS: 33

SOFTWARE: FASTESEQ for Windows Version 4.0

SEQ ID NO 7

LENGTH: 62
Score 40; DB 2; Length 62;
Pred. No. 19;
2; Mismatches 2; Indels
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red. No. 19;
Mismatches 2
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Pred. No.
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APPLICATION NUMBER: US 08/608,845
FILING DATE: 16-UUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: MCMORYOW Jr., RODERT G
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,526
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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66.7%;
            64.5%;
                                                                                              Conservative
                                                                                                                                                                       2 LEENKELENALK 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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STATE: Delaware
COUNTRY: U.S.A.
            Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
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Gaps

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GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
FILE REFERENCE: PATHOO 0.7A
CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR PILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-05-12
PRIOR FILING DATE: 1998-05-12
PRIOR FILING DATE: US 60/051,553
PRIOR FILING DATE: US 60/051,553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 340;
                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Camerini-Otero, Rafael D.
APPLICANT: Angov, Evangelina
TITLE OF INFORTON: Cloning and Expression of Tag recA
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/097 8.1
2;
                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR STREET: 620 Newport Center Drive 16th Floor CITY: Newport Beach STATE: CA
2; Mismatches .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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N. ...
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Patent No. 6699703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS OSTWARE: Patentin Policy
                                                                                                                                                                           Sequence 2, Application US/08097831
Patent No. 5510473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Altman, Daniel B.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: NIF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 71.4%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 340 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 LEEN--KELENALK 13
                                                                177 LEENKSLKNDLR 188
  8; Conservative
                                       2 LEENKELENALK 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: protein US-08-097-831-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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US-09-583-110-2803
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                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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    Matches
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Pred. No. 84;
                                                                                                                                                                                  DB 2; Length 218;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: GOAGO C. Shore et al.

TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING

TITLE OF INVENTION: APOPTOSIS

FILE REFERENCE: 50013/004002

CURRENT APPLICATION NUMBER: US/09/033,524B

CURRENT PILING DATE: 1998-03-02

PRIOR PILING DATE: 1997-03-03

NUMBER OF SEQ ID NOS: 33

NUMBER OF SEQ ID NOS: 33

SEQ ID NO 33

LENGTH: 245

TYPE: RT
                                                                                                                                                                                                                                                                                                                                                                                  US-09-180-167A-33

Sequence 3.3 Application US/09180167A

Patent No. 6558960

GENERAL INFORMATION:

APPLICANT Gordon C. Shore et al.

TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING

TITLE OF INVENTION: ADOPTOSIS

FILE REFERRICE: 50013/004003

CURRENT FILING DATE: 1999-09-10

PRIOR APPLICATION NUMBER: CA 2,198,988

PRIOR APPLICATION NUMBER: PCT/1B98/00706

PRIOR PILING DATE: 1999-03-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 84;
2; Mismatches
                                                                                                                                                                                                                             Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 33
LENGTH: 245
TYPE: PRT
                                                                                                                                                                                  Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 33, Application US/09033524B Patent No. 6607880
      (302) 658-9141
                      TELEFAX: (302) 658-5613
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||||| |:| |:
177 LEENKSLKNDLR 188
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Best Local Similarity 66.7
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , ORGANISM: Mus musculus
US-09-033-524B-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , ORGANISM: Mus musculus
US-09-180-167A-33
                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                        TOPOLOGY: linear
      TELEPHONE:
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US-09-033-524B-33
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Relating to Streptococcus

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ADPLICANT: MIXSON, James A
TITLE OF INVENTION: CARTER: DNA COMPLEXES CONTAINING DNA
TITLE OF INVENTION: CARTER: DNA COMPLEXES CONTAINING DNA
TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 43
CORRESPONDENCE S.
STREET: 1220 Market Street, P.O. Box 2207
CITY: Wilhington
STATE: Delaware
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
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1.6e+02;
--- 2; Indels
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Sequence 67, Application US/09914259
Sequence 77, Application US/09914259
Sequence 77, Application US/09914259
SERENCE 1000 SEQUENCE 1000 SEQUENCE 1000 SEPTIMENT APPLICATION NUMBER 1000 SEQUENCE 1000 SEQ
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COMPUTER READABLE FORM:
MEDIUM TYER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64.5%; Score 40; DB 2; 72.7%; Pred. No. 1.6e+02;ive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/608,845
FILING DATE: 16-JUL-1996
ATTORNEY/AGENT INFORWATION:
NAME: MCMORTSOW Jr., Robert G
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 658-9141
                                                                                                                              RESULT 22
US-08-985-526-3
Sequence 3, Application US/08985526
Patent No. 6080728
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (302) 658-5613
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
||||:| |:||||
281 LEENREKSLKNALK 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
COGANISM: Rattus norvegicus
US-09-914-259-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          i: 441 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-914-259-67
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Patent No. 6800744
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A DOUCETTE ACID AND AMINO ACID
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
THERE OF INVENTION: THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
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                                                                                                                                                                                                                                         Length 391;
                                                                                                                                                                                                                                         Score 40; DB 2; Length 391
Pred. No. 1.4e+02;
2; Mismatches 0; Indels
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ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTATION OF A PARTICATION NUMBER: 0.05134

COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660

COMPUTER: «Unknown»
OPERATING SYSTEM: «Unknown»
SOFTWARE: «Unknown»
SOFTWARE: «Unknown»
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
PRIOR APPLICATION NUMBER: 60/085131
FILING DATE: MAY 12, 1998
APPLICATION NUMBER: 60/08153
FILING DATE: MAY 12, 1998
APPLICATION NUMBER: 60/08153
FILING DATE: JULY 2, 1998
ATTONEY/AGENT INFORMATION:
NAME: ATTAILING DATE: JULY 2, 1997
ATTONEY/AGENT INFORMATION:
NAME: ATTAILING DATE: JULY 2, 1997
ATTONEY/AGENT INFORMATION:
NAME: ATTAILING DATE: JULY 2, 1997
ATTONEY/AGENT INFORMATION:
REFERENCE/DOCKET UNBER: GTC-011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...403
SEQUENCE DESCRIPTION: SEQ ID NO: 3191:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 3191:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 100 Beaver Street
                                                                                                             ; TYPE: PRT; ORGANISM: Streptococcus pneumoniae
US-09-583-110-2803
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Massachusetts
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MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                     Query Match
Best Local Similarity 71.4%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 269 LEENREKSLKNALK 282
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
      NUMBER OF SEQ ID NOS:
SEQ ID NO 2803
LENGTH: 391
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US-09-107-433-3191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-107-433-3191
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2 LEENKE--LENALK 13

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LENGTH: 2285
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LENGTH: 411
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US-09-646-403-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 961;
             Length 959;
Score 40; DB 2; Length 959
Pred. No. 3.7e+02;
2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Genencor International, Inc.
TITLE OF INVENTION: Proteases From Gram-Positive Organisms
FILE REFERENCE: GC394-PCT
CURRENT FILING DATE: 1999-05-14
EARLIER APPLICATION NUMBER: EP9719636.4
EARLIER FILING DATE: 1997-09-15
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US-09-914-259-66
Sequence 66, Application US/09914259
Patent No. 649-5336
GENERAL INFORMATION:
APPLICANT: MAKOWSKI, Lee
APPLICANT: Hyman, Paul
HTLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
FILE REFERENCE: 8471-010-999
CURRENT APPLICATION NUMBER: US/09/914,259
CURRENT FILING DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 180
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 66
LENGTH: 961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 40; DB 2;
Pred. No. 9.5e+02;
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Pred. No. 3.7e4
4; Mismatches
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                                            4; Mismatches
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 2285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-308-375-2
; Sequence 2, Application US/09308375
; Patent No. 6300117
; GENERAL INFORMATION:
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ilarity 61.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64.5%;
53.8%;
           Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
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; ORGANISM: Bacillius subtilis
US-09-308-375-2
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                                                                                                853 LLQETKELKNEIK 865
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852 LLQETKELKNEIK 864
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Best Local Similarity 53.8
Matches 7; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: BOS taurus
US-09-914-259-66
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US-09-932-183A-2
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APPLICANT: KOVALENKO, Addrei
TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF RECEPTORS OF THE TNF/NGF RECEPTOR
TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF RECEPTORS OF THE TNF/NGF RECEPTOR
TITLE OF INVENTION: AND OTHER PROTEINS
TITLE REFERENCE: WALLACH=27
CURRENT APPLICATION NUMBER: US/09/646,403
CURRENT APPLICATION NUMBER: LL 123758
PRIOR PLING DATE: 1998-03-19
PRIOR FILING DATE: 1999-03-18
PRIOR FILING DATE: 1999-03-18
PRIOR FILING DATE: 1999-03-18
PRIOR FILING DATE: 1999-09-01
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Patent No. 6680366
GENERAL INFORMATION:
APPLICANT: SHOJI, YAMAOKA
TITLE OF INVENTION NUCLEOTIDE SEQUENCE ENCODING A MODULATOR OF NF-KB
FILE REFERENCE: 0660-0146-55
CURRENT APPLICATION NUMBER: US/09/253,701
CURRENT FILING DATE: 1999-02-22
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TITLE OF INVENTION: Proteases From Gram-Positive Organisms FILE REFERENCE: GC394C1-US
CURRENT APPLICATION NUMBER: US/09/932,183A
CURRENT APPLICATION NUMBER: US/09/332,183A
CURRENT APPLICATION NUMBER: US 09/308,375
PRIOR APPLICATION NUMBER: PC7/US98/18828
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-09-08
PRIOR PRIOR APPLICATION NUMBER: EP9719636.4
PRIOR FILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 2285;
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Pred. No. 2.1e+02;
4; Mismatches 1,
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Pred. No. 9.5e+02;
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Patent No. 6734174
GENERAL INFORMATION:
APPLICANT: WALLACH, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PatentIn version 3.0
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58.3%;
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Best Local Similarity 61.5%;
Matches 8; Conservative
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847 ILKTNKELEKAIE 859
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Best Local Similarity 58.3
Matches 7; Conservative
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56 LEENQELRDAIR 67
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is Sequence 728, Application US/09438185A

j Sequence 728, Application US/09438185A

j Setent No. 6822071

i GENERAL INFORMATION:
    APPLICANT: Stephens, Richard
    APPLICANT: Mitchell, Wayne
    APPLICANT: Mitchell, Wayne
    APPLICANT: Mitchell, Wayne
    APPLICANT: The Regents of the University of California
    APPLICANT: The Regents of the University of California
    APPLICANT: The Regents of the University of California
    APPLICANT: The Regents of the University of California
    APPLICANT: NUMBER: O8094138,185A
    CURRENT PILING DATE: 2002-03-13
    PRIOR FILING DATE: 1999-04-08
    NUMBER OF SEQ ID NOS: 1074
    SOFTWARE: FastSEQ for Windows Version 3.0
    SEQ ID NO 758
    LENGTH: 835
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Pred. No. 4.7e+02;
1; Mismatches 2; Indels
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                                                                        Length 438;
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62.9%; Score 39; DB 2; L
Best Local Similarity 72.7%; Pred. No. 4.5e+02;
Matches 8; Conservative 2; Mismatches 1;
                                                                    62.9%; Score 39; DB 2; I
ilarity 72.7%; Pred. No. 2.3e+02;
Conservative 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 4768, Application US/09543681A; Patent No. 6605709
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; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-771
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Best Local Similarity 72.7%;
Matches 8; Conservative
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; ORGANISM: Proteus mirabilis
US-09-543-681A-4768
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US-09-438-185A-728
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                                                       RESULT 32
US-09-543-681A-4768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Heiss, Nina Treatment of Medical Conditions Associated with Def TITLE OF INVENTION: Disgnosis and Treatment of Medical Conditions Associated with Def FILE OF INVENTION: NFKAPPA B (NF-kB) Activation FILE REPERBNCE: HO-PO1961US1 CURRENT APPLICATION NUMBER: US/09/863,049B CURRENT FILING DATE: 2001-05-22 PRIOR APPLICATION NUMBER: US 60/206,223
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Pred. No. 2.1e+02;
4; Mismatches 1; Indels
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Pred. No. 2.1e+02;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09863049B
Patent No. 6824972
GENERAL INFORMATION:
APPLICANT: Kenwrick, Sue J.
APPLICANT: Nelson, David L.
APPLICANT: Nethys, Swarcop
APPLICANT: Worfendin, Hayley
APPLICANT: Woffendin, Hayley
APPLICANT: Munnich, Arnold
                   SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 419
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                         62.9%;
58.3%;
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Lewis, Richard A
Levy, Moise
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SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 419
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58.3%;
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Best Local Similarity 58.3°
                                                                                                                                                         Query Match 62.9
Best Local Similarity 58.3
Matches 7; Conservative
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55 LEENQELRDAIR 66
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55 LEENQELRDAIR 66
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Israel, Alain
   NUMBER OF SEQ ID NOS: 8
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                                                                                                                                                                                                                                                                                                                            RESULT 29
US-09-863-049B-2
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                                                                                                                      US-09-646-403-4
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TITLE OF INVENTION: Diagnosis and Treatment of Medical Conditions Associated with Def
TITLE OF INVENTION: NFKARPA B (NF-kB) Activation
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pred. No. 11;
4; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Clarke, Howard RG
APPLICANT: Clarke, Howard RG
APPLICANT: Clarke, Howard RG
APPLICANT: DuBose, Robert F
APPLICANT: Wiley, Steven R
TITLE OF INVENTION: HUMAN SERPIN POLYPEPTIDES
FILE REFERENCE: 3223-A
CURRENT APPLICATION NUMBER: US/10/094,944
CURRENT FILING DATE: 2002-03-08
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61.3%; Score 38; DB 2; 63.6%; Pred. No. 31;
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                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/863,049B CURRENT FILING DATE: 2001-05-22 PRIOR APPLICATION NUMBER: US 60/206,223 PRIOR FILING DATE: 2000-05-22
                                Sequence 76, Application US/09863049B
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Patent No. 6958387
GENERAL INFORMATION:
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Lewis, Richard A
Levy, Moise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 79
SOFTWARE: PatentIn version 3.1
SEQ ID NO 76
                                                                                                                                                                                Woffendin, Hayley
Munnich, Arnold
                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: HO-P01961US1
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Best Local Similarity 63.6
Matches 7; Conservative
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Best Local Similarity 58.3
Matches 7; Conservative
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LEENQELPDAIR 16
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                                                                                                                                                                                                                                                                                                                              Heiss, Nina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Human
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               JS-09-863-049B-76
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LENGTH: 51
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APPLICANT:
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                                                                                                                        Sequence 11433, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CLOOKINGTON: US/09/949,016
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
PRIOR PLING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 11433
LENGTH: 2733
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Sequence 6507, Application US/09949016

Batent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILE REFERENCE: CLOOD1307

CURRENT PILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-0-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FEALSEQ for Windows Version 4.0
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Best Local Similarity 77.8%;
Matches 7; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
                                  754 LEENIELENTI 764
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2559 LQQNKELEN 2567
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US-09-949-016-6507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Human
                                                                                                                      US-09-949-016-11433
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Sequence 6977, Application US/09543681A
Fatent No. 6605709
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: UNCLEIC ACID AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: UNDERS. 2009-001
TITLE OF INVENTION: UNDBER: US/09/543,681A
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-0-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR APPLICATION NUMBER: US 60/128,706
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 6977
LENGTH: 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 23418, Application US/09252991A

Sequence 2418, Application US/09252991A

Sequence 251795

GENERAL INFORMATION:
APPLICANT:
MAIC J. Rubenfield et al.
APPLICANT:
MAIC J. Rubenfield et al.
TITLE OF INVENTION:
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR PELING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-01-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 617
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                                          Length 373;
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61.3%; Score 38; DB 2; Length 617
Best Local Similarity 63.6%; Pred. No. 4.7e+02;
Matches 7; Conservative 2; Mismatches 2; Indels
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                                          61.3%; Score 38; DB 2; L 100.0%; Pred. No. 2.7e+02;
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Pred. No. 4.3e+02;
1; Mismatches 2;
                                                                                     0; Mismatches
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US-09-252-991A-23418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61.3%;
72.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Proteus mirabilis US-09-543-681A-6977
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Best Local Similarity 72...
Best Local Similarity 72...
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340 VLERTRELENA 350
                                                                                       Conservative
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                        Query Match
Best Local Similarity
---- 8; Conserve
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  US-09-248-796A-19926
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US-08-887-534A-45
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Sequence 19926, Application US/09248796A

Sequence 19926, Application US/09248796A

Sequence 19926, Application US/09248796A

Sequence 19926, Application US/09248796A

Sequence 19926, Application US/09248796A

TITLE OF INVENTION: NOTECT ACID AND THERAPEUTICS

TITLE OF INVENTION: NOTECT ACID AND THERAPEUTICS

TITLE OF INVENTION: NOTECT ACID AND THERAPEUTICS

FILE REFERENCE: 107196-132

CURRENT ELLING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13

SEQ ID NO 19926

SEQ ID NO 19926

SEQ ID NO 19926

SEQ ID NO 19926

SEQ ID NO 19926
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US-09-270-767-50148

US-09-270-767-50148, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburge et al.

TITLE OF INVENITON: Nucleic acids and proteins of Drosophila melanogaster.

FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

UNMBER OF SEQ ID NOS: 62517

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 50148
US-09-270-767-34931

Sequence 34931, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster:

FILE REPRENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 34931

LENGTH: 144
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Pred. No. 96;
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Pred. No. 96;
4; Mismatches
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; ORGANISM: Drosophila melanogaster
US-09-270-767-34931
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US-09-270-767-50148
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63.6%;
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Best Local Similarity 63.6%;
Matches 7; Conservative
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Matches 7; Conservative
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Patent No. 6740485
GENERAL INFORMATION:
APPLICANT: Holden, David W.
TITLE OF INFORTION: ANTI-BACTERIAL METHODS AND MATERIALS
NUMBER OF SEQUENCES: 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: IL.
COUNTRY: United States of America
ZIP: 60606
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 28341/6314.PCP
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 38; DB 2; 1
Pred, No. 7.3e+02;
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REPLICATION NUMBER: US/09/446,861
FILING DATE: 22-Mar-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 45: US-09-446-861-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Li-Haien Rin-Laures, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (312)474-6300
TELEPAX: (312)474-0448
INFORMATION FOR SEQ ID NO: 45
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TYPE: amino acid
                                                                                                         TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-6408
TELEFAX: (312) 474-6600
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 932 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                NAME: Rin-Laures, Li-Heien
REGISTRATION NUMBER: 33,547
                                                                      REFERENCE/DOCKET NUMBER: 2
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66.7%;
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Best Local Similarity 66.7
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919 LVQNKIIENALK 930
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Best Local Similarity
Matches 8; Conserva
                                                                                                                                                                                                                                                                 linear
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Patent No. 6485899
GENERAL INFORMATION:
APPLICANT: Holden, David W.
TITLE OF INVENTION: ANTI BACTERIAL METHODS AND MATERIALS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
                   GENERAL INC. 6455323
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
COTTY:
CLICAGO
STATE: 1111nois
COUNTRY: United States of America
                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,534A
                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 28341/33996
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/887,534
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APPLICATION NUMBER: US/09/527,431
Application US/08887534A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LELEFAX: (312) 474-6300
TELEX: (312) 474-648
TELEX: (312) 474-6600
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
TYDE
TYDE
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Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-887-534A-45
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US-09-538-092-706
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                                                                                                   TYPE: PRT
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APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REPERENCE: File Reference: 7326-094
CURRENT PAPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 60453
LENGTH: 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-538-092-706
US-09-538-092-706
US-09-538-092-706
Sequence 706, Application US/09538092
Patent No. 6753314
GENERAL INFORMATION:
APPLICANT: Gloct, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same;
FILE REPERBECE: 15866-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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      Sequence 621, Application US/09640211A

Patent No. 6833446

GENERAL INFORMATION:
APPLICANT: Wood, Marion
APPLICANT: Wood, Marion
APPLICANT: McGrath, Annette
APPLICANT: Glann, Matthew
APPLICANT: Glann, Matthew
APPLICANT: Glann, Matthew
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Transcription
FILE REPRESENCE: 11000.1021C1U
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SEQ ID NO 621
LENGTH: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59.7%; Score 37; DB 2; Length 76; 80.0%; Pred. No. 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 37; DB 2; Length 72;
Pred. No. 65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 60453, Application US/09270767 Patent No. 6703491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                  59.7%;
                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Eucalyptus grandis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 66.7
Matches 8; Conservative
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Matches 8; Conservative
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US-09-270-767-60453
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US-09-640-211A-621
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US-09-248-796A-20281

US-09-248-796A-20281

Sequence 20281, Application US/09248796A

Sequence 20281, Application US/09248796A

Sequence 20281, Application US/09248796A

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-12

PRIOR FILING DATE: 1999-02-13

FRIOR FILING DATE: 1998-08-13

WUMBER OF SEQ ID NOS: 28208
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US-09-861-451A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 18, Application US/09861451A;
Sequence 18, Application US/09861451A;
Patent No. 6759516
GENERAL INFORMATION:
APPLICANT: COMMONWEATH Scientific & Industrial Research Orga
TITLE OF INVENTION: Methods of Identifying Antigen Gene Sequences;
FILE REFERENCE: FF34033/01;
CURRENT APPLICATION NUMBER: US/09/861,451A;
CURRENT PILING DATE: 2001-05-21
PRIOR PILING DATE: 1998-11-20
NUMBER OF SEQ ID NOS: 84
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 18
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59.7%; Score 37; DB 2; Length 530
Best Local Similarity 61.5%; Pred. No. 5.7e+02;
Matches 8; Conservative 2; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: (0)._.(0)
OTHER INFORMATION: Polypeptide Accession Number YOL069W
                                                                                                                                                                                                                                                                                                                                                                                                              59.7%; Score 37; DB 2; I
72.7%; Pred. No. 4.8e+02;
tive 1; Mismatches 2;
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR PRILATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuraPatSeqFormatter Version 0.9
SOFTWARE: 451
                                                                                                                                                                                                                                        ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
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Matches 8; Conservative
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Sequence 1. Application US/09150867

Fatent No. 645748

GRERAL INPORMATION:

APPLICANT: Wood, Kenneth W.

APPLICANT: Sakowicz, Roman

APPLICANT: Goldstein, Lawrence S.B.

APPLICANT: Goldstein, Lawrence S.B.

APPLICANT: Goldstein, Lawrence S.B.

APPLICANT: The Regents of the University of California

TITLE OF INVENTION: Plus End-Directed Microtubule Motor Required for TITLE OF INVENTION: Plus End-Directed Microtubule Motor Required for TITLE OF INVENTION: Chromosome Congression

FILE REFERENCE: 18557C-00011001

FILE REFERENCE: 18557C-00011001

FILE RAPLICATION NUMBER: US 60/058,645

FARLIER APPLICATION NUMBER: US 60/058,645

FARLIER PILING DATE: 1997-09-11

NUMBER OF SEQ ID NOS: 11

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Xenopus centromere-associated protein-E (XCENP-E) OTHER INFORMATION: member of the kinesin superfamily of microtubule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Hebera, Ledare
APPLICANT: Hebera, Ledare
APPLICANT: Reddick, Bradford B.
TITLE OF INVENTION: Waize Chlorotic Dwarf Virus Genome and
TITLE OF INVENTION: Uses Therefor
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30B
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Pred. No. 3.7e+03;
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LOCATION: (1)..(472)
OTHER INFORMATION: kinesin like motor domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (2753). (2854)
COTHER INFORMATION: tail domain US-09-150-867-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (473)..(2752)
OTHER INFORMATION: rod domain
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Best Local Similarity 63.0.
T; Conservative
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ZIP: 32606
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 2954
TYPE: PRT
ORGANISM: Xenopus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: DOMAIN
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US-08-416-603-4
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Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICANTON NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 42870
LENGTH: 841
                                                                                                                                                                                 Gaps
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pred. No. 1.2e+03;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 37; DB 2; Length 841;
Pred. No. 9.4e+02;
1; Mismatches 3; Indels
                                                                                                                                 DB 2; Length 810;
9e+02;
                                                                                                                                                                                 2; Indels
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US-09-270-767-44973
                                                                                                                                                                                   4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , OTHER INFORMATION: Xaa means any amino acid US-09-270-767-42870
                                                                                                                                      Score 37;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 42870, Application US/09270767
Patent No. 6703491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Drosophila melanogaster
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Best Local Similarity 66.7%;
Matches 8; Conservative
                                                                                                                                   Query Match 59.7%;
Best Local Similarity 53.8%;
Matches 7; Conservative
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755 IIKENKKLERELE 767
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744 ILEENENQENPL 755
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Best Local Similarity 80.0
Matches 8; Conservative
                                             .TYPE: PRT
ORGANISM: Candida albicans
                                                                                                                                                                                                                               1 ILEENKELENALK 13
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                                                                                        US-09-248-796A-20281
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LENGTH: 1024
SEO ID NO 20281
                       LENGTH: 810
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Length 2954;

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US-09-248-796A-26906

US-09-248-796A-26906

Sequence 26906, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN:

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: WOMBER: US/09/248,796A

CURRENT PELLING DATE: 1999-02-12

PRIOR PELLING DATE: 1998-02-13

PRIOR PELLING DATE: 1998-02-13

PRIOR PILLING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 26506

LENGTH: L57
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Length 153;
Score 36; DB 2; Length 153
Pred. No. 2.1e+02;
2; Mismatches 3; Indels
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Pred. No. 2.2e+02;
3; Mismatches 0; Indels
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Patent No. 649536

GENERAL INFORMATION:

APPLICANT: MAKWWEK, Lee

APPLICANT: Williams, Mark

TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES

TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES

CURRENT APPLICANION NUMBER: US/09/914,259

CURRENT FILING DATE: 2000-11-21

NUMBER OF SEQ ID NOS: 180

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 65

LENGTH 245
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Pred. No. 3.5e+02;
2; Mismatches 3;
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  Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative
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US-09-914-259-65
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228 LEQNRRLTNELK 239
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Best Local Similarity 66.7
Matches 6; Conservative
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Patent No. 6605709
Patent No. 6605709
Patent No. 6605709
APPLICANT GARY BRETON
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT APPLICATION NUMBER: US 60/128,706
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR SEQ ID NOS: 8344
LENGTH: 148
TYPE: PRT
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Batent No. 6562954

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BADMANNII FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 6203

LENGTH: 153
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Pred. No. 4.3e+03;
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                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/416,603
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lloyd, Jeffrey
REGISTRATION NUMBER: 35,589
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3457 mmino acide
TYPE: amino acide
TYPE: amino acide
TYPE: TOPOLOGY: linear
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; ORGANISM: Acinetobacter baumannii
US-09-328-352-6203
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2257 LERNKELKAALE 2268
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Best Local Similarity 66.7
Matches 8; Conservative
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Matches 8; Conservative
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US-09-328-352-6203
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APPLICANT: Kebith Weinstock et al
APPLICANT: Kebith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILER REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT APPLICATION DATE: 1999-02-12
APPLICANT: Origene Technologies, Inc
TITLE OF INVENTION: Regulated Angiogenesis Genes and Polypeptides
FILE REFERENCE: 1U 103 R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 281;
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APPLICANT: Hyman, Paul
APPLICANT: Hyman, Paul
APPLICANT: Hilitams, Mark
TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
FILE REFERENCE: 8471-010-999
CURRENT APPLICATION NUMBER: US/09/914,259
CURRENT FILING DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 180
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 36; DB 2; 1
Pred, No. 4.1e+02;
2; Mismatches 3
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                                                              CURRENT APPLICATION NUMBER: US/10/164,595
CURRENT FILING DATE: 2002-06-10
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn version 3.1
SEQ ID NO 34
LENGTH: 245
TYPE: PRT
TYPE: PRT
US-10-164-595-34
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PRIOR PELING DATE: 1999-02-12

PRIOR FILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR PILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 25451

LENGTH: 294
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Sequence 25451, Application US/09248796A
Patent No. 6747137
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Patent No. 6495336
GENERAL INFORMATION:
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Best Local Similarity 58.3%;
Matches 7; Conservative
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ORGANISM: Candida albicans
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Best Local Similarity 58.3
Matches 7; Conservative
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          h 58.1%;
Similarity 50.0%;
6; Conservative
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Search completed: March 11, 2006, 12:27:22 Job time : 34.0789 secs

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Sequence 136, App
Sequence 4171, App
Sequence 131, Appl
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sequence 286959, A
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                                                                    March 11, 2006, 12:26:08; Search time 101.947 Seconds (without alignments) 53.280 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
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            GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-733-368-34 US-10-470-48B-561 US-10-472-928-246 US-10-472-928-2246 US-10-424-929-238292 US-10-282-122A-76580 US-10-282-122A-76580 US-10-382-122A-76580 US-10-313-977-9442 US-10-313-977-9433 US-10-313-977-9433 US-10-424-599-206504 US-10-424-599-266696 US-10-424-599-266696 US-10-424-599-260504 US-10-282-122A-7116 US-10-424-599-260504 US-10-424-599-260504 US-10-424-999-260286 US-10-424-999-260286 US-10-424-999-260286 US-10-424-999-260286 US-10-424-999-260286 US-10-424-999-260286 US-10-424-999-260286 US-10-424-999-260387 US-10-425-114-5698 US-10-425-114-5698 US-10-425-114-5698 US-10-425-114-5698 US-10-425-114-5698 US-10-425-114-5698 US-10-425-114-65105 US-10-425-114-65105 US-10-425-114-65105 US-10-425-114-65105 US-10-425-114-65105 US-10-425-114-65105 US-10-425-114-65105 US-10-425-114-65105 US-10-425-114-65105 US-10-425-114-65105 US-10-425-114-65105 US-10-425-114-65105 US-10-425-114-65105 US-10-425-114-65105 US-10-425-114-65105 US-10-425-114-65105 US-10-425-114-65105 US-10-425-114-65105 US-10-425-114-65105 US-10-425-113-35-384 US-10-425-113-35-384 US-10-425-113-35-384 US-10-425-113-35-384 US-10-425-113-35-384 US-10-425-113-35-384 US-10-425-113-35-384 US-10-425-113-35-384 US-10-425-113-35-384 US-10-425-113-35-384 US-10-425-113-35-384 US-10-425-113-35-384 US-10-425-113-35-384 US-10-425-113-35-384 US-10-425-113-35-384 US-10-425-113-35-384 US-10-425-113-35-384 US-10-425-113-35-384 US-10-425-113-35-384 US-10-425-113-35-384 US-10-425-113-35-384 US-10-425-113-35-384 US-10-425-113-35-384 US-10-425-113-35-384 US-10-425-113-35-384 US-10-425-113-35-384 US-10-425-113-35-384 US-10-425-113-35-384 US-10-425-113-35-384 US-10-425-113-35-384 US-10-425-113-35-384 US-10-425-113-35-384 US-10-425-113-35-384 US-10-425-113-35-384 US-10-425-113-35-384 US-10-425-113-35-384 US-10-425-113-35-384 US-10-425-113-35-384 US-10-425-113-35-384 US-10-425-113-35-384 US-10-425-113-35-384 US-10-425-113-35-384 US-10-425-113-35-384 US-10-425-113-35-384 US-10-	US-10-425-115-36636 US-09-801-574-65 US-10-092-9000A-340 US-10-169-493-22825 US-09-788-626-4322 US-10-494-541-96 US-10-437-963-141471 US-10-437-963-149503 US-10-425-115-231231 US-10-425-115-231231
6.00 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	6.5 6.5 6.5 6.5 913 6.5 962 6.5 962 6.5 962 6.5 963 6.5 963 6.5
UUUUUUUU 44444444444444444444444444444	1 M M M M M M M M M M M M M M M M M M M

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APPLICANT: Mills, Gordon B.
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Berger, Alison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Guillemette, Tracy L.
APPLICANT: Guillemette, Tracy L.
APPLICANT: Schlagel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Monahan, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF COLON CANCER
TITLE OF INVENTION: THERAPY OF COLON CANCER
TITLE OF INVENTION: THERAPY OF COLON CANCER
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE REFERENCE: MPMOI-029PZRNM
CURRENT FILING DATE: 2002-11-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 760;
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100.0%; Score 62; DB 4; Length 760;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                     FILE REFERENCE: MRI-038
CURRENT APPLICATION NUMBER: US/10/177,293
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: US 60/299,887
PRIOR FILING DATE: 2001-06-21
PRIOR FILING DATE: 2001-06-27
PRIOR FLING DATE: 2001-06-27
PRIOR FLING DATE: 2001-06-27
PRIOR FLING DATE: 2001-06-27
PRIOR FLING DATE: 2001-06-27
PRIOR FLING DATE: 2001-06-27
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 506
SOUTWARE: PRESEG FOR WINDOWS VERSION 4.0
SEQ ID NO 136
LENGTH: 760
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PRIOR PILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361, 978
PRIOR PLING DATE: 2002-03-05
PRIOR PLING DATE: 2002-06-20
PRIOR PLING DATE: 2002-06-20
PRIOR PLING DATE: 2002-06-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Millennium Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 55, Application US/10301822
Publication No. US20030148410A1
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100.0%; Pr
tive 0;
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Best Local Similarity 100.
Matches 13; Conservative
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US-10-177-293-136
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LENGTH: 760
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                                                               APPLICANT: Zimmermann, Rainer; Park, John E.;
APPLICANT: Rettig, Wolfgang; Old, Lloyd J.
TITLE OF INVENTION: ISOLATED DIMERIC FIBROBLAST ACTIVATION PROTEIN
TITLE OF INVENTION: ALPHA, AND USES THEREOF
WUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/619,280
FILING DATE: 18-MARCH-1996
APPLICATION NUMBER: 08/230,491
FILING DATE: 20-APRIL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. US20020034789Alman D.
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 2.0 MB
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WOrdperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265,606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
pplication US/09265606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gannavarpu, Manjula
Kamatkar, Shubhangi
Mertens, Maureen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ortobagyi, Gabriel
usztai, Laios
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oersch, Sebastian
onahan, John
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                                                                                                                                                                                                                                    SEE: Felfe & Lynch
: 805 Third Avenue
New York City
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 13; Conservative
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                           US20020034789A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear
US-09-265-606-2
                                                                                                                                                                                                                                                                                                                    New York
                                                                                                                                                                                                                                                                                                                                          USA
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                                                                                                                                                                                                                                       ADDRESSEE:
STREET: 80
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US-10-767-701-53059

US-10-767-701-53059

Sequence 53059, Application US/10767701

Publication No. US20040172684A1

GENERAL INFORMATION:

APPLICANT: Kovalic, David K.

APPLICANT: APPLICANT: Avoid Wolecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

TITLE OF INVENTION: NUCLEIC ACID NUBER: US/10/767,701

CURRENT APPLICATION NUMBER: US/10/767,701

NUMBER OF SEQ ID NOS: 63128

SEQ ID NO 53059

LENGTH: 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 286978, Application US/10425115
; Sequence 286978, Application US/10425115
; Publication No. US20040214272A1
; Garrant No. US20040214272A1
; Garrant No. US20040214272A1
; APPLICANT: Law Rowalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Plants
; TITLE OF INVENTION: Plants
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 286978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79.0%; Score 49; DB 4; Length 187; 69.2%; Pred. No. 6.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: MRT4577_24818C.1.pep
US-10-425-115-286978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79.0%; Score 49; DB 4; 69.2%; Pred. No. 4.8; tive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: 13239136.pep
US-10-767-701-53059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
US-10-425-114-52777
Sequence 52777, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
487 ILEENKELENALK 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 69.2-
Best Local Similarity
Propertive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ILEENKELENALK 13
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77 VLEENQSLENALR 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :||||: |||||:
77 VLEENQSLENALR 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 69.2
Matches '9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Liu, Jingdong
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US-10-425-115-286978
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APPLICANT: Aziz, Watasha
APPLICANT: Glaburg, Wendy M.
APPLICANT: Zlotnik, Albert
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
FILE REFERENCE: 05882.0193.NPUS01
CURRENT APPLICATION NUMBER: US/10/723,860
CURRENT FILING DATE: 2003-11-26
NUMBER OF SEQ ID NOS: 8393
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
LENGTH: 760
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Williams D.
APPLICANT: Williams D.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: TEATMENT OF TUMOR
FILE REFERENCE: P5036R1-US
CURRENT APPLICATION NUMBER: US/10/884,070A
CURRENT FILING DATE: 2004-07-02
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 13
LENGTH: 760
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 62; DB 5; Length 760;
Pred. No. 0.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                             US-10-723-860-4171
Sequence 4171, Application US/10723860
Publication No. US20040253606A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 13, Application US/10884070A Publication No. US20050170368A1 GENERAL INFORMATION:
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100.0%;
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Frantz, Gretchen
French, Dorothy
Gonzalez, Lino
Polakis, Paul
Smith, Victoria
Wolf, Beni B.
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                                                     Ouery Match
Best Local Similarity luv...
Best Local 3; Conservative
                         1 ILEENKELENALK 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ILEENKELENALK 13
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; ORGANISM: Homo sapiens
US-10-884-070A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-860-4171
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APPLICANT:
APPLICANT:
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Gaps

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Gaps

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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B CURRENT APPLICATION NUMBER: US/10/437,963 CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966 SEQ ID NO 186821 LENGTH: 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELLCOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                Indele
                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: PAT_MRT4530_83584C.1.pep
US-10-437-963-186821
                                                                                                                                                                                                                                                                                                                     Score 49; DB 4;
Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...223
SEQUENCE DESCRIPTION: SEQ ID NO: 8596:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: TP PP C COMPALIBLE
COMPATER: TP PP C COMPALIBLE
OPERATING SYSTEM: Windows NT 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Mandragouras, Amy E. REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: LAHIVE & COCKFIELD STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8596, Application US/10335977
Publication No. US20040052799A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 223 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 8596:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                       79.0%;
69.2%;
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                      :||||: ||-||:
83 VLEENOSLENALR 95
                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                         TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
9, Conserve
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US-10-335-977-8596
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APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Avoid K.
APPLICANT: Avoid K.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants
FILE OF INVENTION: Plants
FILE REFERENCE: 30-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 268692
LENGTH: 604
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Pred. No. 25;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 49; DB 4; Length 562;
Pred. No. 23;
3; Mismatches 1; Indels
                                                                                                                     TITLE OF INVENTION: Nucleic Acid Molecules and Other MY TITLE OF INVENTION: Plants and Uses Thereof for Plant FILE REFERENCE: 38-21(53313) B CURRENT APPLICATION NUMBER: US/10/425,114 CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 73128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Clone ID: MRT4577_24821C.1.pep
                                                                                                                                                                                                                                                                                                                                                                    , OTHER INFORMATION: Clone ID: 700236753_FLI.pep
US-10-425-114-52777
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 186821, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: La ROSS, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
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                                                                                     Tabaska, Jack E
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43 VLEENQSLENALR 55
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1 VLEENQSLENALR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 79.0
Best Local Similarity 69.2
Matches 9; Conservative
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                               SEQ ID NO 52777
LENGTH: 562
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APPLICANT:
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APPLICANT: Selig, Luc
APPLICANT: Selig, Luc
APPLICANT: Rain, Jean-Christophe
APPLICANT: Rain, Jean-Christophe
TITLE OF INVENTION: Collection of Prokaryotic DNA for Two-Hybrid System, Helicobacter
TITLE OF INVENTION: Oplori Protein-Protein Interactions and Applications thereof
FILE REFERENCE: B5053
CURRENT APPLICATION NUMBER: US/10/012,819
CURRENT FILING DATE: 2001-10-30
PRIOR APPLICATION NUMBER: EP 99401066.8
PRIOR APPLICATION NUMBER: EP 99401066.8
SPRIOR FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 278
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 82.
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Publication No. US20040052799A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLETC ACID AND AMINO ACID SEQUENCES
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 706;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 346;
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Pred. No. 1.2e+02;
2; Mismatches 2; Indels
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US-10-172-094-6
| Sequence 6, Application US/10172094
| Sequence 6, Application US/10172094
| Publication No. US20030161830A1
| GENERAL INFORMATION:
| APPLICANT: LORENZI, MATTHEW
| APPLICANT: LORENZI, MATTHEW
| APPLICANT: GOTTARDIS, MARCO
| TITLE OF INVENTION: NOVEL HUMAN HISTONE PEPTIDES
| FILE REFERENCE: 3053-4145US1
| CURRENT APPLICATION NUMBER: 00/298,296
| PRIOR APPLICATION NUMBER: 60/298,296
| PRIOR PELLING DATE: 2001-66-14
| PRIOR PELLING DATE: 2001-66-14
| NUMBER OF SEQ ID NOS: 127
| SOFTWARE: Patentin Ver. 2.1
| SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69.4%; Score 43; DB 4; 181.8%; Pred. No. 2.7e+02;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-172-094-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 69.2%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Helicobacter pylori
US-10-012-819-82
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157 ILTESKEIBEALK 169
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Best Local Similarity 81.8
Matches 9; Conservative
        APPLICANT: Legrain, Pierre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 LEENKELENAL 12
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US-10-335-977-8599
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TYPE: PRT
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                                                              Gaps
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                                                                                                                                                                                                                                                                                          Sequence 8597, Application US/10335977

Publication No. US20040052799A1

GENERAL INPORMATION:

APPLICANT: DOUGLAS SMITH et al

APPLICANT: DOUGLAS SMITH et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES

RELATING TO HELICOBACTER PYLORI FOR
Score 43; DB 4; Length 223; Pred. No. 74; 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69.4%; Score 43; DB 4; Length 296; 69.2%; Pred. No. 1e+02;
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CORRESPONDENCE ADDRESS: LAHIUF & COCKFIELD
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRET APPLICATION DATA:

APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragourae, Amy E.
REFERENCE/DOCKET NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 36,207
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-7400
TELEPHONE: (617)727-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...296
SEQUENCE DESCRIPTION: SEQ ID NO: 8597:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 82, Application US/10012819
Publication No. US20030017478A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 296 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Massachusetts
COUNTRY: USA
          69.4%;
69.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176 ILTESKEIEEALK 188
                                                                                                                                             208 ILTESKEIEEALK 220
                                                                                                                 1 ILEENKELENALK 13
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          Query Match
Best Local Similarity 69.2
Matches 9; Conservative
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Matches 9, Conservative
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US-10-012-819-82
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RESULT 19
US-10-419-462-10
S-10-419-462-10
S-20-410-462-10
S-20-410-462-10
S-20-410-462-10
S-20-410-462-10
S-20-410-462-10
GENERAL INFORMATION:
APPLICANT: Kevin J.
APPLICANT: Williams, Kevin J.
TITLE OF INVENTION: Thrombospondin Fragments and Uses Thereof In Clinical Assays for TITLE OF INVENTION: Cancer and Generation of Antibodies and Other Binding Agents;
TITLE REPERENCE: W1107-20005
CURRENT APPLICATION NUMBER: US/10/419,462
CURRENT FILING DATE: 2003-04-17
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.2
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Thrombospondin Region which includes an N-terminal Cys added to OTHER INFORMATION: aid conjugation
                                                                                                                                                           APPLICANT: Kevin J. Williams
APPLICANT: Kevin J. Williams, Kevin J.
APPLICANT: Kevin J. Williams, Kevin J.
TITLE OF INVENTION: Thrombospondin Fragments and Uses Thereof In Clinical Assays fr
TITLE OF INVENTION: Cancer and Generation of Antibodies and Other Binding Agents
TITLE OF INVENTION: Cancer and Generation of Antibodies and Other Binding Agents
FILE REFERENCE: WILO7-20005
CURRENT PILING DATE: 2004-02-20
PRIOR APPLICATION NUMBER: US/10/419,462
PRIOR APPLICATION NUMBER: US/10/419,462
PRIOR FILING DATE: 2003-04-21
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.2
SEQ ID NO 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 42; DB 4;
Pred. No. 6.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Thrombospondin Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 10, Application US/10782968
; Publication No. US20050065324A1
; GENERAL INFORMATION:
                                                                                          US-10-782-968-9
; Sequence 9, Application US/10782968
; Sequence 9, Application US-10782968
; GENERAL INFORMATION:
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Best Local Similarity 61.5
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3 VTEENKELANELR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-419-462-10
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Publication No. US20040053392A1
GENERAL INFORMATION
APPLICANT: Kevin J. Williams
APPLICANT: Kevin J. Williams
APPLICANT: Williams, Kevin J.
TITLE OF INVENTION: Thrombospondin Fragments and Uses Thereof in Clinical Assays for TITLE OF INVENTION: Thrombospondin Fragments and Generation of Antibodies and Other Binding Agents FILE REFERENCE: WINDER: US/10/419,462
CURRENT APPLICATION NUMBER: US/10/419,462
CURRENT FILING DATE: 2003-04-17
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                    CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 37.007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)72-7400
TELEPHONE: (617)72-4214
INFORMATION FOR SEQ ID NO: 8599:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ilarity 61.5%; Score 42; DB 4 ilarity 61.5%; Pred. No. 6.1; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature; LOCATION: (B) LOCATION 1...806; SEQUENCE DESCRIPTION: SEQ ID NO: 8599: US-10-335-977-8599
                                                ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 806 amino acids
TYPE: amino acid
       STATE: Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
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155 ILTESKEIEEALK 167
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Best Local Similarity 69.2
Matches 9; Conservative
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Best Local Similarity
Matches 8; Conserv
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1 ILEENKELENALK 13

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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rovalic David K
APPLICANT: About Yihua
APPLICANT: About Yihua
APPLICANT: Tabou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 257798
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Sequence 1020, Application US/10741600

Sequence 1020, Application WS.

Publication No. US20050026169A1

SEQUENCE 1020

Publication No. US20050026169A1

TITLE OF INVENTION: MYCOARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: MYCOARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF

TITLE REFERENCE: CL001499

CURRENT APPLICATION NUMBER: US/10/741,600

CURRENT FILING DATE: 2003-12-22

NUMBER OF SEQ ID NOS: 73997

SOFTWARE: FABLESEQ for Windows Version 4.0

SEQ ID NO 1020

LENGTH: 432
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                                                                                                                                                                                       ; OTHER INFORMATION: Thrombospondin Region plus Procollagen homology domain
US-10-782-968-42
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                                                                                                                                                                                                                                                                                            Length 98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: PAT_MRT3847_74815C.1.pep
US-10-424-599-257798
                                                                                                                                                                                                                                                                                         Query Match 67.7%; Score 42; DB 5; Best Local Similarity 61.5%; Pred. No. 43; Matches 8; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 42; DB 4;
Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (1)..(384)
OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 257798, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
PRIOR FILING DATE: 2003-04-21
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn version 3.2
SEQ ID NO 42
LENGTH: 98
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Similarity 72.7%;
8; Conservative
                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                    1 ILEENKELENALK 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 VTEENKELANELR 33
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ORGANISM: Homo sapiens
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ORGANISM: Glycine max
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Best Local Similarity
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                                                                                                                                      TYPE: PRT
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APPLICANT: Kevin J. Williams
APPLICANT: Williams, Kevin J.
TITLE OF INVENTION: Thrombospondin Fragments and Uses Thereof In Clinical Assays for TITLE OF INVENTION: Cancer and Generation of Antibodies and Other Binding Agents FILE REFERENCE: Wil07-20005
CURRENT APPLICATION NUMBER: US/10/782,968
CURRENT FILING DATE: 2004-02-20
PRIOR APPLICATION NUMBER: US/10/419,462
PRIOR PILING DATE: 2003-04-21
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn version 3.2
SEQ ID NO 10
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-419-462-42
| Sequence 42, Application US/10419462
| Sequence 42, Application US/10419462
| Sequence 42, Application US/10419462
| Sequence 42, Application US/104104019
| Sequence 42, Application US/104104019
| APPLICANT: Kevin J. Williams
| APPLICANT: Williams, Kevin J. TITLE OF INVENTION: Thrombospondin Fragments and Uses Thereof In Clinical Assays for TITLE OF INVENTION: Cancer and Generation of Antibodies and Other Binding Agents | FILE REFERENCE: WillOT-20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 42, Application US/10782968
Sequence 42, Application US/10782968
Publication No. US20050065324A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kevin J. Williams
APPLICANT: Williams, Kevin J.
TITLE OF INVENTION: Thrombospondin Fragments and Uses Thereof in Clinical Assays for TITLE OF INVENTION: Cancer and Generation of Antibodies and Other Binding Agents
FILE REFERENCE: W1107-20005
CURRENT APPLICATION NUMBER: US/10/782,968
CURRENT FILING DATE: 2004-02-20
PRIOR APPLICATION NUMBER: US/10/419,462
                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Thrombospondin Region which includes an N-terminal Cys added to CTHER INFORMATION: aid conjugation US-10-782-968-10
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US-10-419-462-42
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Pred. No. 43;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67.7%; Score 42; DB 5; Length 18; 61.5%; Pred. No. 6.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
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CURRENT FILING DATE: 2003-04-17
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 61.5%;
Matches 8; Conservative :
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21 VTEENKELANELR 33
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Best Local Similarity 61.5
Matches 8; Conservative
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LENGTH: 98
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RESULT 28
US-10-425-115-226623
US-10-425-115-226623
i Sequence 226624, Application US/10425115
i Publication No. US20040214272A1
i GENERAL INFORMATION:
i APPLICANT: La Roba. Thomas J.
APPLICANT: La Roba. Thou, Yihua
APPLICANT: Cao, Yongwei
ITILE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
ITILE OF INVENTION: Plants
ITILE REPRENUE: 38-21(53222)
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 226623
LENGTH: 584
                                                                                                                                                                                                                APPLICANT: Aziz, Natasha
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Ginsburg, Albert
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
FILE REFERENCE: 05882.0193.NPUS01
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US-10-425-115-226623
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61.5%; Pred. No. 3.1e+02;
iive 2; Mismatches 3.
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Publication No. US20040034888A1
                                                                                                                                            Sequence 4109, Application US/10723860 Publication No. US20040253606A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67.7%;
illarity 61.5%;
Conservative
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SOFTWARE: PatentIn version 3.2
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108 LLERNKELEGSLQ 120
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                             354 VTEENKELANELR 366
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Best Local Similarity 61.5
Matches 8; Conservative
1 ILEENKELENALK 13
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US-10-723-860-4109
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Matches 8; Conserv
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ORGANISM: Zea mays
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US-10-425-114-64494
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LENGTH: 535
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Sequence 1022, Application US/10741600
Publication No. US20050026169A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT APPLICATION NUMBER: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SEQ ID NO 1022
LENGTH: 432
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Patent No. US2020205230841

GENERAL INFORMATION:

APPLICANT: ROSEN et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106

CURRENT FILING DATE: 2001-08-10

PRIOR FILING DATE: 2000-03-08

PRIOR FILING DATE: 1999-03-12

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1694

SOFTWARE: PATENTIN NUMBER: 60/124,270

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1694
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Pred. No. 2.2e+02;
2; Mismatches 3; Indels
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i OTHER INFORMATION: Xaa = Any Amino Acid
US-10-741-600-1022
                      ; NAME/KEY: VARIANT
; LOCATION: (1)...(432)
; CTHER INVERMATION: Xaa = Any Amino Acid
US-10-741-600-1020
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Best Local Similarity 61.5%;
Matches 8; Conservative
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Best Local Similarity 61.5-
Best Local 8; Conservative
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ORGANISM: Homo sapiens
US-09-925-301-1047
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LENGTH: 466
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APPLICANT: Aventis Pasteur Limited
TITLE OF INVENTION: Enhancement of the Immune Response Using CD-36 Binding Domain
FILE REPERENCE: API-01-17-PCT
CURRENT APPLICATION NUMBER: 105/10/317,8218
CURRENT FILING DATE: 2050-12-12
PRIOR PILING DATE: 2001-12-12
PRIOR FILING DATE: 2001-12-12
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Pred. No. 6.7e+02;
2; Mismatches 3;
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Pred. No. 6.6e+02;
2; Mismatches 3;
FILE REFERENCE: 1440.2009002; CURRENT APPLICATION NUMBER: US/10/296,733; CURRENT FILING DATE: 2002-11-25; PRIOR APPLICATION NUMBER: 60/207,994; PRIOR FILING DATE: 2000-05-26; NUMBER OF SEQ ID NOS: 27; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 1
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Patent No. US20020137679A1
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SOFTWARE: Patentin version 3.2
SEQ ID NO 7
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Best Local Similarity 61.5%;
Matches 8; Conservative
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Best Local Similarity 61.5%;
Matches 8; Conservative
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283 VTEENKELANELR 295
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CORGANISM: Homo sapiens
US-10-296-733-1
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US-09-919-603-1
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ORGANISM: Homo sapiens
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US-09-939-853A-97

US-09-939-853A-97

Sequence 97, Application US/09939853A

Publication No. US20040039163A1

GENERAL INFORMATION:

APPLICATION:

APPLICATION:

TITLE OF INVENTION:

CURRENT FILING DATE: 2001-08-27

PRIOR APPLICATION NUMBER: 60/264,191

PRIOR APPLICATION NUMBER: 60/267,300

PRIOR APPLICATION NUMBER: 60/267,300

PRIOR PILING DATE: 2001-08-08

PRIOR FILING DATE: 2001-02-08

PRIOR FILING DATE: 2001-02-08

PRIOR FILING DATE: 2001-03-20

PRIOR FILING DATE: 2001-03-20

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                                                                     APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cor, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 18131313 B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 64494
LENGTH: 625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 42; DB 4; Length 625;
Pred. No. 3.4e+02;
2; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) OTHER INFORMATION: Clone ID: LIB3060-111-G1_FLI.pep
US-10-425-114-64494
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Publication No. US20040110131A1
GENERAL INFORMATION:
APPLICANT: Beth Island Deaconess Medical Center
APPLICANT: Lawler, John W.
TITLE OF INVENTION: Thrombospondin-1 Type 1 Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
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Best Local Similarity 61.5%;
Matches 8; Conservative
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Best Local Similarity 61.5%;
Matches 8; Conservative
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432 VLEEKAELENRMK 444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Zea mays
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APPLICANT: MILEAY, ALCHAICA
APPLICANT: Watson, Susan R.
APPLICANT: Watson, Susan R.
APPLICANT: Watson, Susan R.
APPLICANT: BOS Biotechnology, Inc.
APPLICANT: BOS Biotechnology, Inc.
TITLE OF INVENTION: No. US20030152926A1e1 Methods of Diagnosis of Angiogenesis
TITLE OF INVENTION: Modulators
FILE REPERENCE: 018501-000710US
CURRENT APPLICATION NUMBER: US/10/021,660
CURRENT PILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: US/09/784,356
PRIOR PLIING DATE: 2001-02-14
PRIOR FILING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 135
SOFTWARE: FeatSEQ for Windows Version 3.0
SEQ ID NO 114
LENGTH: 1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: MCCATLAN, Jeannette Just
APPLICANT: MCCATLAN, Jeannette Just
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE IDENTIFICATION,
TITLE OF INVENTION: CARDIOVASCULAR DISEASE
TITLE OF INVENTION: CARDIOVASCULAR DISEASE
CURRENT APPLICATION NUMBER: US/10/008,093
CURRENT APPLICATION NUMBER: US 60/248,185
PRIOR APPLICATION NUMBER: US 60/248,185
PRIOR FILING DATE: 2000-11-09
PRIOR PILING DATE: 2000-12-09
PRIOR FILING DATE: 2000-12-22
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
                                                                                                  Sequence 114, Application US/10021660 Publication No. US20030152926A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/10008093 Publication No. US20030166017A1 GENERAL INFORMATION:
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61.5%;
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301 VTEENKELANELR 313
  301 VTEENKELANELR 313
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Best Local Similarity 61.5'
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Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                                    APPLICANT: Murray, Richard APPLICANT: Glynne, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-008-093-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
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                                                                                       Gaps
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APPLICANT: MCCATCHY, Jeanette
APPLICANT: MCCATCHY, Jeanette
APPLICANT: Ableson, Allen
TILE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
FILE REFERENCE: MMI-002
CURRENT APPLICATION NUMBER: US/10/020,141
CURRENT FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: US 60/313,097
PRIOR PILING DATE: 2001-08-16
PRIOR PELING DATE: 2001-08-16
PRIOR PILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 4.0
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Publication No. US20030096248A1
GENERAL INFORMATION:
APPLICANT: MCCarthy, Jeanette
APPLICANT: Bolk, Seacy
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
FILE REFERENCE: MMI-003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 67.7%; Score 42; DB 4; Length 1170; Best Local Similarity 61.5%; Pred. No. 6.8e+02; Matches 8; Conservative 2; Mismatches 3; Indels
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Pred. No. 6.8e+02;
2; Mismatches 3; Indels
                                                Length 1169;
                                                                                          3; Indels
                                              Score 42; DB 5;
Pred. No. 6.8e+02;
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PRIOR APPLICATION NUMBER: US 60/317,033
PRIOR FILING DATE: 2001-09-04
PRIOR FILING DATE: 2001-09-04
PRIOR PAPLICATION NUMBER: US 60/330,248
PRIOR FILING DATE: 2001-10-17
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                  Sequence 12, Application US/10020141
Publication No. US20030092013A1
                                                67.7%;
61.5%;
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300 VTEENKELANELR 312
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301 VTEENKELANELR 313
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                                                                                          Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                            Query Match
Best Local Similarity
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LENGTH: 1170
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LENGTH: 1170
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    US-10-317-821B-7
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TYPE: PRT
ORGANISM: Human
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US-10-211-462-38

Sequence 38, Application US/10211462

Publication No. US20040033495A1

GENERAL INFORMATION:
APPLICANT: Murray, Richard
APPLICANT: Atson, Susan R.
APPLICANT: Atson, Susan R.
APPLICANT: Atson, Susan R.
APPLICANT: Atson, Methods of Diagnosis of Angiogenesis, Compositions and TITLE OF INVENTION: Methods of Screening for Angiogenesis Modulators
FILE REFERENCE: 018501-006200US
FILE REFERENCE: 2003-02-13

CURRENT FILING DATE: 2003-02-13

PRIOR APPLICATION NUMBER: US 09/784,356
                                                                                                            GENERALD INFORMATION:
APPLICANT: Affar, Daniel
APPLICANT: Affar, Daniel
APPLICANT: Glanebeag, Wendy M.
APPLICANT: Glanebeag, Wendy M.
APPLICANT: Glanebeag, Wendy M.
APPLICANT: Glanebeag, Wendy M.
APPLICANT: Glane, Richard
APPLICANT: Marson, Susan
APPLICANT: Marson, Susan
APPLICANT: Marson, Susan
APPLICANT: Marson, Susan
APPLICANT: Marson, Susan
APPLICANT: Marson, Susan
APPLICANT: Marson, Susan
APPLICANT: Wethods of Excening for Modulators of Cancer
APPLICANT: Methods of Screening for Modulators of Cancer
APPLICANT: Methods of Screening for Modulators of Cancer
APPLICANT: Methods of Screening for Modulators of Cancer
APPLICANT: Wethods of Screening for Modulators of Cancer
APPLICATION NUMBER: US 00/350,666
PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-13
PRIOR PILING DATE: 2001-11-15
PRIOR PILING DATE: 2001-11-15
PRIOR PILING DATE: 2001-11-15
PRIOR PILING DATE: 2001-11-24
PRIOR PILING DATE: 2001-11-24
PRIOR PILING DATE: 2001-11-24
PRIOR PILING DATE: 2002-11-10
PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR PILING DATE: 2002-11-10
PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR PILING DATE: 2002-01-08
PRIOR PILING DATE: 2002-01-08
PRIOR PILING DATE: 2002-01-08
PRIOR PILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 60/347,349
PRIOR PILING DATE: 2002-01-08
PRIOR PILING DATE: 2002-01-08
PRIOR PILING DATE: 2002-02-08
PRIOR PILING DATE: 2002-02-08
PRIOR PILING DATE: 2002-02-08
PRIOR PILING DATE: 2002-02-08
PRIOR PILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 60/347,349
PRIOR PILING DATE: 2002-02-08
PRIOR PILING DATE: 2002-02-08
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PRIOR PILING DATE: 2002-02-08
PRIOR PILING DATE: 2002-02-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 1386
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1170
LENGTH: 1170
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Pred. No. 6.8e+02;
2; Mismatches 3; Indels
                      ; Sequence 1170, Application US/10295027; Publication No. US20030232350A1; GENERAL INFORMATION:
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Best Local Similarity 61.5%;
Matches 8; Conservative 5
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US-10-295-027-1170
US-10-295-027-1170
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US-10-419-462-38
US-10-419-462-38
Sequence 38, Application US/10419462
Sequence 38, Application US/04005332A1
Publication No. US2004005332A1
APPLICANT: Kevin J. Williams
APPLICANT: Kevin J. Williams, Kevin J.
TITLE OF INVENTION: Thrombogondin Fragments and Uses Thereof In Clinical Assays for TITLE OF INVENTION: Cancer and Generation of Antibodies and Other Binding Agents
TITLE REFERENCE: W1107-20005
CURRENT APPLICATION NUMBER: US/10/419,462
CURRENT PILING DATE: 2003-04-17
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn version 3.2
SEQ ID NO 38
LENGTH: 1170
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Pred. No. 6.8e+02;
2; Mismatches 3; Indels
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Best Local Similarity 61.5%; Pred. No. 6.8e+02;
Matches 8; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: US 09/791,390 ,
PRIOR FILING DATE: 2001-02-22
PRIOR PELING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: US 60/310,025
PRIOR APPLICATION NUMBER: US 60/334,244
PRIOR PILING DATE: 2001-11-29
NUMBER OF SEQ ID NOS: 230
SOFTWARE: PATENTIN VEY: 2.1
                                                                                                                                                                                                                                                                                  Query Match 67.7%;
Best Local Similarity 61.5%;
Matches 8; Conservative ;
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                                                                                                                                                                                      LENGTH: 1170
TYPE: PRT
CRGANISM: Homo sapiens
US-10-211-462-38
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US-10-231-956A-482
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Gaps

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Sequence 38, Application US/10782968
Publication No. US20050065324A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Williams, Kevin J.
TITLE OF INVENTION: Thrombospondin Fragments and Uses Thereof In Clinical Assays f.
TITLE OF INVENTION: Cancer and Generation of Antibodies and Other Binding Agents
FILE REFERENCE: WINDER: US/10/782,968
CURRENT APPLICATION NUMBER: US/10/782,968
CURRENT APPLICATION NUMBER: US/10/419,462
PRIOR APPLICATION NUMBER: US/10/419,462
                      MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Guild, Braydon C.
APPLICANT: Liao, Hua
APPLICANT: Liao, Hua
APPLICANT: Jones, Michael D.
APPLICANT: Solg, Johannes W.
TITLE OF INVENTION: Compositions, Kits, and Methods for
TITLE OF INVENTION: Identification, Assessment, Prevention, and Therapy of
TITLE OF INVENTION: Rheumatoid Arthritis
FILE REFERENCE: MP103-037PIRM
CURRENT APPLICATION NUMBER: US/10/849,989
CURRENT FILING DATE: 2004-05-20
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INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
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Pred. No. 6.8e+02;
2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                       Score 42; DB 5; Pred. No. 6.8e+02;
                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
  TITLE OF INVENTION: GENETIC POLYMORPHISMS
TITLE OF INVENTION: MYCCARDIAL INFARCTION
FILE REFERENCE: CLOO1499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/472,330 PRIOR FILING DATE: 2003-05-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 44, Application US/10849989
Publication No. US20050142569A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                          61.5%;
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SOFTWARE: Patentin version 3.2
SEQ ID NO 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 VTEENKELANELR 313
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Best Local Similarity 61.5
Matches 8; Conservative
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Best Local Similarity 61.5
Matches 8; Conservative
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CRGANISM: Homo sapiens
US-10-741-600-1021
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ORGANISM: Human
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US-10-782-968-38
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Sequence 1019, Application US/10741600
Publication No. US20050026169A1
GENERAL INFORMATION:
APPLICAPT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYWORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                          Sequence 1018, Application US/10741600
Sequence 1018, Application US/10741600
Publication No. US20050026169A1
GENERAL INFORMATION:
APPLICANT: CANGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILER REPRENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FeatSEQ for Windows Version 4.0
SEQ ID NO 1018
LENGTH: 1170
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61.5%; Pred. No. 6.8e+02;
tive 2; Mismatches 3; Indels
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                                                            DB 4; Length 1170;
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                                                                                                            3; Indels
                                                                                  6.8e+02;
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                                                                                                              2; Mismatches
                                                              Score 42;
Pred. No.
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                                                         67.7%;
illarity 61.5%;
Conservative
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301 VTEENKELANELR 313
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301 VTEENKELANELR 313
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Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                           1 ILEENKELENALK 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , ORGANISM: Homo sapiens
US-10-741-600-1019
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                                                            Query Match
Best Local Similarity
Matches 8, Conserval
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US-10-741-600-1019
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               US-10-419-462-38
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Publication No. US20040052799A1
GENERAL INFORMATION:
GENERAL INFORMATION:
ITILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RELATING TO HELICOBACTER PYLORI FOR DIAGNOSTICS AND THERAPEUTICS
Score 42; DB 6; Length 1170;
Pred. No. 6.8e+02;
2; Mismatches 3; Indels
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88.9%; Pred. No. 1.2e+02;
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APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 36,207
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                            2; Mismatches
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LOCATION: (B) LOCATION 1...176
SEQUENCE DESCRIPTION: SEQ ID NO: 7129:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT
SOFTWARE: UNIX
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INFORMATION FOR SEQ ID NO: 7129:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Boston
STATE: Massachusetts
      67.7%;
61.5%;
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MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                      : |||||| | |:
301 VTEENKELANELR 313
                                                                                                                                1 ILEENKELENALK 13
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Best Local Similarity 88.9
Matches 8; Conservative
      Query Match
Best Local Similarity 61.5
Matches 8; Conservative
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EENKELKNA 36
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US-11-097-143-2913
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| Sequence 548, Application US/10631467 |
| Publication No. US2005208496A1 |
| Publication No. US2005208496A1 |
| Publication No. US2005208496A1 |
| Publication No. US2005208496A1 |
| Publication No. US2005208496A1 |
| Publication No. US2005208496A1 |
| TITLE OF INVENTION: Method for testing for broncheal asthma, or chronic obstructive prints REFERENCE: 3462.1005-000 |
| TITLE OF INVENTION: Method for testing for broncheal asthma, or chronic obstructive prints REFERENCE: 3462.1005-000 |
| FILE REFERENCE: 3462.1005-000 |
| CURRENT PELING DATE: 2003-07-31 |
| PRIOR PILING DATE: 2003-03-20 |
| PRIOR PILING DATE: 2002-08-06 |
| NUMBER OF SEQ ID NOS: 2086 |
| SOFTWARE: Patentin version 3.1 |
| SEQ ID NO 548 |
| LING DATE: 1700 |
| LINGTH: 1170 |
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Sequence 51, Application US/1103713

Publication No. US20050221398A1

GENERAL INFORMATION:

APPLICANT: JACQUEMIER, JOCELYNE

APPLICANT: BERTUCCI, FRANCOIS

APPLICANT: BERTUCCI, FRANCOIS

APPLICANT: BERRBACA

TITLE OF INVENTION: PROCIEN EXPRESSION PROFILING AND BREAST CANCER

TITLE OF INVENTION: PROCIEN EXPRESSION PROFILING AND BREAST CANCER

TITLE OF INVENTION: PROGNOSIS

FILE REFERENCE: 1016-R-04 (B)

CURRENT APPLICATION NUMBER: US/11/037,713

CURRENT FILING DATE: 2005-01-16

PRIOR FILING DATE: 2004-01-16
                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                             Score 42; DB 5; Length 1170;
Pred. No. 6.8e+02;
2; Mismatches 3; Indels
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            SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : ||||| | |:
301 VTEENKELANELR 313
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301 VTEENKELANELR 313
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SOFTWARE: PatentIn Ver. 3.3
                                                                                                                                                                                                                                                                                                                                                             1 ILEENKELENALK 13
                                                                                                                                                                                                                                      Query Match
Best Local Similarity 61.5
Matches 8; Conservative
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CORGANISM: Homo sapiens
US-11-037-713-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Homo sapiens
                                                                                                         TYPE: PRT
ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-631-467-548
                                                                                1170
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                                                                                LENGTH:
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Gaps
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                                                                                                                                                                                                   Length 847;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: ProKaryotes
FILE REFENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8e+02;
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Pred. No. 6.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURKENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PELING DATE: 2000-03-21
PRIOR PELING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FABELSEQ for Windows Version 4.0
SEQ ID NO 11577
                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66.1%; Score 41; 88.9%; Pred. No. (
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11419
LENGTH: 847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11577, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wall, Daniel
Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                     Query Match
Best Local Similarity 88.9%;
                                                                                                  ; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-815-242-11419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ohlsen, Kari L.
Zyskind, Judith W.
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Best Local Similarity 88.5
Matches 8; Conservative
                                                                                                                                                                                                                                                        8; Conservative
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699 EENKELKNA 707
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                                                  TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DOSOPPHILA GENES.
FILE REFERENCE CLOO0728
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 2005-04-04
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TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prockaryctes
FILE REFERENCE: ELITRA.011A 90/98/15,242
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR PLILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,931
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/253,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/259,308
PRIOR FILING DATE: 2001-02-16
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                                                                                                                                                                           CURRENT APPLICATION NUMBER: 05/11/09/11/19
PRIOR APPLICATION NUMBER: 06/15/,832
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-05
PRIOR PRIOR DATE: 1999-10-19
PRIOR PELING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-11-2
PRIOR FILING DATE: 1999-11-2
PRIOR FILING DATE: 1999-11-2
PRIOR FILING DATE: 1999-11-2
PRIOR FILING DATE: 1999-11-2
PRIOR FILING DATE: 1999-11-2
PRIOR FILING DATE: 2000-01-1
PRIOR FILING DATE: 2000-01-1
PRIOR FILING DATE: 2000-01-2
PRIOR FILING DATE: 2000-01-3
PRIOR FILING DATE: 2000-03-3
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: PABLESEQ for Windows Version 4.0
SENGTHAL: 790
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Patent No. US20020061569A1
GENERAL INFORMATION:
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Carr, Grant J.
Yamamoto, Robert T.
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Zyskind, Judith W.
Wall, Daniel
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Best Local Similarity 61.5%;
Matches 8; Conservative
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Publication No. US20040052799A1

GENERAL INFORMATION:

APPLICANT: DOUGLAS SMITH et al

APPLICANT: DOUGLAS SMITH et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

DIAGNOSTICS AND THERAPEUTICS
                                                                                                                             Length 847;
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tive 1; Mismatches 0; Indels
                                                                                                                             Score 41; DB 4; 1
Pred. No. 6.8e+02;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...847
SEQUENCE DESCRIPTION: SEQ ID NO: 7131:
US-10-335-977-7131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOUNCE:
ORGANISM: Hellcobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 847 amino acids
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SEQUENCE CHARACTERISTICS:
                           ; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-282-122A-58924
                                                                                                                               66.1%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
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Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                             Query Match
Best Local Similarity 88.5
Matches 8; Conservative
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699 EENKELKNA 707
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US-10-335-977-7131
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LENGTH: 847
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                     APPLICANT: Tomb, Jean Francois
APPLICANT: Obmen, Raymond P.
TITLE OF INVENTION: Identification of Polynucleotides
TITLE OF INVENTION: Encoding No. US20020160456Alel Helicobacter Polypeptides in the
TITLE OF INVENTION: Genome
TITLE OF INVENTION: Genome
FILE REPERBUES: 66132/04302.
CURRENT APPLICATION NUMBER: US/09/895, 913A
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 08/881,227
PRIOR APPLICATION NUMBER: US 08/881,227
NUMBER OF SEQ ID NOS: 368
SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-06
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
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PRIOR PILING DATE: 2001-02-06
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Pred. No. 6.8e+02;
1; Mismatches 0; Indels
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangeu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Haselbeck, Robert
APPLICANT: Obleen, Kari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.1%;
88.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
  Miller, Charles
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Best Local Similarity 88.9
Matches 8; Conservative
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US-10-282-122A-58924
                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-895-913A-164
                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 164
LENGTH: 847
  APPLICANT:
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Sequence 226060, Application US/10425115

Publication No. US20040214272A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yongua

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

TITLE OF INVENTION: NUMBER: US/10/425,115

CURRENT APPLICATION NUMBER: 2003-04-28

CURRENT FILING DATE: 2003-04-28

SEQ ID NOS: 369326

LENGTH: 386
                                                                                                                                                                                                                                                                                                                                                                         Sequence 42480, Application US/10767701
Sequence 42480, Application US/10767701
Sequence 42480, Application US/10767701
Sequence 42480, Application OS/107684A1
GENERAL INFORMATION:
Sequence Applicant: Kovaluc, Vihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535) B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 42480
LENGTH: 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64.5%; Score 40; DB 4; Length 275; illarity 72.7%; Pred. No. 2.88+02; Conservative 1; Mismatches 2; Indels
                                                                                                                                Length 245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C52891_1.pep
US-10-767-701-42480
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                                                                                                                                                          2.5e+02;
                                                                                                                                       Score 40;
Pred. No.
                                                                                                                                  64.5%;
                                                                                                               Query Match
Best Local Similarity 66...
Best Local 8; Conservative
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177 LEENKSLKNDLR 188
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Matches 8; Conservative
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ORGANISM: Sorghum bicolor
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; TYPE: PRT
; ORGANISM: Mus musculus
; PEATURE:
; OTHER INFORMATION: BAP31
US-10-205-194-99
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Matches 8; Conserv
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ORGANISM: Zea mays
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US-10-425-115-226060
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US-10-767-701-42480
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                                                                                                                  CARRIER: DNA COMPLEXES CONTAINING DNA
ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE
THERAPY
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APPLICANT: Dixon, Alietair
APPLICANT: Dixon, Alietair
APPLICANT: Brooksbank, Robert
TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
FILE REPERENCE: WL-A-018201
CURRENT APPLICATION NUMBER: US/10/205,194
CURRENT FILING DATE: 5200-07-24
PRIOR APPLICATION NUMBER: GB 0118354.0
PRIOR PILING DATE: 2001-07-27
WUMBER OF SEQ ID NOS: 177
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                         ZIP: 19899
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                            NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Connolly, Bove, Lodge, & Hutz
STREET: 1220 Market Street, P.O. Box 2207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/036,869
FILING DATE: 29-No. US20020151516A1-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64.5%; Score 40; DB 4; 172.7%; Pred. No. 2.2e+02; tive 1; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/985,526
FILING DATE: «Unknown»
APPLICATION NUMBER: US 08/608,845
FILING DATE: 16-UL-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: MCMORTOW Jr., Robert G
TELECOMMUNICATION INFORMATION:
                                               Sequence 1, Application US/10036869
Publication No. US20020151516A1
GENERAL INFORMATION:
APPLICANT: Mixeon, James A
TITLE OF INVENTION: CARRIER: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (302) 658-9141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 99, Application US/10205194 Publication No. US20030134301A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 218 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (302) 658-9
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                        CITY: Wilmington
STATE: Delaware
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Conservative
                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A.
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Best Local Similarity
Matches 8; Conserv
                            -10-036-869-1
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US-09 185-242-13407

US-09 185-242-13407

US-09 185-242-13407

Determen 13407, Application US/09815242

Perent No. US-02020006556A1

APPLICANT: Handsleck, Robert

APPLICANT: Trawick, John User, Robert

APPLICANT: Trawick, John D.

APPLICANT: Trawick, John D.

APPLICANT: Trawick, John D.

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APPLICANT: Trawick, John D.

APPLICANT: Trawick, John D.

APPLICANT: Trawick, John D.

FILE OF INVENTION: Proverse

TITLE OF INVENTION: Proverse

FILE REFRENCE: ELIXA, 011A

CURRENT FILING DATE: 2000-03-24

PRIOR PILING DATE: 2000-03-25

PRIOR PILING DATE: 2000-01-25

PRIOR PILING DATE: 2000-01-25

PRIOR PILING DATE: 2000-10-21-6

PRIOR PILING DATE: 2000-11-21-6

PRIOR PILING DATE: 2000-11-21-6

PRIOR PILING DATE: 2000-11-21-6

PRIOR PILING DATE: 2000-11-21-6

NUMBER OF SEQ ID NOG: 14110

SEQ ID NOG: 14110

SEQ ID NOG: 14110

SEQ ID NOG: 14110

SEQ ID NOG: 14110

APPLE FREE RESECUTE WINDOWN VERSION 4.0

SEQ ID NOG: 13417

QUARTY MARCH: Trawick Trawick DATE: 2001-02-02-02

APPLE TREE FREE RESECUTE WINDOWN VERSION 4.0

SEQ ID NOG: 14110

OMET WARCHER IN TRAWICK: 13447

OMET WARCHER IO: CORRESTATIVE 2; MISSMATCHES 2; Gaps 1;

BRICK MARCHER 10; CORRESTATIVE 2; MISSMATCHES 2; Gaps 1;
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Search completed: March 11, 2006, 12:32:33 Job time : 109.947 secs

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Jef, A
Lequence 11150, A
Sequence 10418, A
Sequence 92, Appl
Sequence 98, Appl
Sequence 101
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Sequence 3500, Ap
Sequence 7907, Ap
Sequence 917, Ap
Sequence 31147, Ap
Sequence 32146, A
Sequence 32146, A
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7682, Ap
7755, Ap
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7680, Ap
81356, Ap
21335, A
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3, Appli
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192, App
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1080, App
7832, Ap
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3432, Ap
7178, Ap
29, Appl
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1217, Ap
3852, Ap
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Sequence 4911, Al
Sequence 1418, Al
Sequence 6587, Al
Sequence 16576, A
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Sequence 7680, P
Sequence 8356, P
Sequence 21380,
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Sequence 6
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340 7 US-II-096-56BA-27013 Sequence 270348 6 US-IO-793-656-1702 Sequence 118349 6 US-IO-793-656-1702 Sequence 118351 7 US-II-018-866-118 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequence 11865 Sequ	50.0         604         7         US-11-096-568A-27015         Sequence           1         50.0         610         7         US-11-096-568A-27015         Sequence           50.0         610         7         US-11-096-568A-27015         Sequence           50.0         610         7         US-11-124-368A-260         Sequence           50.0         635         7         US-11-124-368A-262         Sequence           50.0         663         7         US-11-124-368A-262         Sequence           50.0         663         7         US-11-124-368A-269         Sequence           50.0         683         7         US-11-124-368A-269         Sequence           50.0         683         7         US-11-124-368A-269         Sequence           50.0         683         7         US-11-108-172-131         Sequence           50.0         844         7         US-11-109-463-4         Sequence           50.

Sequence 1269, Ap Sequence 238, App Sequence 245, App Sequence 241, App Sequence 242, App Sequence 28352, A Sequence 1542, Ap Sequence 1542, Ap Sequence 135, App Sequence 134, App Sequence 712, App Sequence 712, App Sequence 712, App	Sequence 22, Appli Sequence 22, Appli Sequence 29,00, Appli Sequence 29100, A Sequence 27, Appli Sequence 27, Appli Sequence 11, Appli Sequence 11, Appli Sequence 13, Appli Sequence 13, Appli Sequence 28, Appli Sequence 28, Appli Sequence 29099, A Sequence 5370, Appli Sequence 5370, Appli Sequence 131, Appli Sequence 310, Appli Sequence 310, Appli Sequence 114, Appli Sequence 116, Appli Sequence 117, Appli Sequence 117, Appli Sequence 118, Appli Sequence 118, Appli Sequence 118, Appli Sequence 118, Appli Sequence 118, Appli	AND ISSMENT, PREVENTION, AND
	6 US-10-857-780-22 6 US-10-828-831-9 7 US-11-231-59100 7 US-11-096-568A-29100 7 US-11-096-568A-29100 7 US-11-096-568A-29100 6 US-10-755-092-9 6 US-10-755-092-9 6 US-10-755-092-15 6 US-10-755-092-15 6 US-10-755-092-15 6 US-10-755-092-15 7 US-11-087-099-5370 8 US-11-087-099-5370 9 US-11-087-099-5370 1 US-11-087-099-5370 1 US-11-087-099-5370 1 US-11-087-099-5370 1 US-11-087-099-5370 1 US-11-087-099-5370 1 US-11-087-099-5370 1 US-11-087-099-5370 1 US-11-087-099-5370 1 US-11-087-099-5370 1 US-11-087-099-5370 1 US-11-087-099-5370 1 US-11-087-099-5370 1 US-11-087-099-5370 1 US-11-087-099-5370 1 US-11-087-099-5370	RESULT 1  US-11-166-284-55  Sequence 55, Application US/11186284  Publication No. US2050266493A1  GENERAL INFORMATION:  APPLICANT: Millennium Pharmaceuticals, Inc.  APPLICANT: Millennium Pharmaceuticals, Inc.  APPLICANT: Millentet, Tracy L.  APPLICANT: Kamatkar, Shubhangi  APPLICANT: Kamatkar, Shubhangi  APPLICANT: Kamatkar, Shubhangi  APPLICANT: Kamatkar, Shubhangi  APPLICANT: Calillemette, Tracy L.  APPLICANT: Monahan, John E.  APPLICANT: Thibodeau, Stephen N.  APPLICANT: Thibodeau, Stephen N.  APPLICANT: Thibodeau, Stephen N.  APPLICANT: MONEMATON: UNOVEL GENES, COMPOSITIONS, KITS, AND  TITLE OF INVENTION: THERAPY OF COLON CANCER  FILE OF INVENTION: THERAPY OF COLON CANCER  FILE OF INVENTION: THERES US/11/186,284  CURRENT APPLICATION NUMBER: US/01301,822  PRIOR FILING DATE: 2002-11-21  PRIOR FILING DATE: 2002-11-21  PRIOR FILING DATE: 2002-11-21  PRIOR PILING DATE: 2002-11-21  PRIOR PILING DATE: 2002-11-21  PRIOR PILING DATE: 2002-05-00  PRIOR PILING DATE: 2002-05-00  PRIOR PILING DATE: 2002-05-00  PRIOR PILING DATE: 2002-05-00  PRIOR PILING DATE: 2002-05-00  PRIOR PILING DATE: 2002-05-00  PRIOR FILING DATE: 2002-05-00  PRIOR PILING DATE: 2002-05-00  PRIOR PILING DATE: 2002-05-00  PRIOR PILING DATE: 2002-05-00  PRIOR PILING DATE: 2002-05-00  PRIOR PILING DATE: 2002-05-00  PRIOR PILING DATE: 2002-05-00  PRIOR PILING DATE: 2002-05-00  PRIOR PILING DATE: 2002-05-00  PRIOR PILING DATE: 2002-05-00  PRIOR PILING DATE: 2002-05-00  PRIOR PILING DATE: 2002-05-00  PRIOR PILING DATE: 2002-05-00  PRIOR PILING DATE: 2002-05-00  PRIOR PILING DATE: 2002-05-00  PRIOR PILING DATE: 2002-05-00  PRIOR PILING DATE: 2002-05-00  PRIOR PILING DATE: 2002-05-00  PRIOR PILING DATE: 2002-05-00  PRIOR PILING DATE: 2002-05-00  PRIOR PILING DATE: 2002-05-00  PRIOR PILING DATE: 2002-05-00  PRIOR PILING DATE: 2002-05-00  PRIOR PILING DATE: 2002-05-00  PRIOR PILING DATE: 2002-05-00  PRIOR PILING DATE: 2002-05-00  PRIOR PILING DATE: 2002-05-00  PRIOR PILING DATE: 2002-05-00  PRIOR PILING DATE: 2002-05-00  PRIOR PILING DATE: 2002-05-00  PRIOR
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Pred. No. 52;
2; Mismatches
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Score 42; DB 6; Pred. No. 52; 2; Mismatches
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Pred. No.
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US-11-046-456-28
; Sequence 28, Application US/11046456
; Publication No. US20050256044A1
; GENERAL INFORMATION:
; APPLICANT: Boyle, Bryan
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Best Local Similarity 61.5
Best Local 8; Conservative
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                                      Conservative
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US-10-995-561-595
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Best Local Similarity
Matches 8; Conserv
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION WUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FASTERO for Windows Version 4.0
SEQ ID NO 5594
LENGTH: 1170
                                                                                                                 Gaps
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APPLICANT: Cargill, Michele
APPLICANT: Cargill, Michele
APPLICANT: Bolk, Stacey
APPLICANT: Bolk, George O.
APPLICANT: Bolk, George O.
APPLICANT: Bolk, George O.
APPLICANT: McCarthy, Jeanette J.
TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
FILE REFRENCE: 2825.1027-001
CURRENT APPLICATION NUMBER: US/10/831,997
CURRENT FILING DATE: 2004-04-26
PRIOR PELLON NUMBER: US 60/153,357
PRIOR PILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: US 60/153,357
PRIOR APPLICATION NUMBER: US 60/220,947
PRIOR PILING DATE: 1999-09-10
PRIOR PELLON NUMBER: US 60/220,947
PRIOR PILING DATE: 2000-07-26
PRIOR FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2551
SOFTWARE FASISEQ for Windows Version 4.0
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52;
                                                                           Score 62; DB 7; Length 760; Pred. No. 0.018;
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                                                                           Query Match 100.0%; Score 62; DE Best Local Similarity 100.0%; Pred. No. 0.0 Matches 13; Conservative 0; Mismatches
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Pred. No.
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Publication No. US20050244834A1
GENERAL INFORMATION:
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61.5%;
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Best Local Similarity 61.5
Matches 8; Conservative
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ORGANISM: Homo sapiens
US-10-995-561-594
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                       , ORGANISM: Homo Sapiens
US-11-186-284-55
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US-10-995-561-594
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LENGTH: 1170
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       TYPE: PRT
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US-10-95-561-595
US-10-95-561-595
Sequence 595, Application US/10995561
Fublication No. US20050272054A1
GENERAL INFORMATION:
TITLE OF INVENTION:
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Sequence 596, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REPERENCE: CLO01559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT PILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SEQ ID NOS: 85702
SEQ ID NO 596
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TYPE: PRT
ORGANISM: Arabidopsis thaliana
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RESULT 8
US-11-087-099-12226
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US-11-087-099-5401
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APPLICANT: Boyle, Bryan
APPLICANT: Funk, Walter
APPLICANT: Funk, Walter
APPLICANT: Saktitani, Makoto
APPLICANT: Park, Emily
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Tomizuka, Kazuma
APPLICANT: Tomizuka, Kazuma
APPLICANT: Yagi, Mikio
TITLE OF INVENTION: Gastrointestinal Proliferative Factor and uses thereof
FILE REFERENCE: 11926-19401
CURRENT APPLICATION NUMBER: US 60/539,605
PRIOR FILING DATE: 2004-01-27
PRIOR FILING DATE: 2004-01-15
PRIOR FILING DATE: 2004-10-15
NUMBER OF SEQ ID NOS: 178
SOFTWARE: Patentin version 3.3
SEQ ID NO 28
LENGTH: 1170
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                                                                APPLICANT: Tang, Y. Tom
PEPLICANT: Yaddi, Mikio
APPLICANT: Tomizuka, Kazuma
TITLE OF INVENTION: Gastrointestinal Proliferative Factor and uses thereof
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Pred. No. 52;
2; Mismatches 3; Indels
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Pred. No. 52;
2; Mismatches
                                                                                                                                          THILE REFERENCE: 18824-003301
CURRENT APPLICATION NUMBER: US/11/046,456
CURRENT FILING DATE: 2005-01-27
PRIOR APPLICATION NUMBER: US 60/539,605
PRIOR FILING DATE: 2004-01-27
PRIOR FILING DATE: 2004-01-15
PRIOR FILING DATE: 2004-01-15
PRIOR FILING DATE: 2004-03-03
PRIOR FILING DATE: 2004-03-03
PRIOR FILING DATE: 2004-03-03
PRIOR FILING DATE: 2004-03-03
PRIOR FILING DATE: 2004-03-03
SEQ ID NO 28
LENGTHARE: PATENTIN VERSION 3.3
SEQ ID NO 28
LENGTHARE: PATENTIN VERSION 3.3
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Publication No. US20050256036A1
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Kakitani, Makoto
Oshima, Takeshi
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301 VTEENKELANELR 313
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Best Local Similarity 61.5
Matches 8; Conservative
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Best Local Similarity 61.5
Matches 8; Conservative
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; ORGANISM: Homo sapiens
US-11-046-456-28
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ORGANISM: Homo sapiens
US-11-046-644-28
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APPLICANT: Alexandrov, Nickolai et al.

TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 29720
LENGTH: 291
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Sequence 12226, Application US/11087099; Publication No. US20060041961A1; GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.; TILLE OF INVENITON: Genes and Uses for Plant Improvement; FILE REFERENCE: 38-21(53450)B EP; CURRENT APPLICATION NUMBER: US/11/087,099; CURRENT FILING DATE: 2006-03-22; NUMBER OF SEQ ID NOS: 12464; SEQ ID NO 12226; LENGTH: 291
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PUDlication No. US20060041961A1
GENERAL INFORMATION.
APPLICANT: Abad, Mark S. et al.
APPLICANT: Abad, Mark S. et al.
TILLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38 21 (53450) B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
SEQ ID NOS: 12464
LENGTH: 298
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80.0%; Pred. No. 15;
tive 1; Mismatches
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                                                                                                                                                                                                                                                                            ) ORGANISM: Arabidopsis thaliana US-11-087-099-12226
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ORGANISM: Arabidopsis thaliana
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Best Local Similarity 80.v
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25 EENKKFENAL 34
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25 EENKKFENAL 34
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Score 37; DB 7;
Pred. No. 40;
3; Mismatches
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; OTHER INFORMATION: Ceres Seq. ID no. 15227121
US-11-096-568A-8539
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; OTHER INFORMATION: Ceres Seq. ID no. 15227122
US-11-096-568A-8540
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Pred. No.
                                                                                                                                            Sequence 8540, Application US/11096568A Publication No. US20060048240A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59.7%;
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                                                   322 IAEGNKTRENALK 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      165 LLEENQNLRNQLQ 177
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Best Local Similarity 53.8
Matches 7; Conservative
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ORGANISM: Glycine max
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Best Local Similarity
Matches 7; Conserv
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US-11-096-568A-8538
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US-11-096-568A-8539
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APPLICANT: Zelder, Oskar
APPLICANT: Kolpprogge, Corinna
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Stefan for Zymotic Production of Fine Chemicals Containing
TITLE OF INVENTION: Bulphur (metY)
FILE REFERENCE: 13111-00106-018/10
CURRENT APPLICATION NUMBER: US/10/525,710
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Pred. No. 72;
                                   Score 41; DB 7; Length 298;
Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                          APPLICANT: Immunex Corporation
APPLICANT: Clarke, Howard RG
APPLICANT: Dubose, Robert F
APPLICANT: Wiley, Steven R
TITLE OF INVENTION: HUMAN SERPIN POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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PRIOR APPLICATION NUMBER: PCT/EP 2003/009453
PRIOR FILING DATE: 2003-08-26
PRIOR APPLICATION NUMBER: DE 102 39 082.7
                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/11/219,282
CURRENT FILING DATE: 2005-09-02
PRIOR PAPLICATION NUMBER: US/10/094,944
PRIOR FILING DATE: 2002-03-08
NUMBER OF SEO ID NOS: 35
SOFTWARE: Patentin version 3.1
SEO ID NO 31
LENGTH: S1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 30, Application US/10525710 Publication No. US20050260721A1 GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 79
SOFTWARE: Patentin version 3.3
SEQ ID NO 30
LENGTH: 430
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Best Local Similarity 69.2%;
Matches 9; Conservative
                                     66.1%;
80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61.3%;
63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 63.6
Matches 7; Conservative
                                                                           Conservative
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31 LEENRSMESAL 41
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                                                                                                                  3 EENKELENAL 12
                                                                                                                                                        32 EENKKFENAL 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-219-282-31
                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 3223-A
                                       Query Match
Best Local Similarity
Matches 8; Conserv
US-11-087-099-5401
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APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 8540
LENGTH: 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Publicant: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE REPRENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT APPLICATION NUMBER: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 8539
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Sequence 4493, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 4433
LENGTH: 308
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Sequence 2317, Application US/11087099
Publication No. US20060041961A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genea and Uses for Plant Improvement
FILE REPERBACE: 38-21(53450) B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT APPLICATION NUMBER: US/11/087,099
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 2317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 37; DB 7;
Pred. No. 71;
2; Mismatches
                                                                                                                         59.7%; Score 37; DB 7;
80.0%; Pred. No. 64;
tive 0; Mismatches
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                       NAME/KEY: misc_feature
i LOCATTON: (1).:(284)
i OTHER INFORMATION: Ceres Seq. ID no. 15220412
US-11-096-568A-4494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (1). (308)
OTHER INFORMATION: Ceres Seq. ID no. 15220411
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Best Local Similarity 66.79,
Best Local Similarity 67.79,
Best Local Similarity
                                                                                                          Query Match
Best Local Similarity 80.v.
Best Local 8; Conservative
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Best Local Similarity 80.0
Matches 8; Conservative
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                                                                                                                                                                                                             3 EENKELENAL 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                    US-11-096-568A-4493
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US-11-096-568A-8537
US-11-096-568A-8537
Sublication No. US20060048240A1
Sublication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 8537
LENGTH: 246
APPLICANT: Alexandrov, Nickolai et al.

TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT APPLICATION NUMBER: US/11/096,568A
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 8538
LENGTH: 222
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TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-15922PUS2
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
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Pred. No. 48;
                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
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LOCATION: (1). (246)
OTHER INFORMATION: Ceres Seq. ID no. 15227119
                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
| LOCATION: (1)..(122)
| MTHER INDOMATION: Ceres Seq. ID no. 15227120
US-11-096-568A-8538
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Sequence 4494, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
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Best Local Similarity 53.8%;
Matches 7; Conservative
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Best Local Similarity 53.8%;
Matches 7; Conservative
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195 LLEENQNLRNQLQ 207
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ORGANISM: Glycine max
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ORGANISM: Glycine max
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ORGANISM: Glycine max
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LENGTH: 284
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RESULT 24

US-10-763-712A-23

US-10-763-712A-23

Sublication No. US20050266541A1

Sublication No. US20050266541A1

GENERAL INFORMATION:

APPLICANT: Solazyme, Inc.

TITLE OF INVENTION: Methods and Compositions for Evolving Microbial Hydrogen

TITLE OF INVENTION: Methods and Compositions for Evolving Microbial Hydrogen

TITLE OF INVENTION: Methods and Compositions for Evolving Microbial Hydrogen

TITLE OF INVENTION: PLOGATION-CIP

CURRENT TILING DATE: 2004-01-21

PRIOR FILING DATE: 2004-01-21

PRIOR PILING DATE: 2003-04-12

PRIOR PLING DATE: 2003-04-12

PRIOR APPLICATION NUMBER: US 10/411,910

PRIOR PLING DATE: 2003-04-12

PRIOR PLING DATE: 2003-04-12

PRIOR PLING DATE: 2003-04-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 334;
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Publication No. US20060041961A1
GENERAL INFORMATION:
APPLICAT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement FILE REFERENCE: 38-21(53450) B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 8967
                                                                                                                                                                                                  Score 36; DB 7; I
Pred. No. 1.1e+02;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 36; DB 7; Pred. No. 1.1e+02;
                                                                                                                 ; TYPE: PRT
; ORGANISM: Oryza Bativa (japonica cultivar-group)
US-11-087-099-10594
CURRENT APPLICATION NUMBER: US/11/087,099 CURRENT FILING DATE: 2005-03-22 NUMBER OF SEQ ID NOS: 12464 SEQ ID NO 10594
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ORGANISM: Trichomonas vaginalis
                                                                                                                                                                                                         58.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 184
SOFTWARE: Patentin version 3.2
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Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                      Query Match
Best Local Similarity 70.0
7; Conservative
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                                                                                                                                                                                                                                                                                                 3 EENKELENAL 12
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31 EENKQFERAL 40
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US-11-087-099-8967
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                                                                                              LENGTH: 330
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LENGTH: 582
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                                                                                                               APPLICANT: Zelder, Oskar
APPLICANT: Zelder, Oskar
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Hafner Stefan
TITLE OF INVENTION: Method for Zymotic Production of Fine Chemicals Containing
TITLE OF INVENTION: Sulphur (metY)
TITLE OF INVENTION: Sulphur (metY)
TITLE OF INVENTION: Sulphur (metY)
FILE REFERENCE: 13111-00006-US
CURRENT APPLICATION NUMBER: US/10/525,710
CURRENT APPLICATION NUMBER: PT/FP 2003/009453
PRIOR APPLICATION NUMBER: DE 102 39 082.7
PRIOR PILING DATE: 2003-08-26
NUMBER OF SEQ ID NOS: 79
SOFTWARE: PatentIn version 3.3
SEQ ID NO 42
LENGTH: 421
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Pred. No. 1e+02;
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Publication No. US20060041961A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53450) B EP
CURRENT APPLICATION UNDBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
SEQ ID NOS: 12464
LENGTH: 289
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Publication No: US20060041961A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genee and Uses for Plant Improvement
FILE REFERENCE: 38-21(53450) B EP
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Pred. No. 95;
1; Mismatches
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CTHER INFORMATION: unsure at all Xaa locations
US-11-087-099-8567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                 Sequence 42, Application US/10525710 Publication No. US0050260721A1 GENERAL INFORMATION: APPLICANT: Kroger, Burkhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Clostridium difficile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58.1%;
70.0%;
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Best Local Similarity 66.7.
Best Local Similarity 67.7.
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Best Local Similarity 70.v
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31 EENKQFERAL 40
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US-11-087-099-10594
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Sequence 19857, Application US/11096568A
Publication No. US20060048240A1
Publication No. US20060048240A1
Publication No. US20060048240A1
Publication No. US20060048240A1
APPLICANT: ALEXANDRON:
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 19857
LENGTH: 791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 19856, Application US/11096568A

Sequence 19856, Application US/11096568A

Publication No. US20060048240A1

GENERAL INFORMATION:
APPLICANT: Albarandrow, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION: 105-1952P025
TITLE OF INVENTION: 2005-04-01
TITLE OF INVENTION THERES. 2005-04-01
TITLE OF 1850 ID NOS: 34471
SEQ ID NO 19566
LENGTH: 848
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Publication No. US20060013813A1
GENERAL INFORMATION:
APPLICANT: Macse et al.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same FILE REPERENCE: 21402-240CIP
CURRENT APPLICATION NUMBER: US/11/054,281
CURRENT FILING DATE: 2005-02-08
PRIOR FILING DATE: 2001-01-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 848;
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Pred. No. 3.1e+02;
5; Mismatches 2; Indels
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Pred. No. 3.3e+02;
5; Mismatches 2,
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i LOCATION: (1).:(1848)
cother information: Ceres Seq. ID no. 12375066
US-11-096-5688-19856
                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature

! LOCATION: (1)...(791)

! OTHER INFORMATION: Ceres Seq. ID no. 12375067

US-11-096-5688-19857
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Best Local Similarity 46.2
Matches 6; Conservative
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Matches 6; Conservative
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US-11-054-281-116
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TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUSC
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 19958
LENGTH: 729
                                                                                                                                    US-10-763-712A-101

US-10-763-712A-101

US-10-763-712A-101

Sequence 101, Application US/10763712A

Publication No. US20050266541A1

GENERAL INFORMATION:

APPLICANT: Solazyme, Inc.

APPLICANT: Dillon, Harrison F.

TITLE OF INVENTION: Preduction

TITLE OF INVENTION: Production

TITLE OF INVENTION: Production

TITLE OF INVENTION: Production

FILE REFRENCE: H2042101-CIP

CURRENT TILING DATE: 2004-01-21

PRIOR FILING DATE: 2004-01-21

PRIOR FILING DATE: 2003-04-12

PRIOR PLICATION NUMBER: US 10/411,910

PRIOR FILING DATE: 2003-04-12

PRIOR APPLICATION NUMBER: US 6/500,032

PRIOR FILING DATE: 2003-09-03

NUMBER OF SEQ ID NOS: 184

SOFTWARE: Patentin version 3.2

SEQ ID NO 101

LENGTH: 582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 582;
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Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0;
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| LOCATION: (1): (729)
| THER INORWATION: Ceres Seq. ID no. 12375068
US-11-096-568A-19858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 19858, Application US/11096568A Publication No. US20060048240A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Zea mays subsp. mays
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488 VMEETKEKKNAVE 500
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US-10-763-712A-101
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Matches 6; Conservative
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                                                             435 ENKELEN 441
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                 4 ENKELEN 10
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APPLICANT: KUMIMOTO, ROGERICK W
APPLICANT: GUTTERSON, Neal
APPLICANT: REUBER, T. Lynne
APPLICANT: SHERMAN, Bradley K
TITE OF INVENTION PLANT TRANSCRIPTIONAL REGULATORS OF DROUGHT STRESS
FILE REFERENCE: MB10058-CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 255;
                                                                                                       Length 247;
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Pred. No. 1.2e+02;
4; Mismatches 1;
                                                                                                                              1.1e+02;
                                                                                                                                                                                                                                                                                                                        Sequence 29, Application US/11219282; Sequence 29, Application US/11219282; Sequence 29, Application US/11219282; Publication No. US20060018892A1; GENERAL INFORMATION: APPLICANT: Clarke, Howard RG APPLICANT: Dubose, Robert F APPLICANT: Dubose, Robert F APPLICANT: Wiley, Steven R; TITLE OF INVENTION: HUMAN SERPIN POLYPEPTIDES; CURRENT PAPLICATION UNMBER: US/11/219,282; CURRENT FILING DATE: 2005-09-02; PRIOR FILING DATE: 2005-09-02; PRIOR PILING DATE: 2005-09-02; PRIOR PLILING DATE: 2005-03-08
                                                                                                         56.5%; Score 35; DB 7; 58.3%; Pred. No. 1.1e+0
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CURRENT FILING DATE: 2003-11-13
PRIOR APPLICATION NUMBER: 10/412,699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Mendel Biotechnology, Inc.
APPLICANT: HEARD, Jacqueline
APPLICANT: RIECHMANN, Jose Luis
APPLICANT: CREELMAN, Robert
APPLICANT: RATCLIFPE, Oliver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-714-887-274; Sequence 274, Application US/10714887; Sequence 1000 No. US2066015972A1; Publication No. US2066015972A1; GENERAL INFORMATION:
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APPLICATION NUMBER: 60/135,134
FILING DATE: 1999-05-20
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SOFTWARE: PatentIn version 3.1
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Best Local Similarity 54.5
Matches 6; Conservative
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REPETTI, Peter
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235 LQENRSMESAL 245
                                                                                                                                                       7; Conservative
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65 LEKNFEMENKLE 76
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; LENGTH: 247
; TYPE: PR:
; ORGANISM: Zinnia elegans
US-11-087-099-7178
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                                                                                                         Query Match
Best Local Similarity
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LENGTH: 255
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Publication No. US20060041961A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement;
FILE REPERENCE: 38-21(53450) B.F.
CURRENT RAPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 3432
LENGTH: 186
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Publication No. US20060041961A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REPERENCE: 38-21(53450)B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT PILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58.1%; Score 36; DB 7; 177.8%; Pred. No. 3.4e+02;
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OTHER INFORMATION: unsure at all Xaa.locations
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                      PRIOR FILING DATE: 2001-01-11
PRIOR PELING DATE: 2001-01-11
PRIOR PELING DATE: 2001-09-10
PRIOR FILING DATE: 2001-09-10
PRIOR FILING DATE: 2001-01-11
PRIOR FILING DATE: 2001-01-11
PRIOR FILING DATE: 2001-01-11
PRIOR PILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/261,029
PRIOR PILING DATE: 2001-01-11
PRIOR PELING DATE: 2001-08-17
PRIOR PILING DATE: 2001-08-17
PRIOR FILING DATE: 2001-08-17
PRIOR FILING DATE: 2002-01-11
NUMBER OF SEQ ID NOS: 324
SEGTHARE: PARENTIN VET: 2.1
SEQ ID NO 116
LENGTH: 656
    60/261,018

    i TYPE: PRT
    j ORGANISM: Drosophila melanogaster
    US-11-054-281-116

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 77...
Triconservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 70.0
Matches 7; Conservative
         APPLICATION NUMBER:
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33 EENKRFESAL 42
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US-11-087-099-7178
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CURRENT FILING DATE: 2003-08-11
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US-10-793-626-2250
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LENGTH: 481
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                            PRIOR FILING DATE: 1995-09-13
PRIOR PILING DATE: 2000-03-22
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PRIOR PLING DATE: 1990-03-22
PRIOR PLING DATE: 1999-03-23
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PRIOR PLING DATE: 1999-03-23
PRIOR PLING DATE: 2000-11-16
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US-10-467-657-3852
; Sequence 3852.
; Sequence 3852.
; Sequence 3852.
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: FOHTANA Maria Rita
; APPLICANT: FONTANA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 56.5%; Score 35; DB 6; Length 277; Best Local Similarity 70.0%; Pred. No. 1.3e+02; Matches 7; Conservative 1; Mismatches 2; Indels
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Sequence 1217, Application US/11087099

Publication No. US20060041961A1

GENERAL INFORMATION:

APPLICANT: Abad, Mark S. et al.

TITLE OF INVENTION: Genes and Uses for Plant Improvement

FILE REFERENCE: 38-21(53450) B EP

CURRENT APPLICATION NUMBER: US/11/087,099

CURRENT FILING DATE: 2005-03-22

NUMBER OF SEQ ID NOS: 12464

LENGTH: 277
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APPLICATION NUMBER: 09/394,519
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Matches 7; Conservative
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34 EENKKFERAL 43
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34 EENKKFERAL 43
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Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAHYLOCCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT PELING DATE: 2004-03-04
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2250
LIENGTH: 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: RADIL., Vivek and Gebhart, Connie J.
APPLICANT: RADIL., Vivek and Gebhart, Connie J.
TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIOE SEQUENCES
FITLE OF INVENTION: FORM LAWSONIA INTRACELLULARIS AND METHODS OF USING
FILE REPERENCE: 05531-122001
CURRENT APPLICATION NUMBER: US/11/098,686
CURRENT APPLICATION NUMBER: US/05-04-04
PRIOR APPLICATION NUMBER: PCT/US03/31318
PRIOR FILING DATE: 2003-10-01
PRIOR FILING DATE: 2003-10-04
NUMBER OF SEQ ID NOS: 11433
SOFTWARE: FASTESQ for Windows Version 4.0
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                                                                                                                                                                                                                                           Length 338;
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Pred. No. 1.6e+02;
5; Mismatches 1;
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54.5%; Pred. No. 2.3e+02;
tive 3; Mismatches 2;
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SEQ ID NO 3852
LENGTH: 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 10757, Application US/11098686; Publication No. US20060024696A1; GENERAL INFORMATION:
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ORGANISM: Lawsonia intracellularis
                                                                                                                                                ; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3852
                                                                                                                                                                                                                                         56.5%;
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Best Local Similarity 53.0.
7; Conservative
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Matches 6; Conservative
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401 MRENKSIKNAL 411
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PRIOR FILING DATE: 2004-02-04
PRIOR APPLICATION NUMBER: US 60/444,771
PRIOR FILING DATE: 2003-02-04
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Strongyloides stercoralis
US-11-191-588-3
                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Strongyloides stercoralis
US-11-191-375-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/11191588 Publication No. US20050282222A1 GENERAL INFORMATION:
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Best Local Similarity 58.3%;
Matches 7; Conservative
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58.3%;
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Best Local Similarity 58.5-
Best T, Conservative
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LENGTH: 1122
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APPLICANT:
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                                                     Score 35; DB 7; Length 481;
Pred. No. 2.5e+02;
2; Mismatches 3; Indels
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APPLICANT: Chiapelli, Brandi
APPLICANT: Chiapelli, Brandi
APPLICANT: Aloek, Andrew P.
APPLICANT: Aloek, Andrew P.
APPLICANT: Bandley, John D.
APPLICANT: Xu, Siqun
APPLICANT: Xu, Siqun
APPLICANT: Xu, Siqun
TITLE OF INVENTION: NEMATODE PAN AND ZP RECEPTOR-LIKE
TITLE OF INVENTION: SEQUENCES
FILE REFERENCE: 12557-015001
CURRENT PELLOR DATE: 2005-07-28
PRIOR APPLICATION NUMBER: US/10/771,708
PRIOR FILING DATE: 2004-02-04
PRIOR APPLICATION NUMBER: US/10/771,708
PRIOR APPLICATION NUMBER: US 60/444,771
PRIOR APPLICATION NUMBER: 2003-02-04
SPRIOR APPLICATION NUMBER: 2003-02-04
SPRIOR APPLICATION NUMBER: 2003-02-04
SPRIOR APPLICATION NUMBER: US/10/771,708
SPRIOR APPLICATION NUMBER: US/10/771
SPRIOR APPLICATION NUMBER: US/10/771
SPRIOR APPLICATION NUMBER: US/10/771
SPRIOR APPLICATION NUMBER: US/10/771
SPRIOR APPLICATION NUMBER: US/10/771
SPRIOR APPLICATION NUMBER: US/10/771
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TITLE OF INVENTION: NEMATODE PAN AND ZP RECEPTOR-LIKE
TITLE OF INVENTION: SEQUENCES
TITLE REFERENCE: 12557-015001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
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PRIOR APPLICATION NUMBER: US/10/771,708
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Bradley, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Strongyloides stercoralis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hresko, Michelle Coutu
APPLICANT: McLaird, Merry B.
APPLICANT: Williams, Deryck J.
APPLICANT: Frevert, Anita M.
APPLICANT: Chiapelli, Brandi
APPLICANT: Raudite, Catherine
APPLICANT: Kloek, Andrew P.
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                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/11191374 Publication No. US20050260673A1 GENERAL INFORMATION:
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APPLICANT: McLaird, Merry B.
APPLICANT: Williams, Deryck J.
                                                             Query Match
Best Local Similarity 58.3%;
Matches 7; Conservative
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215 IAVENKQIENEL 226
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Best Local Similarity 58.3
Matches 7; Conservative
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352 LDENEELRNEWK 363
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                 US-11-098-686-10757
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APPLICANT:
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APPLICANT:
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APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THA
TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
FILE REPERBURES: D0273A CIP
CURRENT BEPEIGNES: D0273A CIP
CURRENT PELLOS 1005-03-05
CURRENT FILING DATE: 2005-03-05
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                                                                   Gaps
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Score 35; DB 7; Length 1122;
Pred. No. 6.7e+02;
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Pred. No. 6.7e+02;
                                                             3; Indels
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TITLE OF INVENTION: NEMATODE PAN AND ZP RECEPTOR-LIKE
TITLE OF INVENTION: SEQUENCES
FILE REFERENCE: 12557-015001
CURRENT APPLICATION NUMBER: US/11/191,588
CURRENT APPLICATION NUMBER: US/10/771,708
PRIOR APPLICATION NUMBER: US/040-02-04
PRIOR PELLING DATE: 2004-02-04
PRIOR FILING DATE: 2003-02-04
NUMBER OF FILING DATE: 2003-02-04
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FASESQ for Windows Version 4.0
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                                                                2; Mismatches
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APPLICANT: McLaird, Merry B.
APPLICANT: Williams, Deryck J.
APPLICANT: Frevert, Anita M.
APPLICANT: Chiapelli, Brandi
APPLICANT: Baublite, Catherine
APPLICANT: Baublite, Catherine
APPLICANT: Baylla-Aponte, Jennifer A.
APPLICANT: Bradlay, John D.
APPLICANT: Bradlay, John D.
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; Sequence 192, Application US/11072175
; Publication No. US20060029944A1
; GENERAL INFORMATION:
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Query Match
Best Local Similarity
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                                              FEATURE:
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Sequence 3, Application US/11196400

Publication No. US20050287166A1

GENERAL INFORMATION:

APPLICANT: DAUBERSIES, PIERRE

APPLICANT: DAUBERSIES, PIERRE

TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES

TITLE REFERENCE: 200773US0UT)

CURRENT FILING DATE: 2005-08-04

PRIOR APPLICATION NUMBER: US/99/742,096

PRIOR APPLICATION NUMBER: US 08/973,462

PRIOR FILING DATE: 1998-0-12

PRIOR FILING DATE: 1998-0-6-12

PRIOR FILING DATE: 1996-06-12

PRIOR FILING DATE: 1996-06-12

PRIOR FILING DATE: 1995-06-13

NUMBER OF SEQ ID NOS: 29

SEQ ID NO 3

LENGTH: 1786

***LENGTH: 1786

***LENGTH: 1786

***LENGTH: 1786
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US-10-793-626-1080
is Sequence 1080, Application US/10793626
is Publication No. US20050255478A1
is GENERAL INFORMATION:
i APPLICANT: KIMMERLY, WILLIAM JOHN
if TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
if FILE REFERENCE: PU3480US
i CURRENT APPLICATION NUMBER: US/10/793,626
i PRIOR FILING DATE: 1999-11-09
i NUMBER OF SEQ ID NOS: 4472
i SEQ ID NO 1080
i LENGTH: 582
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                                                                                                                                                                                                                                                 Score 35; DB 7; Length 1261;
Pred. No. 7.7e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                         1; Mismatches
PRIOR APPLICATION NUMBER: US 60/406,385
PRIOR FILING DATE: 2002-08-27
PRIOR APPLICATION NUMBER: US 10/648,593
PRIOR FILING DATE: 2003-08-26
NUMBER OF SEQ ID NOS: 571
SOFTWARE: Patentin version 3.2
SEQ ID NO 192
                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 69.2%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                         314 EQNKMLEAENALK 326
                                                                                                                                                                                                                                                                                                                                   3 EENK--ELENALK 13
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Best Local Similarity 77.ه-
ابات 7، Conservative
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, ORGANISM: P. falciparum
US-11-196-400-3
                                                                                                                                                                                      ORGANISM: Homo sapiens
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                                                                                                                                              LENGTH: 1261
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RESULT 45
US-11-096-568A-12955

Sequence 32955, Application US/11096568A

Publication No. US-2060048240A1

GENERAL INFORMATION:

APPLICANT: Alexandrov, Nickolai et al.

TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides

TITLE OF INVENTION: Therby

TITLE OF INVENTION: 19-205-04-01

TITLE OF INVENTION UNMBER: US/11/096,568A

CURRENT APPLICATION NUMBER: US/11/096,568A

CURRENT PILNG DATE: 2005-04-01

SEQ ID NO 32955

LENGTH: 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                              OTHER INFORMATION: Description of Artificial Sequence: synthetic; OTHER INFORMATION: amino acid sequence US-10-793-626-1080
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APPLICANT: CHIRON SPA
APPLICANT: CHIRON Amaria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNAI Vega
APPLICANT: MONACI Bisabetta
ITILE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT FILING DATE: 2003-08-11
PRIOR FILING DATE: 2003-08-11
PRIOR FILING DATE: 2001-02-12
NUMBER: OF SEQ ID NOS: 9218
SOCTWARE: Seqwing9, version 1.04
SEQ ID NO 7832
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Pred. No. 34;
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! LOCATION: (1)..(125)
! OTHER INFORMATION: Ceres Seq. ID no. 13601567
US-11-096-5688-32955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7832, Application US/10467657, Publication No. US20050260581A1, GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7832
                                                                                                                                                                                                                                                                                                  ORGANISM: Arabidopsis thaliana
TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 58.3.
7; Conservative
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Gaps
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GENERAL INCOMMINION
GENERAL TRUNCHAPILE, Raymond J.
APPLICANT: Gomes Solecki, Maria J. C.
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
TITLE OF INVENTION: Recombinant Constructs of Borrelia
TITLE OF INVENTION: Burgdorferi
FILE REPERENCE: 2631.1001-011
CURRENT APPLICATION NUMBER: US 11/196,475
CURRENT FILING DATE: 2005-08-03
FRIOR FILING DATE: 1993-11-01
FRIOR FILING DATE: 1994-04-29
FRIOR PELICATION NUMBER: US 08/25,836
FRIOR FILING DATE: 2000-09-19
FRIOR FILING DATE: 2000-09-19
FRIOR APPLICATION NUMBER: US 60/266,017
FRIOR APPLICATION NUMBER: US 60/266,484
FRIOR FILING DATE: 2000-09-19
FRIOR APPLICATION NUMBER: PCT/US01/24736
FRIOR FILING DATE: 2000-09-18
FRIOR FILING DATE: 2000-09-09
TITLE OF INVENTION: Genes and Uses for Plant Improvement FILE REFERENCE: 38-21(53450) B. EP CURRENT APPLICATION NUMBER: US/11/087,099 CURRENT FILING DATE: 2005-03-22 NUMBER OF SEQ ID NOS: 12464 SEQ ID NO 11150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10418, Application US/11087099
Publication No. US20060041961A1
Publication No. US20060041961A1
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53450)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 34; DB 7;
Pred. No. 1.8e+02;
0; Mismatches 3.
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Pred. No. 1.8e+02;
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Publication No. US20050271682A1
GENERAL INFORMATION:
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; ORGANISM: Arabidopsis thaliana
US-11-087-099-10418
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US-11-087-099-11150
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Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                    Best Local Similarity 58.3
Matches 7; Conservative
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25 LEKNFEVENKLE 36
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PRIOR FILING DATE: 2001-0:
NUMBER OF SEQ ID NOS: 213
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US-11-087-099-10418
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TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT PRILICE DEPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
                                                                                                                                                                                                                                                          APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1532PUS2
CURRENT APPLICATION VUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
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           Gaps
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           Indela
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Pred. No. 1.3e+02;
4; Mismatches 3;
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LOCATION: (1). (218)
OTHER INFORMATION: Ceres Seq. ID no. 13601565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
i LOCATION: (1)..(206)
cother inFormation: Ceres Seq. ID no. 13601566
US-11-096-5688-32954
           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 32953, Application US/11096568A Publication No. US20060048240A1 GENERAL INFORMATION:
                                                                                                                                                                                                Sequence 32954, Application US/11096568A Publication No. US20060048240A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54.8%;
46.2%;
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194 LLEDNQNLRNQLE 206
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182 LLEDNONLRNOLE 194
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101 LLEDNQNLRNQLE 113
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                                                   1 ILEENKELENALK 13
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Best Local Similarity 46.2
Matches 6; Conservative
             6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                  US-11-096-568A-32954
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LENGTH: 218
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LENGTH: 206
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             Matches
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Query Match 54.8%; Score 34; DB 7; Length 273; Best Local Similarity 87.5%; Pred. No. 1.9e+02; Matches 7; Conservative 1; Mismatches 0; Indels
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54.8%; Score 34; DB 7; Length 273;

Best Local Similarity 87.5%; Pred. No. 1.9e+02;

Matches 7; Conservative 1; Mismatches 0; Indels
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APPLICANT: Gomes Solecki, Maria J. C.
APPLICANT: Gomes Solecki, Maria J. C.
APPLICANT: Gomes Solecki, Maria J. C.
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
TITLE OF INVENTION: Recombinant Constructs of Borrelia
TITLE OF INVENTION: Burgdorferi
FILE OF INVENTION: Burgdorferi
FILE REFERENCE: 2631.1001-011
CURRENT APPLICATION NUMBER: US/11/196,475
CURRENT FILING DATE: 1993-11-01
PRIOR FILING DATE: 1993-11-01
PRIOR FILING DATE: 1993-11-01
PRIOR FILING DATE: 1994-04-29
PRIOR APPLICATION NUMBER: US 60/226,484
PRIOR FILING DATE: 2000-09-19
PRIOR APPLICATION NUMBER: US 60/226,484
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-08-18
PRIOR FILING DATE: 2000-08-18
PRIOR FILING DATE: 2000-08-18
PRIOR FILING DATE: 2000-08-18
NUMBER OF SEQ ID NOS: 213
CURRENT FILING DATE: 2005-08-03

PRIOR APPLICATION NUMBER: US 08/148,191

PRIOR FILING DATE: 1993-11-01

PRIOR FILING DATE: 1994-04-29

PRIOR FILING DATE: 1994-04-29

PRIOR FILING DATE: 2000-09-19

PRIOR PRILING DATE: 2000-09-19

PRIOR PRILING DATE: 2000-09-18

PRIOR PRILING DATE: 2000-09-18

PRIOR PRILING DATE: 2001-08-07

NUMBER: OF SEQ ID NOS: 213

SEQ ID NO 101

LENGTH: 273

LENGTH: 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 142, Application US/11196475; Publication No. US20050271682A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , OTHER INFORMATION: Chimeric Protein US-11-196-475-101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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266 KELKNALK 273
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266 KELKNALK 273
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LENGTH: 273
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                                                                                                                                                                                                                                                     Query Match 54.8%; Score 34; DB 7; Length 273; Best Local Similarity 87.5%; Pred. No. 1.9e+02; Matches 7; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-11-196-475-98

US-11-196-475-98

Sequence 98, Application US/11196475

Publication No. US200S0271682A1

GENERAL INFORMATION:

APPLICANT: Dattwylor:

APPLICANT: Dattwylor:

APPLICANT: Luft, Benjamin J.

APPLICANT: Luft, Benjamin J.

TITLE OF INVENTION: Recombinant Constructs of Borrelia

TITLE OF INVENTION: Burgdorferi

FILE REFERENCE: 2631.1001-011

CURRENT APPLICATION NUMBER: US 08/11/196,475

CURRENT FILING DATE: 2005-08-03

PRIOR FILING DATE: 1994-04-29

PRIOR FILING DATE: 1994-04-29

PRIOR FILING DATE: 2000-09-19

PRIOR FILING DATE: 2000-09-19

PRIOR FILING DATE: 2000-09-19

PRIOR FILING DATE: 2000-09-19

PRIOR FILING DATE: 2000-09-19

PRIOR FILING DATE: 2000-09-19

PRIOR FILING DATE: 2000-09-19

PRIOR FILING DATE: 2000-09-19

PRIOR PELICATION NUMBER: PCT/US01/24736

PRIOR PELICATION NUMBER: PCT/US01/24736

PRIOR PELING DATE: 2001-08-07

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 98

LENGTH: 273
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     SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 92 LENGTH: 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 52
US-11-196-475-101
; Sequence 101, Application US/11196475
; Publication No. US20050271682A1
; GENERAL INFORMATION:
APPLICANT: Dattwyler, Raymond J.
; APPLICANT: Gomes Solecki, Maria J. C.
; APPLICANT: Luft, Benjamin J.
; APPLICANT: Dunn, John J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOTHER INFORMATION: Chimeric Protein US-11-196-475-98
                                                                                                                                                                          ) OTHER INFORMATION: Chimeric Protein US-11-196-475-92
                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
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266 KELKNALK 273
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266 KELKNALK 273
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                                                                                            TYPE: PRT
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Length 274;

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Sequence 66, Application US/10793626;
Sequence 66, Application US/10793626;
Publication No. US20050255478A1
GENERAL INFORMATION:
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS;
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS;
FILE REFERENCE: PUJ480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT PILING DATE: 1999-11-09
PRIOR FILING DATE: 1999-11-09
NUMBER: OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 66
LENGTH: 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTHER INFORMATION: Description of Artificial Sequence: synthetic proper INFORMATION: amino acid sequence US-10-793-626-66
                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53450) B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 2007
LENGTH: 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 34; DB 6; |
Pred. No. 2.1e+02;
5; Mismatches 2;
                                                                    Score 34; DB
Pred. No. 1.9e
1; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                           Sequence 7007, Application US/11087099 Publication No. US20060041961A1 GENERAL INFORMATION:
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US-10-793-626-746
; Sequence 746, Application US/10793626
; ORGANISM: Borrelia burgdorferi
US-11-196-475-9
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US-11-087-099-7007
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                                                                      Query Match
Best Local Similarity 87.5%;
Matchès 7; Conservative
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238 LIKDNPEIDKALK 250
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Best Local Similarity 77.0
Local 7; Conservative
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Best Local Similarity 38.5
Matches 5; Conservative
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267 KELKNALK 274
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APPLICANT: Dattwyler, Raymond J.
APPLICANT: Unit, Benjamin J.
APPLICANT: Luit, Benjamin J.
TITLE OF INVENTION: Recombinant Constructs of Borrelia
TITLE OF INVENTION: Burgdorferi
FILE REFERENCE: 2631.1001-011
CURRENT APPLICATION NUMBER: US/11/196,475
CURRENT FILING DATE: 2005-08-03
                                                                                                                                                                                                                                         TITLE OF INVENTION: Recombinant Constructs of Borrelia TITLE OF INVENTION: Burgdorferi FILE REFERENCE: 2631.1001-011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 34; DB 7;
Pred. No. 1.9e+02;
1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 08/148,191
PRIOR FILING DATE: 1993-11-01
PRIOR FILING DATE: 1993-11-01
PRIOR FILING DATE: 1994-04-29
PRIOR FILING DATE: 1994-04-29
PRIOR FILING DATE: 2000-09-19
PRIOR APPLICATION NUMBER: US 60/226,484
PRIOR FILING DATE: 2000-09-19
PRIOR FILING DATE: 2000-09-19
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-08-18
PRIOR FILING DATE: 2001-08-07
PRIOR SEQ ID NOS: 213
SOFTWARE: FASESQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 08/148,191
PRIOR FILING DATE: 1993-11-01
PRIOR FILING DATE: 1994-04-29
PRIOR FILING DATE: 1994-04-29
PRIOR PILING DATE: 1994-04-29
PRIOR PILING DATE: 2000-09-19
PRIOR FILING DATE: 2000-09-19
PRIOR PILING DATE: 2000-09-19
PRIOR APPLICATION NUMBER: US 60/226,484
PRIOR PILING DATE: 2000-09-18
PRIOR PILING DATE: 2001-08-07
NUMBER: FELING DATE: 2001-08-07
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 144
LENGTH: 273
                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/11/196,475 CURRENT FILING DATE: 2005-08-03
                                                                                                                                                 Dattwyler, Raymond J.
Gomes Solecki, Maria J. C.
Luft, Benjamin J.
Dunn, John J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , OTHER INFORMATION: Chimeric Protein US-11-196-475-144
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; Sequence 9, Application US/11196475
; Publication No. US20050271682A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 87.5%;
Matches 7; Conservative
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LENGTH: 274
TYPE: PRT
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Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STRAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: '2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 746
LENGTH: 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: synthetic; OTHER INFORMATION: amino acid sequence
US-10-793-626-746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
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US-11-087-099-9768
US-11-087-099-9768
; Sequence 9768, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 9768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

54.8%; Score 34; DB 7; Length 307;
Best Local Similarity 77.8%; Pred. No. 2.18+02;
Matches 7; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 54.8%; Score 34; DB 6; Length 297; Best Local Similarity 38.5%; Pred. No. 2.1e+02; Matches 5; Conservative 6; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3424, Application US/11072512
| Publication No. US20060029945A1 |
| GENERAL INFORMATION: APPLICANT: ISOGAI, TAKAO |
| APPLICANT: SUGIYAMA, TOMOYASU |
| APPLICANT: OTSUMI, TETSUJI |
| APPLICANT: STO, HIROYUKI |
| APPLICANT: SATO, HIROYUKI |
| APPLICANT: SATO, HIROYUKI |
| APPLICANT: SATO, HIROYUKI |
| APPLICANT: ISHII | SHIZUKO |
| APPLICANT: YAMAMOTO, JUN-ICHI |
| APPLICANT: YAMAMOTO, YUUKO |
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ORGANISM: Artificial Sequence
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NAGAI, KEIICHI
IRIE, RYOTARO
TAMECHIKA, ICHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 238 LIKDNPEIDKALK 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ILBENKELENALK 13
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## APPLICANT: SEKI, NACHIKO
### APPLICANT: YOSHIKAWA, TSUTCOMU
### APPLICANT: OTSUKA, MOTOVUKI
### APPLICANT: OTSUKA, MOTOVUKI
### APPLICANT: NAGAHARI, KENJI
### APPLICANT: NAGAHARI, KENJI
### APPLICANT: NAGAHARI, KENJI
### APPLICANT: NASUHIKO
### TITLE OF INVENTION: NOVEH full length cDNA
### FILE REFERENCE: 084335-0191
### CURRENT APPLICATION NUMBER: US/11/072,512
### CURRENT FILING DATE: 2002-01-25
### PRIOR FILING DATE: 2002-01-25
### PRIOR FILING DATE: 2002-01-379298
### PRIOR FILING DATE: 2001-11-05
### PRIOR FILING DATE: 2001-11-05
### NUMBER OF SEQ ID NOS: 4096
### SOFTWARE: PRECENTIN VET. 2.1
### SOFTWARE: PRECENTIN VET. 2.1
### SOFTWARE: PRECENTIN VET. 2.1
### CONGANISM: Homo sapien8
### US-11-072-512-3424

### Query Match
### SCOTE 34; DB 7; Length 341;
### Best Local Similarity 60.0%; Pred: No. 2.4e+02;
### Matches 6; Conservative 3; Mismatches 1; Indels
### ON 1 ILLERNKELEN 10
### CONSERVATIVE 158

ON 1 ILLERNKELEN 10
### Search completed: March 11, 2006, 12:33:01

Search completed: March 11, 2006, 12:33:01
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